Research Outputs

โครงการ : เทคโนโลยี RNA interference เพื่อประสิทธิผลของการเพาะเลี้ยงกุ้งในประเทศไทย (ระยะที่ 2)

โดย

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1. Involvement of endocytosis in cellular uptake of injected dsRNA into hepatopancreas but not in gill of *Litopenaeus vannamei*. Maruekawong K, Panyim S, Attasart P. Aquaculture (201)) 500, 393-397.

2. Suppression of argonautes compromises viral infection in *Penaeus monodon*. Ho T, Panyim S, Udomkit A. Developmental and Comparative Immunology (2019) 90, 130-137.

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5. Functional characterization of a cDNA encoding Piwi protein in *Penaeus monodon* and its potential roles in controlling transposon expression and spermatogenesis. Sukthaworn S, Panyim S, Udomkit A. Comparative Biochemistry and Physiology -Part A (2019) 229, 60-68.

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Involvement of endocytosis in cellular uptake of injected dsRNA into hepatopancreas but not in gill of *Litopenaeus vannamei*

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ABSTRACT

RNA interference (RNAi) technology has been widely applied to shrimp research for functional genomics, as well as for investigation of its potential anti-viral applications. While the integral membrane protein SID-1 of *Litopenaeus vannamei* has been reported to participate in the uptake of injected dsRNA into shrimp cells, this may not be the only uptake mechanism. Therefore the possible involvement of endocytosis in the delivery of injected dsRNA into shrimp hepatopancreatic and gill cells was evaluated. Clathrin-mediated endocytosis was inhibited through the injection of shrimp with two pharmacological endocytosis inhibitors (chlorpromazine and bafilomycin-A1) before injection of long dsRNAs directed against STAT (dsSTAT) or Rab7 (dsRab7). Levels of STAT or Rab7 suppression in the treated shrimp as compared to the control shrimp reflect the capability of cells to take up dsRNAs (dsSTAT or dsRab7). Inhibition of clathrin-mediated endocytosis showed a reduction of specific mRNA suppression in the shrimp hepatopancreas. In contrast, neither chlorpromazine nor bafilomycin-A1 effectively blocked dsRNA mediated inhibition of STAT or Rab7 in gill tissue. These results support our conclusion that endocytosis is required in cellular uptake of injected dsRNA into shrimp hepatopancreas but is not participated in the process in gills. This is the first report of the involvement of different pathways of cellular dsRNA uptake into different tissues of shrimp.

1. Introduction

RNA interference (RNAi) technology is widely applied to shrimp research for functional genomics (Phetrungnapha et al., 2015; Sagi et al., 2013), but is additionally investigated for potential anti-viral applications (Assavalapsakul et al., 2014; Escobedo-Bonilla, 2011; Sagi et al., 2013; Shekhar and Lu, 2009). Injection of dsRNA into muscle or the haemocoel is routinely used for delivering dsRNA into shrimp (Labreuche et al., 2010; Sutthangkul et al., 2015), and while in the systemic circulation within the shrimp body cavity, dsRNA may be taken up by cells in different tissues. In invertebrates, at least two pathways for exogenous dsRNA uptake have been described so far, namely the systemic RNA interference defective (SID) transmembrane channel protein-mediated, and an endocytosis-mediated mechanism (Huvenne and Smagghe, 2010). Participation of SID-1 in dsRNA uptake has been demonstrated in *Caenorhabditis elegans* (*C. elegans*) (Feinberg and Hunter, 2003; Winston et al., 2002), *Diabrotica virgifera* (Miyata et al., 2014), *Leptinotarsa decemlineata* (Cappelle et al., 2016), *Nilaparvata lugens* (Xu et al., 2013) and *Apis mellifera* (Aronstein et al., 2006).

However, other studies have shown that endocytosis is a major pathway for cellular dsRNA uptake in some insects. For example, while *Tribolium castaneum* has three SID-1 homologues, they do not participate in dsRNA uptake, and clathrin-mediated endocytosis has been shown to be involved in the process (Tomoyasu et al., 2008; Xu and Han, 2008). Similarly, blocking endocytosis by specific inhibitors of clathrin-coated pit formation or of the vacuolar H^+ ATPase (V-ATPase) required for endocytosis effectively inhibits the internalization of dsRNA in *Drosophila melanogaster* S2 cells (Ulvila et al., 2006; Winston et al., 2002), the red flour beetle (*Tribolium castaneum*) (Xiao et al., 2015) and desert locust (*Schistoceca gregaria*) (Luo et al., 2012). However, the colorado potato beetle (*Leptinotarsa decemlineata*) uses both SID-1 and endocytosis for dsRNA uptake into midgut cells (Cappelle et al., 2016). Our previous study, the role of SID-1 of *Litopenaeus vannamei* (*Lv*SID-1) was evaluated in shrimp by monitoring the uptake efficiency of Cy3-labeled dsRNA as well as the silencing efficiency of target messages after increased expression of *Lv*SID-1 mRNA in a strategy utilizing sequential introduction of long dsRNAs (Maruekawong et al., 2018). The results showed that *Lv*SID-1 is involved in cellular uptake of injected dsRNA into shrimp gills and

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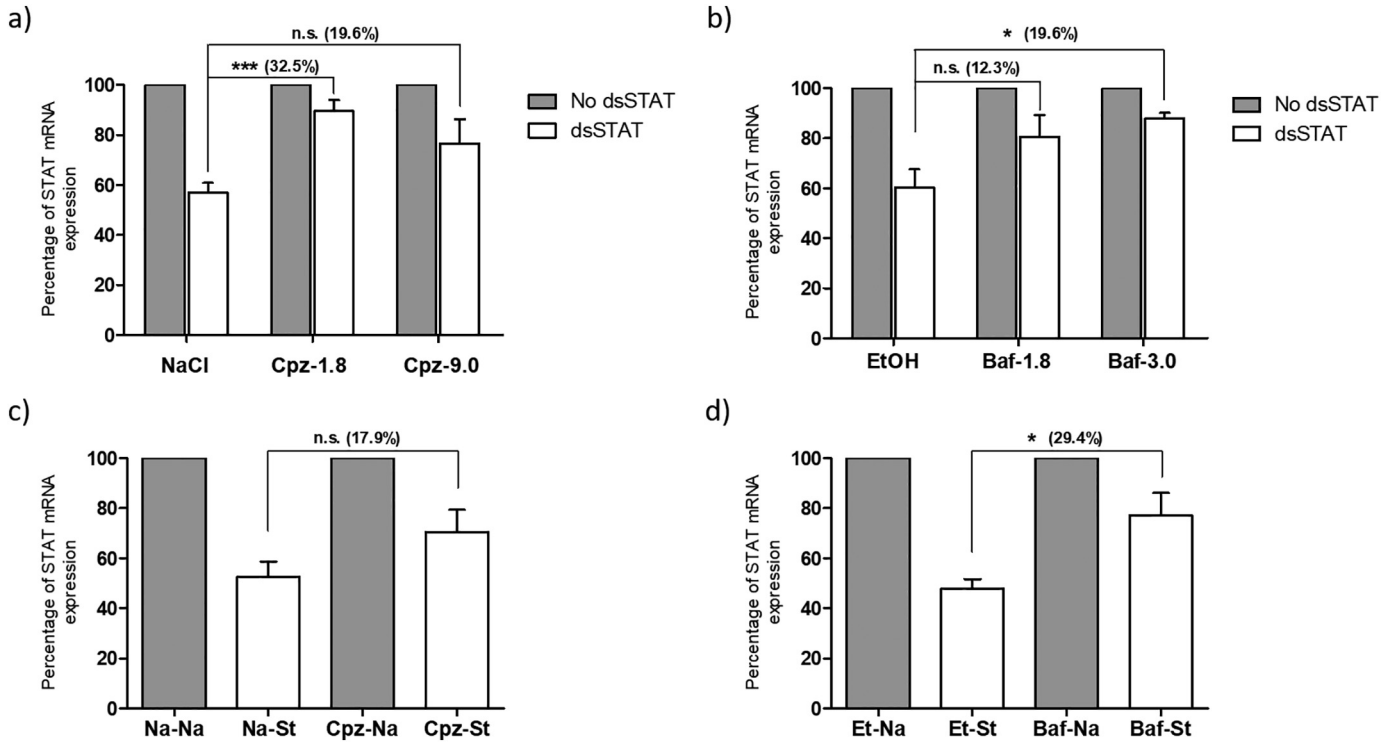

Fig. 1. Effect of inhibitors (chlorpromazine (Cpz) and bafilomycin A1 (Baf)) on endocytic uptake of injected dsSTAT into shrimp hepatopancreatic cells. Shrimp (n = 3–9/group) were pre-injected with the solvents [NaCl (Na) or EtOH (Et)] or drug inhibitors [(a) Cpz (at 1.8 or 9 μg/g of shrimp) or (b) Baf (at 1.8 or 3 μg/g of shrimp)] before injection of NaCl (no dsSTAT) or dsSTAT (St). Twelve hours later, relative expression of STAT mRNA in the hepatopancreas of shrimp in each group was monitored by RT-PCR and plotted as mean ± SEM. The percentage of STAT mRNA expression of the drug treated and untreated shrimp are presented. The statistical analysis was performed using the Mann-Whitney test at p-value < .05 (*) and < 0.001 (***). Another set of experiments was performed (n = 5–10/group) (c and d). The percentage of STAT mRNA expression of the treated (Cpz-St and Baf-St) and untreated (Na-St and Et-St) shrimp are presented. The statistical analysis was performed by a paired t-test at p-value < .05 (*).

hemocytes. However, the *Lv*SID-1 may not be the only mechanism involved in this process. For this reason the possible involvement of endocytosis on the uptake of injected dsRNA into shrimp cells in the hepatopancreas and gill was evaluated. Shrimp were injected with either chlorpromazine (Cpz) to block clathrin-coated pit formation (Wang et al., 1993; Yao et al., 2002), or with bafilomycin-A1 (BafA) to block vacuolar acidification by V-ATPase (Yamamoto et al., 1998), and the treated shrimp were then injected with dsRNAs specific to shrimp signal transduction and transcription protein (STAT) mRNA (dsSTAT) or shrimp small GTP-binding protein (Rab7) mRNA (dsRab7). Levels of STAT or Rab7 suppression in the treated shrimp as compared to the control shrimp reflect the capability of cells to take up dsSTAT/dsRab7.

2. Materials and methods

2.1. Shrimp specimens

Post larval (Pl_{15}-Pl_{20}) white leg shrimp (*L. vannamei*) were purchased from Chuchai farm in Chonburi province, Thailand and were maintained in 10 ppt seawater with aeration in a 500 L tank. A commercial diet (CP) was used to feed shrimp until they reached a juvenile stage of roughly 200–300 mg of body weight. During experiments, shrimp were kept in individual cages in the same tank to avoid cannibalism.

2.2. Production of dsRNA

A previously described plasmid (Maruekawong et al., 2018) containing an expression cassette of dsRNA targeting to the shrimp STAT mRNA (dsSTAT (406 bp)) (Attasart et al., 2013) or Rab7 mRNA (dsRab7 (393 bp)) (Ongvarrasopone et al., 2008) was transformed into *E. coli* HT115 (an RNase III defective strain). Expression of dsRNA was undertaken following the protocol of Ongvarrasopone and colleagues (Ongvarrasopone et al., 2007). Briefly, a single colony was inoculated in LB medium containing 100 μg/ml ampicillin and 12.5 μg/ml tetracycline and grown overnight at 37 °C. This overnight starter culture (0.5 OD) was inoculated into 15 ml of new medium and grown until OD_{600} reached 0.4. Expression of dsRNA was induced with 0.4 mM of isopropyl-β-d thiogalactopyranoside (IPTG) for 4 h. Following the protocol of Posiri and colleagues (Posiri et al., 2013), one OD of bacterial cells was collected by centrifugation at 8,000 ×g at 4 °C for 5 min and resuspended in 100 μl 75% ethanol in phosphate buffer saline (PBS) and incubated at room temperature for 5 min. The treated cells were collected by centrifugation at 8000 ×g for 5 min at 4 °C before resuspending in 100 μl of 150 mM NaCl and incubation at room temperature for 1 h. The cell suspension was centrifuged at 12000 ×g at 4 °C for 5 min to generate a cell-free supernatant. The dsRNA in the supernatant was diluted before loading onto agarose gels to estimate the concentration by comparing with a standard marker.

2.3. Evaluation of inhibition of endocytosis on dsRNA uptake

As suppression of clathrin heavy chain (CHC) by dsRNA is lethal to shrimp (Posiri et al., 2015), clathrin-mediated endocytosis was blocked by injection with specific inhibitors, namely chlorpromazine (Sigma-Aldrich) an inhibitor of clathrin-coated pit formation, and bafilomycin-A1 (Abcam) an inhibitor of v-ATPase. To ensure endocytosis was inhibited, different amounts of the inhibitors (1.8 and 9.0 μg of Cpz and 1.8 and 3.0 μg of BafA per shrimp body weight (g)) were injected into each shrimp. Twelve hours following injection of the inhibitors, dsSTAT or dsRab7 was administered. Targeted mRNAs (STAT or Rab7) expression in shrimp tissues (hepatopancreas and gill) was determined at

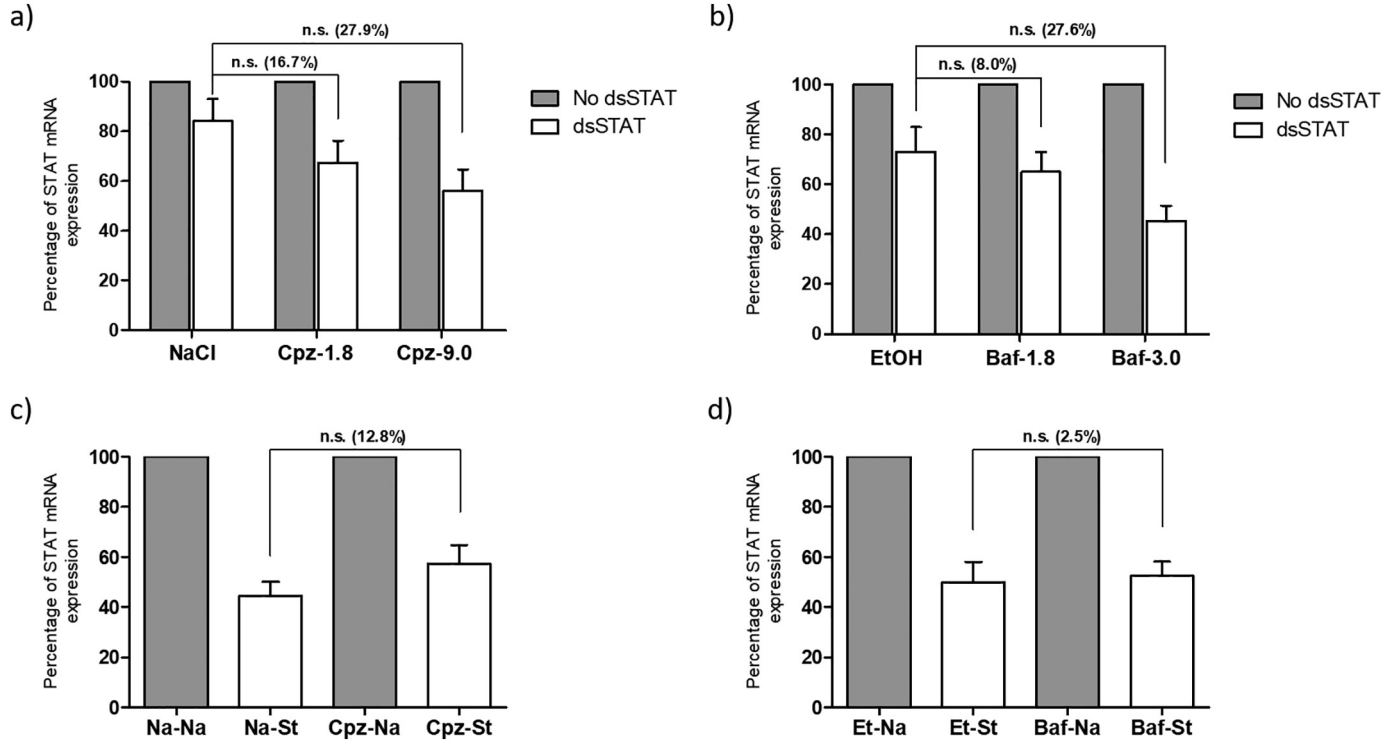

Fig. 2. Effect of inhibitors (chlorpromazine (Cpz) and bafilomycin A1 (Baf)) on endocytic uptake of injected dsSTAT into shrimp gill cells.
Shrimp (n = 3–9/group) were pre-injected with the solvents [NaCl (Na) or EtOH (Et)] or drug inhibitors [(a) Cpz (at 1.8 or 9 μg/g of shrimp) or (b) Baf (at 1.8 or 3 μg/g of shrimp)] before injection of NaCl (no dsSTAT) or dsSTAT (St). Twelve hours later, relative expression of STAT mRNA in hepatopancreas of shrimp in each group was monitored by RT-PCR and plotted as mean ± SEM. The percentage of STAT mRNA expression of the drug treated and untreated shrimp are presented. The statistical analysis was performed using the Mann-Whitney test. Another set of experiments was performed (n = 5–10/group) (c and d). The percentage of STAT mRNA expression of the drug treated (Cpz-St and Baf-St) and untreated (Na-St and Et-St) shrimp are presented. The statistical analysis was performed by a paired *t*-test.

10–12 h post dsRNAs injection.

2.4. Injection of dsRNA into shrimp

The dsRNA solution was diluted in 150 mM NaCl to make 15 ng/μl before injection. Twenty microliters of dsRNA solution (approximately 200–300 ng) was injected into the shrimp haemocoel using a 0.5 ml syringe with 29G needle.

2.5. Shrimp RNA extraction and cDNA synthesis

Hepatopancreas and gill tissues (approximately 10 mg each) were dissected from L. *vannamei* using scissors and forceps. Total RNA was extracted using RiboZol™ (Amresco) following the manufacturer's instruction. The extracted RNA (1–2 μg) was heated at 70 °C for 5 min in a reaction tube containing 2 μM of random primers and RNase-free sterile distilled water and subsequently quickly cooled on ice. The primers were then allowed to anneal with the RNA at 25 °C for 5 min. The following components, 1 × ImProm-II™ reaction buffer, 0.5 mM dNTPs, 30 mM $MaCl_2$, 1 μl of ImProm-II™ reverse transcriptase and RNase-free sterile distilled water were added into the reaction. The cDNA was synthesized at 42 °C for 60 min before termination at 70 °C for 15 min.

2.6. Semi-quantitative RT-PCR

The 25 μl PCR reaction was composed of 2 μl of cDNA template, 1 × PCR buffer (75 mM Tris-HCl (pH 8.8 at 25 °C), 20 mM $(NH_4)_2SO_4$ and 0.01% Tween 20), 0.2 mM dNTPs, 0.2 μM of each primer, 2 mM of MgCl2, 200 μM of dNTPs mix, 1.25 unit (0.25 μl) of *Taq* DNA polymerase (homemade or Aspalagen) and sterile distilled water. For optimal conditions, which did not give saturated amplified products, 1:4 ratio of actin gene primers (5′ GACTCGTACGTCGGGCGACGAGG 3′ and 5′ AGCAGCGGTGGTCATCTCCTGCTC 3′) to STAT gene primers (5′ ATGTCGTTGTGGAACAGAGC 3′ and 5′ GTTTGTTGCATGTGAAACACC TCC 3′) or 1:12 ratio of actin gene primers to Rab7 gene primers (5′ ATGGCATCTCGCAAGAAGATT 3′ and 5′ TTAGCAAGAGCATGCATC CTG 3′) was used. The PCR reactions were held at 94 °C for 2 min, followed by 25 cycles of denaturation at 94 °C for 10 s, annealing at 55 °C for 30 s, and extension at 72 °C for 1 min. Lastly, the amplification was held at 72 °C for 5 min. PCR products were analyzed by agarose gel electrophoresis. Levels of PCR products were quantified using the Scion Image program.

2.7. Statistical analysis

Data are presented as mean ± standard error of mean (SEM) using the GraphPad Prism 5 program. A *p*-value below 0.05 ($p < .05$) of a nonparametric test (Mann-Whitney test) or paired *t*-test comparing between treatment and control groups was considered as statistically significant.

3. Results

3.1. Effect of two endocytosis inhibitors on RNAi in shrimp hepatopancreas

The level of STAT mRNA suppression induced by injection of dsSTAT was used as a marker to determine whether endocytosis is involved in the cellular uptake of dsRNA into shrimp gill and hepatopancreatic cells. Shrimp were pre-injected with drug inhibitors (Cpz and BafA) to block clathrin coated pit endocytosis before injection of dsSTAT. Thereafter, expression of STAT mRNA in the hepatopancreas and gill tissues of the treated shrimp was monitored and compared with

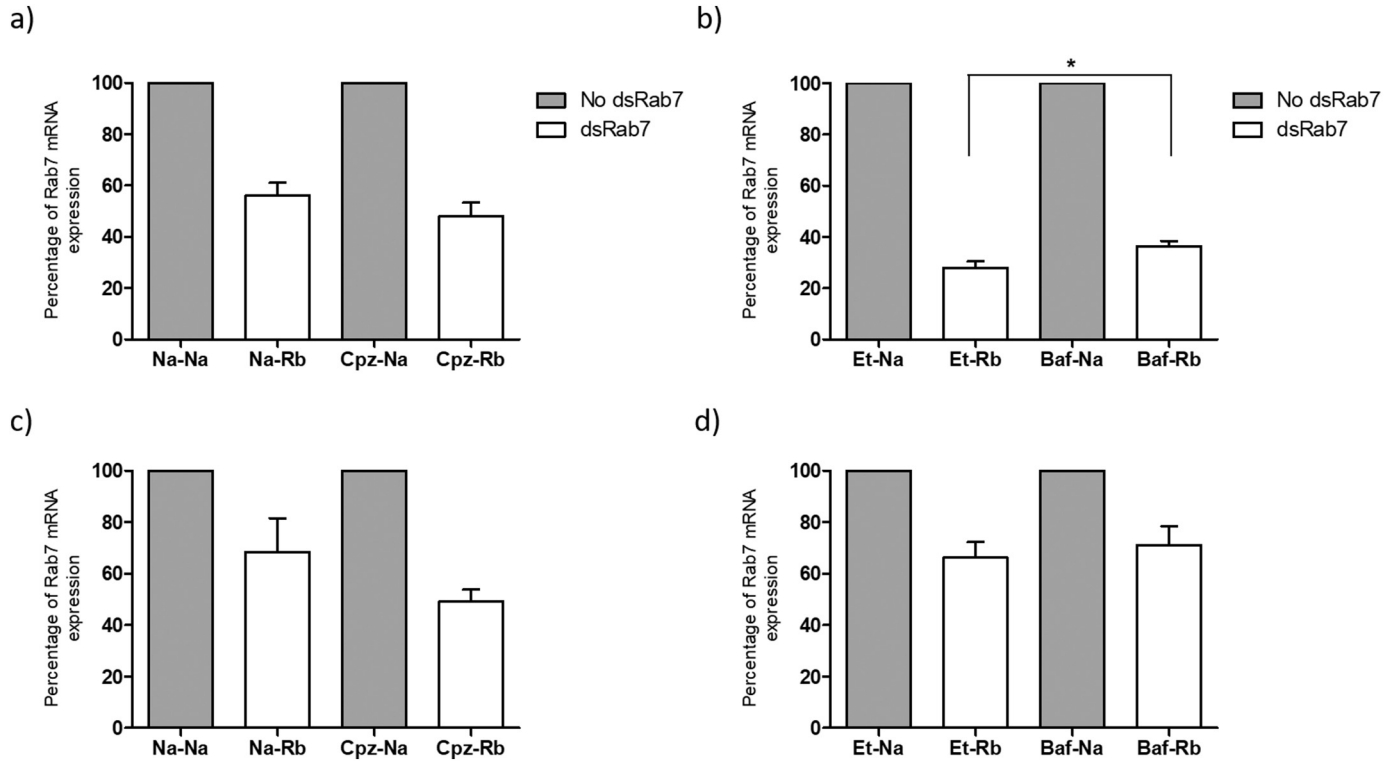

Fig. 3. Effect of inhibitors (chlorpromazine (Cpz) and bafilomycin A1 (Baf)) on endocytic uptake of injected dsRab7 into shrimp cells.
Shrimp (n = 3–10/group) were pre-injected with the solvents [NaCl (Na) or EtOH (Et)] or drug inhibitors [(a, c) Cpz (at 1.8 μg/g of shrimp) or (b, d) Baf (at 3 μg/g of shrimp)] before injection of NaCl (no dsRab7) or dsRab7 (Rb). Twelve hours later, relative expression of Rab7 mRNA in the hepatopancreas (a-b) or gill (c-d) of shrimp in each group was monitored by RT-PCR and plotted as mean ± SEM. The percentage of Rab7 mRNA expression of the drug treated and untreated shrimp are presented. The statistical analysis was performed using the Mann-Whitney test at p-value < .05 (*).

the expression levels of control shrimp (without drug treatment).

In the first experiment, two doses of drugs (1.8 and 9.0 μg of Cpz and 1.8 and 3.0 μg of BafA per one gram of shrimp body weight) were used to block shrimp clathrin-mediated endocytosis. The relative transcript of STAT in the hepatopancreas of the untreated shrimp was significantly suppressed by approximately 40% from the control levels (STAT mRNA level of shrimp injected with drug-dissolving solvents (NaCl for Cpz or EtOH for BafA, respectively) (Fig. 1a and b). However, suppression level of shrimp pre-treated with two doses of Cpz or BafA were significantly reduced to approximately 10% from the control levels (STAT mRNA level of shrimp injected with Cpz or BafA without dsSTAT). In another experiment, doses of 9 μg/g of Cpz and 3.0 μg/g of BafA were used, and shrimp were initially injected with NaCl or drugs before injection with NaCl or dsSTAT. Compared to the suppression control (Na-Na/Na-St and Et-Na/Et-St) in which the RNAi response was not affected, the STAT mRNA suppression of shrimp after blocking with Cpz (Cpz—Na/ Cpz-St) or with BafA (Baf-Na/Baf-St) were approximately 18% and 29%, respectively (Fig. 1c and d). However, the change of RNAi efficiency of STAT after treatment with Cpz was not statistically different. To confirm that endocytosis is required for cellular uptake of not only dsSTAT into shrimp hepatopancreas, the different dsRNA targeted another shrimp endogenous gene (Rab7), dsRab7 was used. Shrimp were initially injected with solvents (NaCl and EtOH) or drugs (1.8 μg/g of Cpz and 3.0 μg/g of BafA) before injection with NaCl or dsRab7. The Rab7 mRNA suppression of shrimp after blocking with BafA was significantly reduced (Fig. 3b). However, the change of RNAi efficiency of Rab7 after treatment with Cpz was not statistically different from the control (Fig. 3a). Taken together the results indicated that inhibition of clathrin-mediated endocytosis affected the dsSTAT/dsRab7 uptake in shrimp hepatopancreas resulting in reduction of RNAi-mediated STAT/Rab7 suppression.

3.2. Effect of two endocytosis inhibitors on RNAi in shrimp gills

The effect of the two endocytosis inhibitors on STAT or Rab7 suppression was also determined in gill tissue of the same shrimp. In contrast to hepatopancreas, the results showed levels of STAT or Rab7 suppression after blocking with two drugs (Cpz and BafA) were not significantly reduced (Figs. 2a–d, 3c–d), indicating that inhibition of clathrin-mediated endocytosis did not affect the uptake of dsRNAs in shrimp gill tissue.

4. Discussion

Over the last few years, the role of endocytosis in the cellular uptake of dsRNA has been studied in several insects either using drug inhibitors (Cappelle et al., 2016; Saleh et al., 2006; Ulvila et al., 2006; Xiao et al., 2015) or RNAi dependent silencing of the key genes in the pathway (Cappelle et al., 2016; Ulvila et al., 2006; Xiao et al., 2015). In most insect species, either the SID-1 like transmembrane protein (Aronstein et al., 2006; Miyata et al., 2014) or endocytosis (Ulvila et al., 2006; Winston et al., 2002; Xiao et al., 2015) or both (Cappelle et al., 2016) are required for cellular importation of dsRNA. There is no consensus about which pathway is involved in dsRNA uptake for several insects.

Our previous study in shrimp (Maruekawong et al., 2018) showed that *Lv*SID-1 is involved in cellular uptake of injected dsRNA into shrimp gills and hemocytes, and this study sought to investigate whether there was a role for endocytosis in dsRNA uptake. Using pharmacological inhibitors (Cpz and BafA) in conjunction with RNAi induced inhibition of STAT or Rab7 as a marker for dsRNA uptake, we observed that both drugs diminished STAT/Rab7 suppression in shrimp hepatopancreas. In contrast, the drugs showed no significant effect on the targeted mRNA silencing in gill tissue. This indicates that injected dsRNA is taken up into shrimp hepatopancreas through the clathrin-

mediated endocytosis pathway, while this pathway does not seem to play an important role in delivering dsRNA into shrimp gill. Combined with our previous study these results indicate that when dsRNA is circulating in the shrimp body cavity, the SID-1 mediated pathway is a major mechanism in the cellular uptake of dsRNA into gill and hemocyte cells (Maruekawong et al., 2018), while endocytosis is required for dsRNA uptake in hepatopancreatic cells. However, because dsRNA does not affect *Lv*SID-1 mRNA expression levels in the shrimp hepatopancreas, the requirement for *Lv*SID-1 in the uptake of dsRNA in this tissue could not be evaluated (Maruekawong et al., 2018). Therefore, the possible combined involvement of *Lv*SID-1 together with endocytosis in dsRNA uptake into the shrimp hepatopancreatic cells cannot be excluded.

It is clear that factors such as species and the nature of specific cells have to be taken into account when elucidating the mechanisms of dsRNA uptake. For instance, two closely related species of coleopteran, *Tribolium castaneum* (Tomoyasu et al., 2008) and *Diabrotica virgifera* (Miyata et al., 2014) utilize different mechanisms for dsRNA uptake. The latter species uses SID-1 for this process, whereas the former species does not, and utilizes endocytic uptake. Uptake of injected dsRNA into shrimp hepatopancreatic cells utilized an endocytic pathway, while this pathway did not play an important role in dsRNA uptake into gill tissue (this study). Moreover, the introduction of dsRNA from different routes may promote different mechanisms of cellular dsRNA uptake. In this study, as in our previous study (Maruekawong et al., 2018) the dsRNA was introduced into shrimp by injection, and it was dsRNA that was being circulated in the shrimp body cavity in the hemolymph that was in contact with cells in the gill and hepatopancreas tissues that was being taken up. Other routes of dsRNA administration, such as feeding and soaking, may utilize different pathways, which needs to be investigated.

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Suppression of argonautes compromises viral infection in *Penaeus monodon*

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ABSTRACT

Argonaute (Ago) proteins, the catalytic component of an RNA-induced silencing complex (RISC) in RNA interference pathway, function in diverse processes, especially in antiviral defense and transposon regulation. So far, cDNAs encoding four members of Argonaute were found in *Penaeus monodon* (*PmAgo1-4*). Two PmAgo proteins, PmAgo1 and PmAgo3 shared high percentage of amino acid identity to Ago1 and Ago2, respectively in other Penaeid shrimps. Therefore, the possible roles of PmAgo1 and PmAgo3 upon viral infection in shrimp were characterized in this study. The level of *PmAgo1* mRNA expression in shrimp hemolymph was stimulated upon YHV challenge, but not with dsRNA administration. Interestingly, silencing of either *PmAgo1* or *PmAgo3* using sequence-specific dsRNAs impaired the efficiency of *PmRab7*-dsRNA to knockdown shrimp endogenous *PmRab7* expression. Inhibition of yellow head virus (YHV) replication and delayed mortality rate were also observed in both *PmAgo1*-and *PmAgo3*-knockdown shrimp. In addition, silencing of *PmAgo3* transcript, but not *PmAgo1*, revealed partial inhibition of white spot syndrome virus (WSSV) infection and delayed mortality rate. Therefore, our study provides insights into *PmAgo1*and *PmAgo3* functions that are involved in a dsRNA-mediated gene silencing pathway and play roles in YHV and WSSV replication in the shrimp.

1. Introduction

Multiple innate defenses including cellular and humoral immune reactions and RNA interference (RNAi) of invertebrates were wildly known as host defense mechanisms against microbial infection. In shrimp, discoveries of several molecules related to both cellular (encapsulation, coagulation, and melanization) and humoral (Toll, Immune deficiency (IMD) and JAK/STAT pathway) immune reactions reveal the existence of innate immune activities to fight against invading pathogens (Borregaard et al., 2000; Hoffmann et al., 1999). In addition, RNAi is also known as one of the potent antiviral immunities in many organisms such as mammals, plants, insects and shrimp (Robalino et al., 2004; Wang et al., 2006; Zambon et al., 2006). The RNAi pathway is triggered by different classes of small regulatory RNAs originating from either endogenous transcripts or exogenous dsRNAs such as small-interfering RNA (siRNA), microRNA (miRNA) and piwi-interacting RNA (piRNA). These small RNAs serve as guide sequences to direct the formation of an RNA-induced silencing complex (RISC), which contains an Argonaute (Ago) family protein as the catalytic core, to regulate viral replication by specific cleavage of the corresponding viral mRNA or translation inhibition (Aliyari et al., 2008).

Regarding their structural features, four domains are identified in a bilobate architecture of Ago proteins; one lobe with N and PAZ domains and the other lobe with MID and PIWI domains. Based on crystal structure analysis, the N domain takes part in unwinding of small RNA duplex (Kwak and Tomari, 2012), while a specific binding pocket on the PAZ domain binds to the 3′ end of small RNA duplex (Lingel et al., 2003; Ma et al., 2004). The 5′ phosphate of small RNAs is held onto the Ago protein by the MID domain (Kiriakidou et al., 2007; Till et al., 2007). A catalytic motif Asp-Asp-His (DDH) in the PIWI domain is responsible for the endonucleolytic activity (Song et al., 2004; Wang et al., 2008).

Multiple members of the Argonaute family exist in a wide range of organisms and are highly conserved among species. Ago proteins can be separated according to their phylogenetic relationships into Ago and Piwi subfamilies (Chen and Meister, 2005; Hammond et al., 2000; Janowski et al., 2006; Leebonoi et al., 2014; Yigit et al., 2006). Members of the Ago subfamily mediate post-transcriptional gene regulation by associating with either miRNA or siRNA. Piwi subfamily proteins are germ cell specific Argonautes associating with piRNAs, which behave as a small RNA-based immune system to safeguard genome integrity against transposon movement in germ cells and to control spermatogenesis and germ cell differentiation (Kalmykova et al., 2005; Kuromochi et al., 2004). In addition, another class of Argonaute

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proteins, a worm-specific Argonaute (WAGO), was exclusively found in the nematodes where they play a role in RNAi pathway to mediate a variety of cellular processes (Yigit et al., 2006). Numbers of Argonaute genes are different among organisms, ranging from a single member in *Schizosaccharomyces pombe* to twenty-seven members in *Caenorhabditis elegans* (Hock and Meister, 2008). So far, Ago2 of *Drosophila* and human were demonstrated to possess slicer activity (Meister et al., 2004; Miyoshi et al., 2005) and mediate antiviral defense via RNAi cleavage mechanism (Chen et al., 2011a; Van et al., 2006).

To date, at least two Ago subfamily members were identified and characterized in Penaeid shrimps. In *Litopenaues vannamei*, two Argonaute genes, *LvAgo1* and *LvAgo2* were identified; only *LvAgo2* was involved in siRNA mediated post-transcriptional gene silencing (Chen et al., 2011b; Labreuche et al., 2010). Likewise, *MjAgo1* and *MjAgo2* were found in *Masupenaeus japonicus*. MjAgo1 play important role in antiviral response in the shrimp (Huang and Zhang, 2012), while MjAgo2 acts as a key protein in viral siRNA biogenesis and function (Huang and Zhang, 2013). These studies suggest that Argonaute 2 proteins were essential for the functional siRNA-associated RISC and play a role in antiviral defense via siRNA-mediated viral mRNA degradation in the shrimp.

Interestingly, cDNAs encoding four types of the Ago subfamily proteins were reported in the black tiger shrimp, *Penaeus monodon* (*PmAgo1-4*). From phylogenetic analysis, PmAgo1 is clustered in the same group with LvAgo1 and MjAgo1, and was demonstrated for its important function in effective RNAi pathway in the primary culture of lymphoid cells (Dechklar et al., 2008). PmAgo3 was classified into the same group of Argonaute 2 proteins in penaeid shrimp i.e. LvAgo2 and MjAgo2, and was shown to be involved in the pathway of dsRNA-mediated gene silencing (Phetrungnapha et al., 2013). In addition, PmAgo2 and PmAgo4 were classified in the same cluster, but located on a separate branch from PmAgo3. The expression of *PmAgo2* was responsive to both viral and bacterial infections, and was also activated upon dsRNA and ssRNA administration (Yang et al., 2014). All members of *PmAgos*, except *PmAgo4* are expressed ubiquitously in all shrimp tissues. Interestingly, *PmAgo4* displays a gonad-specific expression similar to that of the Piwi subfamily. The gonad-specific *PmAgo4* was suggested to be involved in the protection of shrimp genome against transposons invasion (Leebonoi et al., 2014). Although accumulating evidences have demonstrated that *PmAgos* could exhibit diverse-functions, no report has thus far indicated the actual function of Argonaute proteins for innate immunity in shrimp compared to model organisms such as *Drosophila*. In this study, we reported the possible involvement of *PmAgo1* and *PmAgo3*, homologs of DmAgo1 and DmAgo2, respectively in the mechanism of dsRNA-mediated gene silencing. Moreover, the involvement of *PmAgo1* and *PmAgo3* in viral infection was also characterized. Functional analysis of *PmAgo1* and *PmAgo3* in the RNAi mechanism during viral infection will provide a basis for further development of effective strategies to control viral diseases in the economically important Penaeid shrimp.

2. Materials and methods

2.1. Animals

Live adolescent black tiger shrimp (approximately 10–15 g body weight) were purchased from shrimp farms around the central area of Thailand. They were first screened for yellow head virus (YHV) and white spot syndrome virus (WSSV) infection by RT-PCR as previously described (Attasart et al., 2009; Yodmuang et al., 2006). The virus-free shrimp were used in all experiments. Shrimp were gradually acclimatized to the laboratory condition in 10 ppt (parts per thousand) sea water with aeration for 2 days. They were also fed with commercial shrimp feed (CP, Thailand) twice a day for a few days before setting the experiment.

2.2. Viral stock preparation

To obtain fresh viral stock of YHV and WSSV, crude viruses were injected into the healthy virus-free shrimps. After 48 h, the hemolymph was drawn from moribund shrimp, and the viruses were then purified and determined for viral titer (YHV stock; $\sim 2 \times 10^6$ virions ml^{-1}, WSSV stock; $\sim 3 \times 10^5$ virions ml^{-1}) as previously described by Assavalapsakul et al. (2003). Appropriate dilutions of the viral stock (100-fold and 10-fold for YHV and WSSV, respectively) that gave complete mortality within 3 days post-infection (dpi) were freshly prepared before use.

2.3. Detection of gene transcripts by reverse transcription-polymerase chain reaction (RT-PCR)

Gills were dissected from individual shrimp and homogenized in TRI-REAGENT® (Molecular Research Center), while hemolymph was collected and subsequently mixed with TRI-REAGENT®. Total RNA was isolated according to the manufacturer's protocol. The concentration and purity of the extracted total RNA was examined by Nanodrop® ND-1000 spectrophotometer (Nanodrop Technologies). First strand cDNA was reverse-transcribed from 1 to 2 μg of total RNA priming with PRT-oligo-dT_{16} primer by Impromp-II™ reverse transcriptase (Promega) using the following condition: 25 °C for 5 min, 42 °C for 60 min, and 70 °C for 15 min.

One microliter of the first strand cDNA was used as a template to examine mRNA expression. Multiplex-PCR with two primer pairs was applied to determine the expression of the mRNA of interest and *β-actin* mRNA (internal control) simultaneously. The reaction contains the standard components according to Tag DNA polymerase's protocol (Thermo scientific). *PmAgo1* transcript was amplified with PmAgo1-F and PmAgo1-R primers using the following condition: 94 °C for 5 min, 2 cycles of 94 °C for 1 min, 60 °C for 1 min, 72 °C for 1 min and additional 30 cycles of 94 °C for 1 min, 55 °C for 1 min, 72 °C for 1 min (Phetrungnapha et al., 2013). The final extension was performed at 72 °C for 7 min. Amplification of *PmAgo3*, *PmRab7*, *YHV-helicase (YHV-Hel)* and WSSV *vp28* mRNAs were carried out with specific primer pairs and specific conditions as previously described (Attasart et al., 2009; Ongvarrasopone et al., 2008; Phetrungnapha et al., 2013; Yodmuang et al., 2006). In the experiment, two *β-actin* PCR products of either 550 bp or 350 bp were amplified with the same forward primers (Actin-F) and different reverse primers, Actin-R or Actin-R2, respectively. The oligonucleotide sequences of Actin primers and specific conditions are previously described by Posiri et al. (2013). The primers used in this study and their nucleotide sequences are shown in Table 1.

2.4. Double-stranded RNA (dsRNA) production

The hair-pin dsRNA precursor was produced by *in vivo* bacterial expression system as described by Ongvarrasopone et al. (2007). The recombinant plasmids pET17b-st-*PmAgo1* (previously construct in our laboratory), pET17b-st-*PmAgo3* (Phetrungnapha et al., 2013), pET17b-st-*PmRab7* (Ongvarrasopone et al., 2008) and pET3a-st-*GFP* (kindly provided by Asst. Prof.Witoon Tirasophon) harboring the cassette for producing the hair-pin dsRNA of corresponding genes were used to transform ribonuclease III-deficient *Escherichia coli* strain HT115 (DE3). The expression of hair-pin dsRNAs were induced with 0.4 mM IPTG for 4 h with shaking. The hair-pin dsRNAs were extracted by ethanol extraction method (Posiri et al., 2013) before dissolving in 150 mM NaCl. The concentration and purity of the hair-pin dsRNAs were monitored by agarose gel electrophoresis and Nanodrop® ND-1000 spectrophotometer. The hair-pin dsRNAs were verified by RNase digestion assay as described previously (Posiri et al., 2013).

Table 1
List of Primers used in this study.

Primers	Sequence (5′ to 3′)	Experiment
Oligo-dT_{16} (PRT)	CCGGAATTCAAGCTTCTAGAGGATCCTTTTTTTTTTTTTTT	Reverse transcription
PmActin-F	GACTCGTACGTGGGCGACGAGG	Detection of Actin transcript
PmActin-R	AGCAGCGGTGGTCATCTCCTGCTC	
PmActin-R2	CGTAGATGGGCACGGTGTGGG	
PmAgo1-F	CAAGAATTTGGTCTGACGAT	Detection of PmAgo1 transcript
PmAgo1-R	AGTGTCACCCACACGCTTCAC	
PmAgo3-F	GGTGGAAGGATTTCCCACTT	Detection of PmAgo3 transcript
PmAgo3-R	CACTGGGGAGTGAGTTGCTT	
PmRab7-F	ATGGCATCTCGCAAGAAGATT	Detection of PmRab7 transcript
PmRab7-R	TTAGCAAGAGCATGCATCCTG	
YHV-Hel-F	CAAGGACCACCTGGTACCGGTAAAAC	Detection of YHV transcript
YHV-Hel-R	GCGGAAACGACTGACGGCTACATTCAC	
WSSV-Vp28-F	ATGAGAATGAACTCCAACTTTAA	Detection of WSSV transcript
WSSV-Vp28-R	CAGAGCCTAGTCTATCAATCAT	

2.5. Analysis of PmAgo1 expression in response to dsRNA or virus injection

Alteration in *PmAgo*1 transcript level in shrimp hemolymph was investigated upon either dsRNA or viral injections. Shrimp, approximately 10 g body weight (b.w.) were injected with *GFP*-dsRNA at 2.5 μg g^{-1} b.w. or challenged with 50 μl of the 10^{-2} dilution of YHV stock. After that, the hemolymph was collected from individual shrimp from each group (n = 5 and 10 for *GFP*-dsRNA and YHV injected group, respectively) at 0, 3, 6, 9, 12, 24, 36, 48 and 72 h post-injection (hpi) for determination of *PmAgo1* mRNA expression by RT-PCR. Multiplex amplification of *PmAgo*1 and the internal control, *β-actin* transcripts was carried out by specific primers for each gene as described in 2.3, and the PCR products were subsequently analyzed by agarose gel electrophoresis. The Scion image analysis program was applied to quantify the band intensity of *PmAgo1* PCR product normalized with that of *β-actin*, and presented as mean ± standard error of mean (SEM) as relative expression levels of *PmAgo1*. The significant difference of relative *PmAgo1* expression level ($p < 0.05$) between each time point was analyzed by sample T-Test.

2.6. Investigation of the effect of PmAgo1 and PmAgo3 knockdown on the efficiency of RNAi

P. monodon (approximately 10 g b.w.) were injected with *PmAgo1*-or *PmAgo3*-dsRNA at 2.5 μg g^{-1} b.w. Either 150 mM NaCl or *GFP*-dsRNA was injected into shrimp as control groups. At 2 days-post injection, the hemolymph sample from shrimp in each group (n = 5) was collected to determine the expression levels of *PmAgo1* and *PmAgo3*. Subsequently, *PmRab7*-dsRNA was injected into *PmAgo* knocked-down shrimp at 0.63 μg g^{-1} b.w. to suppress *PmRab7* mRNA expression. Expression of *PmRab7* was determined by multiplex RT-PCR analysis as described in 2.3 at 0, 24, 48 and 72 h post *PmRab7*-dsRNA injection.

2.7. Biological assay for antiviral function of PmAgo1 and PmAgo3

Shrimps (approximately 10 g b.w.) were injected with 25 μg g^{-1} b.w of *PmAgo1-, PmAgo3*-or *GFP*-dsRNA (5–10 shrimp per group). The hemolymph was collected at 48 h post-dsRNA injection to determine the transcript levels of *PmAgo1 and PmAgo3* as described in 2.3. The shrimp were subsequently injected with 50 μl of either the 100 fold diluted YHV or 10 fold diluted WSSV stock. Shrimp injected with 150 mM NaCl following with viruses were used as positive control for YHV infection, and shrimp injected with unrelated GFP-dsRNA followed by YHV was used as a control for the effect of dsRNA on viral infection. Multiplex RT-PCR analysis of *helicase* gene of YHV (*hel*) or *Vp28* gene of WSSV was performed to determine viral mRNA expression relative to that of *actin* in the shrimp at 0, 36, and 48 h post viral injection. PCR detection of WSSV genome was also performed to determine the level of WSSV genome. In addition, mortality of individual shrimp in each group was also recorded.

3. Results

3.1. Expression of Ago1 in P. monodon upon YHV and GFP-dsRNA administration

Because the two isoforms of *Ago1* in *P. monodon*, *PemAgo1* (Dechklar et al., 2008) and *PmAgo1* (Unajak et al., 2006) contain the same coding sequences and cannot be differentiated by the RT-PCR detection, they were collectively referred to as *PmAgo1* in this study. In order to determine whether *PmAgo1* expression is correlated to its possible role in antiviral immunity and dsRNA mediated gene silencing as reported earlier, the expression of *PmAgo1* in response to YHV injection or GFP-dsRNA in the hemolymph of shrimp at various time points was determined by multiplex RT-PCR. Successful YHV infection was confirmed at 72 hpi by the detection of YHV *helicase* gene expression in the hemolymph of individual shrimp. The result in Fig. 1A revealed that the expression levels of *PmAgo1* in YHV injected shrimp gradually increased from 0 hpi to the highest level of approximately 2-fold with significant difference ($p < 0.05$) at 9 hpi before continuously decreasing until 72 hpi. On the other hand, *PmAgo1* expression in shrimp hemolymph at every time point post-*GFP*-dsRNA injection was rather constant throughout the course of the experiment (Fig. 1B). These data demonstrated that *PmAgo1* expression was activated by YHV, but not by dsRNA administration.

3.2. Silencing of PmAgo1 and PmAgo3 by specific dsRNAs

To study the function of *PmAgo1* and *PmAgo3*, their expression was first suppressed by dsRNA-mediated gene silencing approach. The injection of *PmAgo1*-dsRNA significantly suppressed *PmAgo1* transcript level ($p < 0.05$) approximately 60% and 50% on day 2 and day 4 post-injection, respectively. More than 95% suppression of *PmAgo3* transcript was found in the hemolymph after one day post-*PmAgo3*-dsRNA injection, and this level of suppression lasted for at least 3 days (Figure S1). Moreover, *PmAgo1*-dsRNA did not have effect on *PmAgo3* expression and *vice versa* (Fig. 2A and B). Therefore, these dsRNAs were able to efficiently and specifically suppress *PmAgo1* and *PmAgo3* expression, and thus could be used for further functional analysis of both *PmAgos*.

3.3. Impairment of RNAi-mediated PmRab7 repression in PmAgo-knockdown shrimp

To investigate possible involvement of *PmAgo1* and *PmAgo3* in dsRNA-mediated RNAi pathway, the efficiency of *PmRab7*-dsRNA to repress shrimp endogenous *PmRab7* mRNA expression was studied in

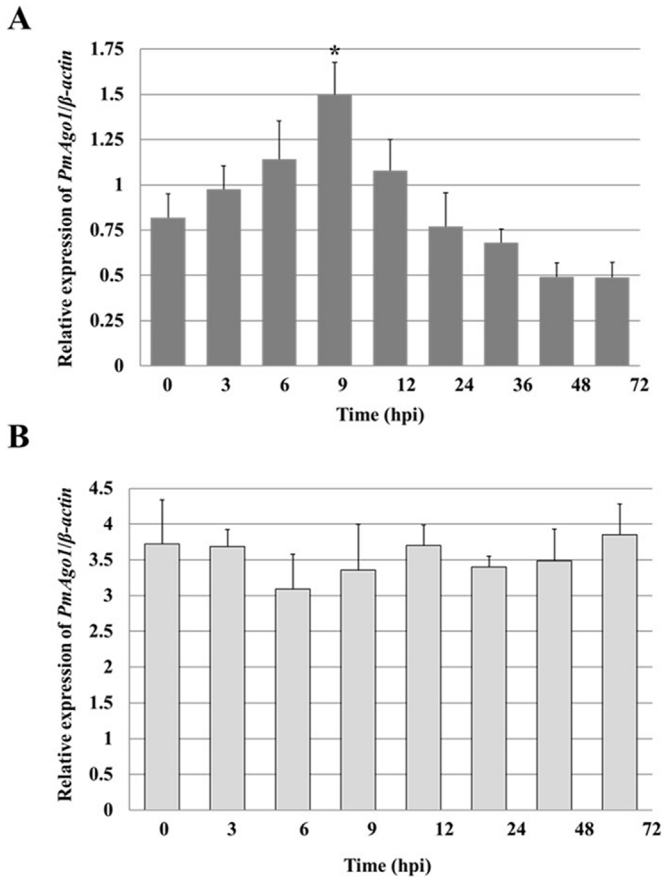

Fig. 1. *PmAgo1* expression in response to yellow head virus (YHV) and GFP-dsRNA administration Multiplex RT-PCR was used to determine the expression of *PmAgo1* in the hemolymph of *P. monodon* at different time points after injected with either 50 µl of 100-fold dilution of purify YHV lysate (A; n = 10) or *GFP*-dsRNA at 2.5 µg g^{-1} shrimp (B; n = 5). The bar-graphs represent expression level of *PmAgo1* normalized with that of *β-actin* as analyzed by Scion image analysis program. Each bar represents mean ± SEM. Asterisk indicates significant difference from 0 hpi ($p < 0.05$).

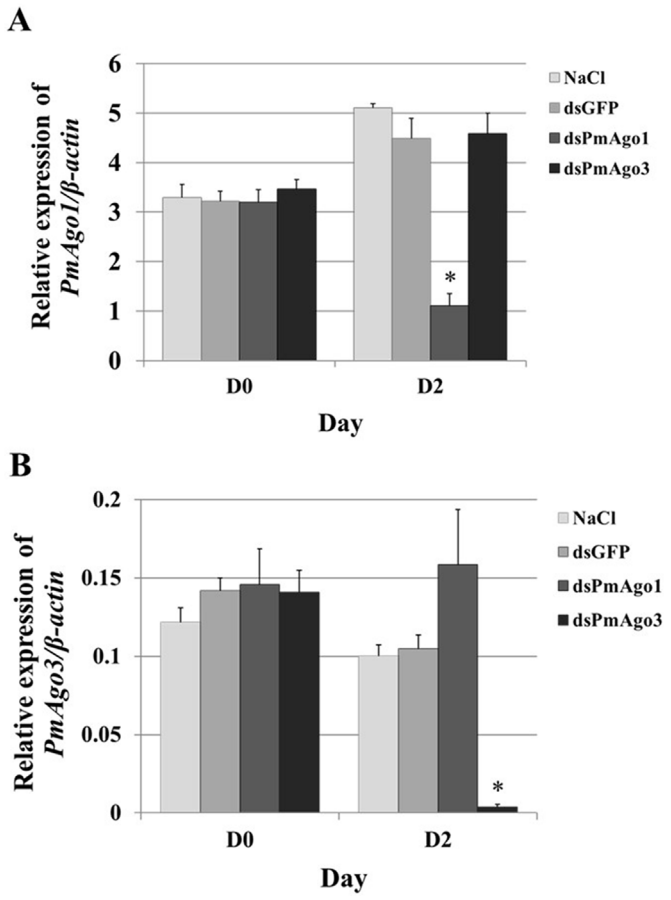

Fig. 2. Suppression of *PmAgo1* and *PmAgo3* transcripts by dsRNA *P. monodon* were injected with 2.5 µg g^{-1} shrimp b.w. of either *PmAgo1*-dsRNA (dsPmAgo1) or *PmAgo3*-dsRNA (dsPmAgo3). The expression of *PmAgos* in the hemolymph was determined by multiplex RT-PCR at 2 days post-injection comparing with that in shrimp injected with NaCl and GFP-dsRNA as the control groups. The levels of *PmAgo1* and *PmAgo3* transcripts in the hemolymph of shrimp in each group were analyzed by agarose gel electrophoresis together with the internal control *β-actin* transcript. The histograms show the relative expression of *PmAgo1* (A) and *PmAgo3* (B) normalized with that of *β-actin* as measured by Scion image analysis program. Each bar represents mean ± SEM (n = 5). Asterisks (*) indicate the significant difference ($p < 0.05$) between *PmAgo1*-dsRNA or *PmAgo3*-dsRNA injection groups and the control groups at each time point.

PmAgo-knockdown shrimp. The silencing of *PmAgo1* and *PmAgo3* expression in shrimp hemolymph was confirmed on day 2 after injected with corresponding dsRNAs compared with that in the control shrimp injected with NaCl or an unrelated *GFP*-dsRNA (Figure S2), whereas the expression of *PmRab7* among each group was not dramatically different (Fig. 3; **Day0**). Shrimp in each group were then injected with *PmRab7*-dsRNA, and *PmRab7* expression was determined at 24 h interval after *PmRab7*-dsRNA injection. The result in Fig. 3 showed the complete suppression of *PmRab7* mRNA expression in both control groups (NaCl or *GFP*-dsRNA injection followed by *PmRab7*-dsRNA) at 24, 48 and 72 h post-*PmRab7*-dsRNA injection. Interestingly, the expression of *PmRab7* could be detected in *PmAgo1*-and *PmAgo3*-knockdown shrimp to a certain extent, but significantly different ($p < 0.05$) from the control shrimp, at all time-points from 24 to 72 h after injected with *PmRab7*-dsRNA. These results indicated that dsRNA-mediated *PmRab7* suppression in *PmAgo*-knockdown shrimp was not as efficient as that in the control shrimp. Moreover, *PmRab7* expression *PmAgo1*-knockdown shrimp was noticeably higher than that in *PmAgo3*-knockdown shrimp at 72 h post-*PmRab7*-dsRNA injection, suggesting that both PmAgos contribute to the dsRNA-mediated gene silencing pathway in shrimp at different extent.

3.4. Effect of PmAgo1 and PmAgo3 knockdown on viral infection in shrimp

To investigate the function of *PmAgo1 and PmAgo3* on virus infection, viral replication and shrimp mortality after YHV or WSSV challenge in *PmAgo*-knockdown shrimp were determined compared with that in the control groups (NaCl or *GFP*-dsRNA injcetion). The expression of *PmAgo1* and *PmAgo3* was knocked down by the injection of specific dsRNA two days before YHV challenge. The YHV-*hel* transcript could be detected in the hemolymph of both control groups at 48 h post-YHV injection (hpi), but not in the hemolymph of *PmAgo1*-knockdown shrimp (Fig. 4A). In addition, the control shrimp that had been injected with NaCl or GFP-dsRNA prior to YHV challenge started to die after 84 hpi, and the cumulative mortality reached 100% at 108 hpi, whereas the mortality of *PmAgo1*-knockdown shrimp was observed after 120 h post-YHV challenge and reached 100% at 138 hpi (Fig. 4B). Similarly, barely detectable level of YHV-*hel* and delayed cumulative mortality rate upon YHV challenge was also observed in *PmAgo3*-knockdown shrimp when compared with the control groups (Fig. 5A and B). The detection of YHV-*hel* gene in the gill tissue from all dead shrimp confirmed that the shrimp were infected with the virus (Figs. 4C and 5C).

Since WSSV is one of major viruses that cause high mortality in the shrimp, the role of *PmAgo1* and *PmAgo3* in WSSV infection was also

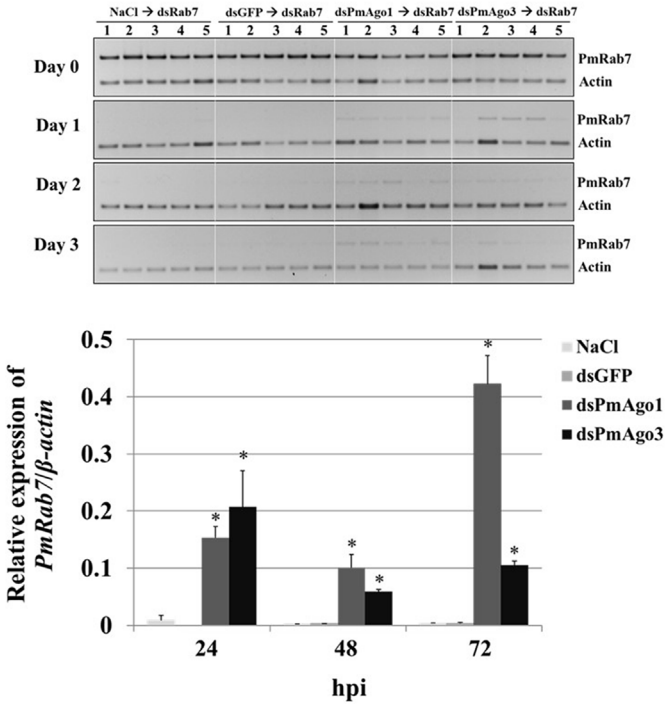

Fig. 3. Impairment of *PmRab7* silencing by *Rab7*-dsRNA in *PmAgo1*-and *PmAgo3*-knockdown shrimp. The expression of *PmAgo1* and *PmAgo3* was suppressed by the injection of *PmAgo1*-or *PmAgo3*-dsRNA at 2.5 μg g^{-1} b.w., whereas NaCl and *GFP*-dsRNA injection were used as the controls. Two days following the dsRNA injection, shrimp in each group were subsequently injected with *PmRab7*-dsRNA (0.6 μg g^{-1} shrimp b.w.), and the expression of *PmRab7* in the hemolymph was determined at 0, 24, 48 and 72 h post-*PmRab7*-dsRNA injection (upper panel). *β-actin* was detected as an internal control. Numbers represent individual shrimp. The histograms (lower panel) show the relative expression of *PmRab7* normalized with that of *β-actin* as measured by Scion image analysis program. Each bar represents mean ± SEM (n = 5). Asterisks (*) indicate the significant difference ($p < 0.05$) between *PmAgo1*-dsRNA (dsPmAgo1) or *PmAgo3*-dsRNA (dsPmAgo3) injection groups and the control groups at each time point.

investigated. The result showed that the levels of WSSV *vp28* transcript as well as WSSV genomic DNA in *PmAgo1*-knockdown shrimp infected with WSSV was comparable to that in both control groups that were injected with either NaCl or GFP-dsRNA prior to viral challenge (Fig. 6A and B). In addition, the cumulative mortality rate of the shrimp in all groups was not different; shrimp started to die after 36 h, and all were dead by 48 h (Fig. 6C). By contrast, lower levels of WSSV *vp28* transcript, notably with undetectable level in two out of five shrimp, and lower amounts of viral DNA genome in the pleopod were detected in *PmAgo3*-knockdown shrimp at 36 h post-WSSV infection compared with that in both control groups (Fig. 6A and B). Moreover, the delay in the cumulative mortality rate in *PmAgo3*-knockdown shrimp was observed upon WSSV challenge when compared to the control groups (Fig. 6C). The WSSV *vp28* transcript could be detected in gill tissue from dead shrimp in all groups confirming that the shrimp died of WSSV infection (Fig. 6D).

4. Discussion

Four types of Argonaute protein were previously identified in *P. monodon*. They are all classified as the Ago subfamily. Nevertheless, the mechanism underlying the Ago-related antiviral immunity in shrimp remains largely unknown. In this study, functional significance of *PmAgo1* and *PmAgo*3 on YHV and WSSV replication and their role in dsRNA-mediated post-transcriptional gene silencing were characterized.

Expression of key proteins in the effective innate antiviral RNAi mechanism was usually stimulated by exogenous RNAs (Choudhary et al., 2007; Garbutt and Reynolds, 2012; Phetrungnapha et al., 2013; Yang et al., 2014). Injection of dsRNA could induce expression of *dicer-2* and *argonaute-2* in tobacco hornworm (Garbutt and Reynolds, 2012). In *Neurospora crassa*, the induction of dicer (DCL-2) and argonaute (QDE-2) expression by dsRNA resulted in an increase in the efficiency of dsRNA-mediated RNAi pathway (Choudhary et al., 2007). These evidences suggested that *dicer-2* and *argonaute-2* are involved in dsRNA-mediated gene silencing pathway. Up-regulation of the expression of genes encoding core RNAi proteins e.g. *Dcr2*, *Ago2* and *Ago3* and associated components such as *TRBP*, *TSN* and *Mov-10* upon dsRNA challenge were also demonstrated in penaeid shrimps (Li et al., 2013; Phetrungnapha et al., 2012, 2013, 2015; Yang et al., 2013, 2014). In

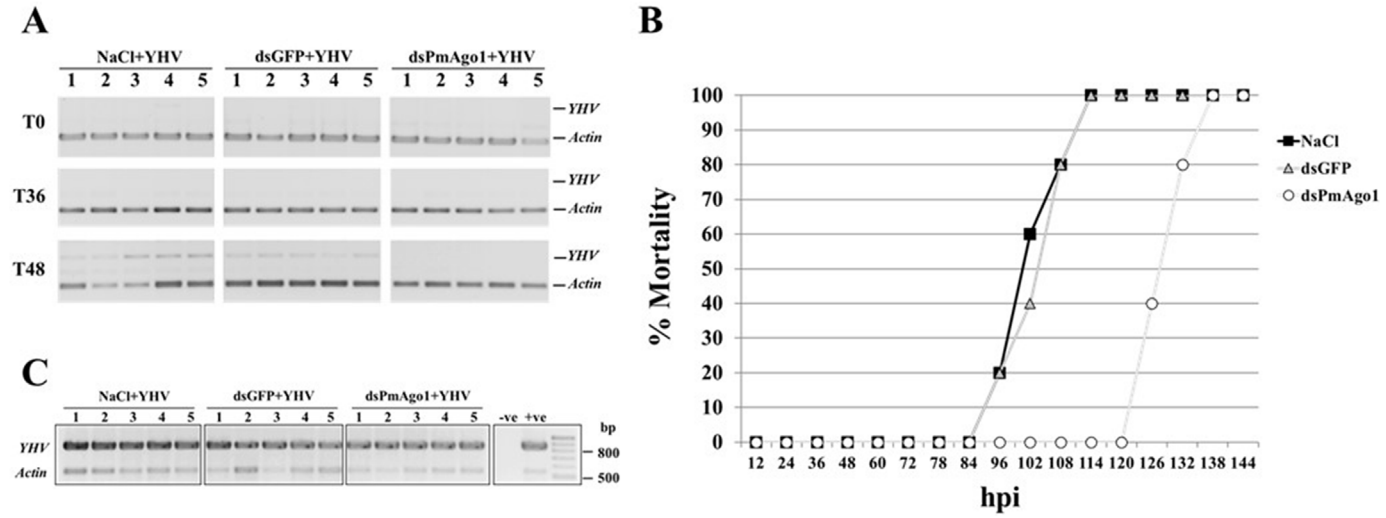

Fig. 4. Effect of *PmAgo1* knockdown on YHV replication and cumulative mortality in shrimp upon YHV infection Suppression of *PmAgo1* expression was carried out by *PmAgo1*-dsRNA injection with NaCl and *GFP*-dsRNA injection as controls. On day 2 after injected with dsRNA, shrimp were subsequently challenged with YHV, and the expression of YHV *helicase* gene (YHV-*hel*) in the hemolymph of *PmAgo1*-knockdown shrimp (dsPmAgo1 + YHV) and the control shrimp (NaCl + YHV, dsGFP + YHV) was detected by multiplex RT-PCR compared with that of *β-actin* at 0, 36 and 48 h post YHV infection (n = 5 at each time point) (A). Mortality of individual shrimp in each group was also recorded, and presented as cumulative percent mortality (B). Virus infection in the shrimp was verified by detection of YHV-*hel* mRNA in gill tissue from dead shrimp in all groups (C).

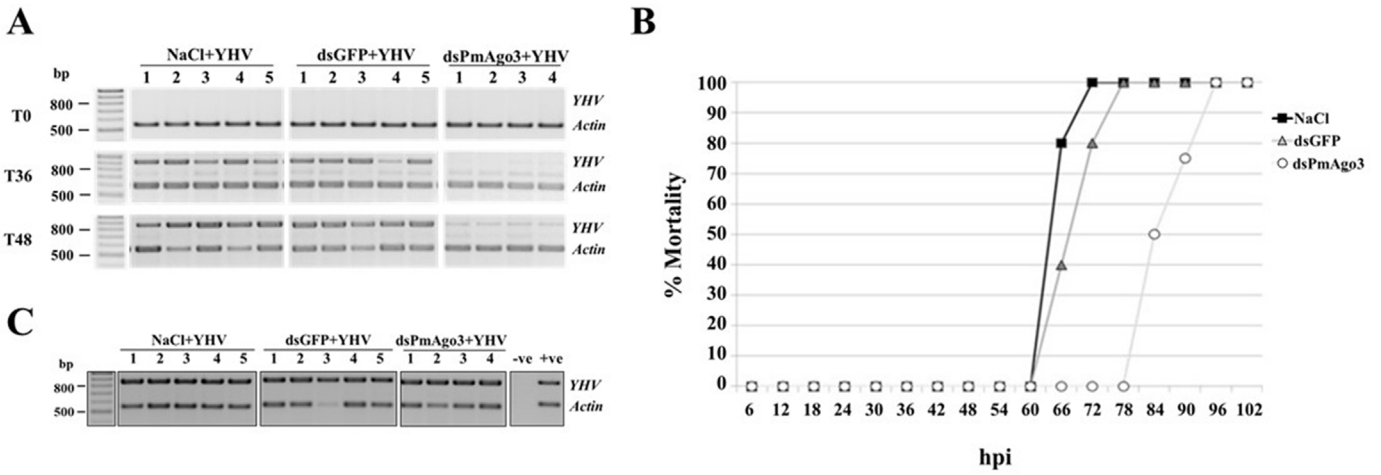

Fig. 5. Effect of *PmAgo3* knockdown on YHV replication and cumulative mortality in shrimp upon YHV infection Suppression of *PmAgo3* expression was carried out by *PmAgo3*-dsRNA injection with NaCl and *GFP*-dsRNA injection as controls. The *PmAgo3*-knockdown shrimp were infected with YHV (dsPmAgo3 + YHV), and the expression of YHV-*hel* gene in the hemolymph was detected by multiplex RT-PCR compared with that of control shrimp (NaCl + YHV, dsGFP + YHV) at 0, 36 and 48 h post YHV infection (n = 5 at each time point) (A). *β-actin* transcript was determined as internal control. Mortality of individual shrimp in each group was also recorded, and presented as cumulative percent mortality (B). Expression of YHV-*hel* mRNA in gill tissue from dead shrimp was examined to confirm virus infection in the shrimp (C).

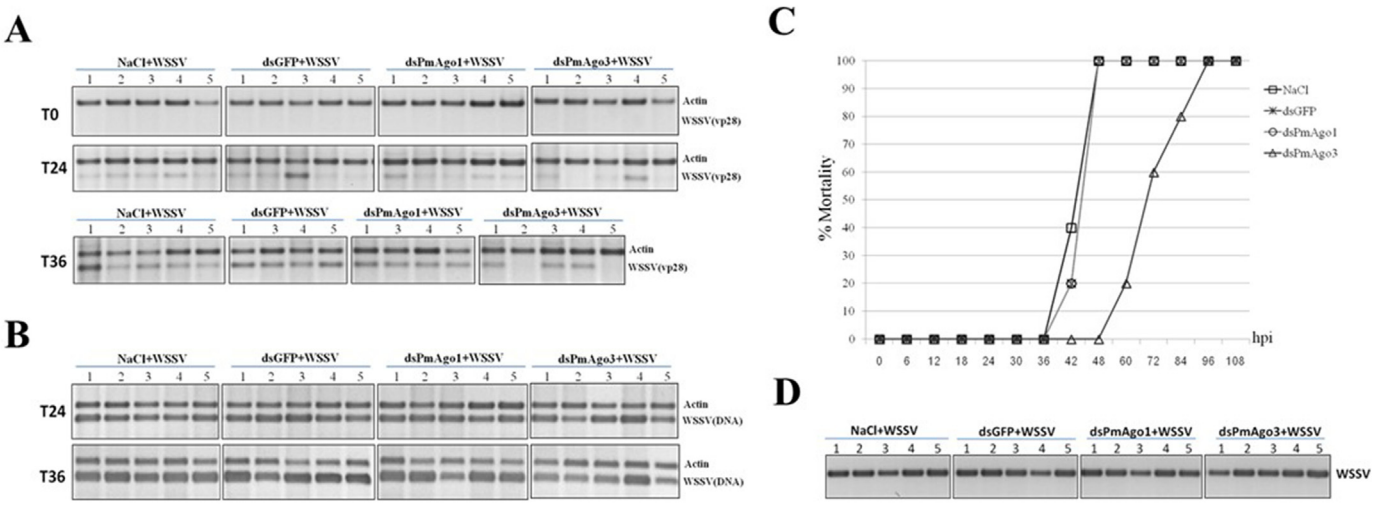

Fig. 6. WSSV replication and shrimp mortality upon WSSV infection in *PmAgo1*-and *PmAgo3*-knockdown *P. monodon*. *P. monodon* were injected with either 2.5 μg g^{-1} shrimp of *PmAgo1*-dsRNA, *PmAgo3*-dsRNA, *GFP*-dsRNA or 150 mM NaCl (n = 5 in each group) 2 days prior to WSSV challenge. WSSV replication in *PmAgo1*-knockdown shrimp (dsPmAgo1 + WSSV), *PmAgo3*-knockdown shrimp (dsPmAgo3 + WSSV) comparing with control shrimp (NaCl + WSSV and dsGFP + WSSV) was determined by both RT-PCR detection of WSSV *Vp28* mRNA (A) and PCR amplification of WSSV genomic DNA (B) at 0, 24 and 36 h post WSSV infection. *β-actin* transcript was determined as an internal control. Mortality of individual shrimp in each group was also recorded, and presented as cumulative percent mortality (C). WSSV infection in all dead shrimp was confirmed by RT-PCR of WSSV-vp28 mRNA in the gill tissue (D).

addition, suppression of *HsAgo2* by *HsAgo2*-siRNA in Human Embryonic Kidney 293 cells (HEK-293) impeded the efficiency of RNAi mechanism to knock-down histone deacetylase 2 (HDAC2) by specific HDAC2-siRNA (Naoghare et al., 2011). Similarly, silencing of *PmAgo1* and *PmAgo3* expression by specific dsRNAs in this study reduced the efficiency of *PmRab7* mRNA suppression by *PmRab7*-dsRNA, indicating the involvement of PmAgo1 and PmAgo3 in dsRNA-mediated gene silencing process. These results strongly supported the study of Dechklar et al. (2008) where repression of *Ago1* reduced the competency of 5HT-dsRNA in suppressing 5HT gene in *P. monodon*'s Oka cells. In addition, the knockdown of *PmTSN* or *MjTRBP* expression by specific dsRNA in shrimp also impaired the efficiency of dsRNA/siRNA mediated gene silencing (Phetrungnapha et al., 2012; Wang et al., 2012). Previous reports on the Argonaute-interacting proteins in shrimp revealed that argonaute-2 of *L. vannamei* and *M. japonicus* bound to dicer-2 and TRBP1, respectively. These Ago2 complexes played a role in dsRNA/siRNA-mediated sequence-specific RNAi process while argonaute-1 primarily functioned in a miRNA pathway (Chen et al., 2011b; Huang and Zhang, 2013). However, the interacting proteins and small RNAs associated with either PmAgo1 or PmAgo3 need to be identified to confirm the precise mechanism of each PmAgo in the RNAi pathway.

Previous studies in other species demonstrated that the responsive expression of *Ago* transcripts upon virus infection enhanced the effective RNAi antiviral defense (Sun et al., 2009; Várallyay et al., 2010). For instance, the increased expression of *Nb*Ago1 mRNA in Cymbidun ringspot virus (CymRSV) infected *Nicotiana benthamiana* and the accumulation of argonaute-1 protein enhanced the RNAi antiviral activity by reducing the levels of CymRSV accumulation in the plant (Várallyay et al., 2010). In addition, high levels of *MjAgo1A* and *MjAgo1B* transcript were accumulated upon WSSV infection in *M. japonicus* (Huang and Zhang, 2012). Similarly, our result showed that the increased levels of *PmAgo1* expression was noticed in the haemolymph of YHV-infected

shrimp. This phenomenon was also observed in YHV-infected as well as WSSV-infected lymphoid organ (Unajak et al., 2006) indicating a possible involvement of *PmAgo1* during viral infection. Our investigation on the expression of *PmAgo3* in WSSV challenge shrimp revealed that *PmAgo3* was gradually up-regulated in WSSV infected shrimp. The significant difference of *PmAgo3* expression was observed after 12 hpi when compared to its expression level at 0 hpi (Fig. S3). These results demonstrated that WSSV infection in shrimp could activate the expression of both *PmAgo1* and *PmAgo3* mRNA. Up-regulation of argonaute 2 (GrAgo2) transcripts was exhibited in grass carp reovirus-infected rare minnow *Gobiocypris rarus* (Su et al., 2009). Likewise, the infection of tomato yellow leaf curl virus in tomato, *Solanum lycopersicum* induced the expression of dicers and Agos (Bai et al., 2012). In *P. monodon*, Yang et al., 2014 demonstrated that *PmAgo2* mRNA expression was escalated by WSSV challenge while the expression of *PmAgo3* and *PmAgo4* was not altered in YHV infected shrimp (Leebonoi et al., 2014; Phetrungnapha et al., 2013). In addition, virus infection in Penaeid shrimps could also evoke other RNAi components such as LvDicer-1, LvDrosha and FcTRBP (Huang et al., 2012; Wang et al., 2009; Yoa et al., 2010). Nonetheless, the responsive expression of *PmAgos* upon viral challenge may not necessarily specify PmAgos' function in antiviral defense. Whether or not PmAgos take part in the response to viral infection in the shrimp was therefore further characterized in this study.

The function of Argonaute proteins in RNAi-mediated antiviral defense in invertebrates was generally demonstrated by an increase in susceptibility to viruses in *Ago*-knockdown animals (Huang and Zhang, 2012). For instance, the hypersensitivity to *Drosophila* C virus infection and high viral RNA accumulation were presented in *DmAgo2* mutant drosophila comparing to wild type and *DmAgo1* mutant flies (Van et al., 2006). A significant increase of viral loads was also observed in the shrimp, in which the expression of RNAi machinery e.g. *Ago1*, *dicer-1*, *TRBP* and *Mov10* had been knocked down (Huang and Zhang, 2012; Phetrungnapha et al., 2015; Su et al., 2008; Wang et al., 2012). Therefore, the functional significance of *PmAgo1* and *PmAgo3* in RNAi upon viral infection were investigated by determining the level of viral transcript and cumulative mortality in *PmAgos*-suppressed shrimp comparing to the control groups.

In general, once the hosts are infected by RNA viruses, the dsRNA replicative intermediates of the viruses are recognized by Dicer and cleaved into viral-derived siRNAs (viRNAs). The complex between viRNAs and Ago proteins in the RISC subsequently trigger the activity of RNA silencing-mediated antiviral immunity (Molnar et al., 2005; Pantaleo et al., 2007; Parameswaran et al., 2010; Weng et al., 2015). However, some viruses could express viRNAs that interfered with host gene expression and promoted viral infection (Adkar-purushothama et al., 2015; Wang et al., 2016). For example, the expression of two callose synthase genes in tomato plant was down-regulated by siRNA derived from potato spindle tuber viroid leading to the accumulation of viroids and the severity of disease (Adkar-purushothama et al., 2015). Likewise, siRNAs derived from Cucumber mosaic virus (CMV) Y satellite RNA (Y-sat) could decrease the expression *chlI* gene in the chlorophyll synthesis pathway, and enhanced the yellowing symptom in tobacco plants (Smith et al., 2011). Our results revealed that inhibition of YHV replication and delay mortality were noticeably observed in *PmAgo1*-and *PmAgo3*-knockdown shrimp when compared with that in both control groups (injection with either NaCl or *GFP*-dsRNA prior to viral challenge). These evidences suggest that the positive single-stranded YHV might produce viRNAs that were subsequently loaded into either PmAgo1 or PmAgo3 RISC to regulate cellular gene expression of shrimp, and accounted for promoting viral replication and disease severity. However, the gene required for YHV replication, whose expression was affected by YHV-derived small RNA in the shrimp needs to be further identified.

In addition to RNA viruses, a number of DNA viruses could also produce viral-derived small RNAs. For example, viRNAs derived from shrimp DNA virus, WSSV were reported in Penaeid shrimps (Huang and Zhang, 2013), and they required shrimp Ago2 protein for the effective function in response to WSSV infection (Yang et al., 2014). Our results also showed that the replication of WSSV in *P. monodon* was suppressed in *PmAgo3*-knockdown shrimp, but not in *PmAgo1*-knockdown shrimp suggesting that PmAgo3 might play an important role in both DNA and RNA virus replication in the shrimp. The preference for each Ago protein in response to RNA and DNA viruses is not surprising as it has been demonstrated that *Arabidopsis* Ago1 and Ago2 played a major role in the anti-RNA viral response (Dzianott et al., 2012; Garcia-Ruiz et al., 2015; Jaubert et al., 2011; Wang et al., 2011), while Ago4 functions in an antiviral activity against several RNA (Bhattacharjee et al., 2009; Hamera et al., 2012) and DNA viruses (Raja et al., 2008, 2014). Nevertheless, what defines these preferential antiviral activities in shrimp is still elusive.

In conclusion, the function of *PmAgo1* and *PmAgo3* during viral infection in *P. monodon* was reported in this study. The elevated *PmAgo1* expression in the hemolymph upon YHV challenge suggests its association with shrimp response to viral infection. Suppression of *PmAgos* by specific dsRNA indicated that *PmAgo1* was preferentially required for YHV replication, whereas *PmAgo3* has more extensive effect on the replication of both YHV and WSSV. Our findings expand an understanding in Argonaute-associated RNA silencing mechanism and host response during viral infection in Penaeid shrimps.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dci.2018.09.008.

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Full length article

PmEEA1, the early endosomal protein is employed by YHV for successful infection in *Penaeus monodon*

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ABSTRACT

Yellow head disease (YHD) is an infectious disease of *Penaeus monodon* which is caused by the yellow head virus (YHV). YHV infection invariably leads to 100% shrimp mortality within 3–5 days. Currently, an effective method to prevent or cure shrimp from YHV infection has not been elucidated. Therefore, the molecular mechanism underlying YHV infection should be examined. In this study, early endosome antigen 1 (EEA1) protein that was involved in the tethering step of the vesicle and early endosome fusion was investigated during YHV infection. The open reading frame of *P. monodon* EEA1 (PmEEA1) was cloned and sequenced (3000 bp). It encoded a putative protein of 999 amino acids and contained the zinc finger C_2H_2 domain signature at the N-terminus and the FYVE domain at the C-terminus. Suppression of PmEEA1 by specific dsRNA in shrimp showed inhibition of YHV replication after 48 h post YHV injection (hpi). On the other hand, shrimp received only NaCl without any dsRNA showed high YHV levels at approximately one hundred thousand times at 24 hpi and 48 hpi. Moreover, silencing of PmEEA1 by specific dsRNA followed by YHV challenge demonstrated a delay in shrimp mortality from 60 hpi to 168 hpi when compared to the control. These results indicated that YHV required PmEEA1 for trafficking within the infected cells, strongly suggesting that PmEEA1 may be a potential target to control and prevent YHV infection in *P. monodon*.

1. Introduction

YHD outbreaks have been reported since 1990 as epizootic events in the eastern, central and southern parts of Thailand, and resulted in shrimp production loss worldwide. A causative agent of this disease is the Yellow head virus (YHV) [1]. YHV is a positive-sense single stranded RNA virus that is classified into genus *Okavirus*, family *Roniviridae*, in the order *Nidovirales* [2,3] and is closely related to gill-associated virus (GAV) from Australia particularly in terms of the nucleotide and amino acid sequences, histological, and morphological observations [4,5]. YHV is approximately 50–60 × 190–200 nm in size, with enveloped bacilliform surrounded by prominent peplomers or spikes [6]. The genome of the virus is approximately 27 kb in length and consists of ORF1a, ORF1b, ORF2 and ORF3. The enveloped glycoprotein, gp116, which is involved in the entry process of YHV into the cells is encoded from ORF3 [7].

Currently, it is believed that the major route of YHV entry into the cells of *Penaeus monodon* is by clathrin-mediated endocytosis via clathrin heavy chain and AP17 protein [8,9]. The clathrin-coated vesicle containing YHV requires a small GTPase Rab5 protein to traffic it from the plasma membrane towards the first sorting station, the early endosome. *P. monodon* Rab5 was identified and showed to colocalize with YHV particles [10,11]. At the early endosomal compartment, Rab5 protein binds to the Rab5 effector protein, the early endosome antigen 1 (EEA1), to promote the fusion between the vesicular and early endosomal membranes, causing the cargo proteins including the virus to be transported inside of the early endosome [12].

Rab5 effector EEA1 works with SNAREs (Soluble NSF (N-Ethylmaleimide-Sensitive Factor) Attachment Protein Receptors) complex which consists of synaptobrevin, syntaxin and two SNAP-25 proteins. This interaction helps to promote the transported vesicle-endosome membrane tethering and fusion [12]. EEA1 location is associated with the early endosome and showed colocalization with Rab5 protein [13]. The EEA1 structure is a long parallel coiled coil homodimer that

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contains C_2H_2 zinc finger (ZF) domain at the N-terminus and FYVE domain at the C-terminus [14]. Interactions between the N-terminal ZF domain of EEA1 with Rab5 protein and the SNAREs complexes facilitate the docking and fusion processes. Furthermore, the fusion step of the vesicle and the early endosome requires phosphatidylinositol-4-5-bisphosphate 3-kinase (PI(3)K) activity whereby the C-terminal FYVE domain of EEA1 can bind directly to the product of PI(3)K, phosphatidylinositol-3-phosphate (PtdIns3P). Taken together, the specific binding of Rab5-GTP bound form, together with PI(3)K activity are needed in the vesicle-early endosome membrane fusion [15–18]. Furthermore, EEA1 has been shown to colocalize with Semliki forest virus (SFV) [19] and hepatitis C virus (HCV) [20]. Our previous study found that YHV utilized clathrin heavy chain, Rab5 and Rab7 proteins to get into the shrimp cells [9,11,21]. It is thus possible that YHV also requires Rab5 effector early endosome antigen 1 (EEA1) protein during infection. Therefore, in this study, the roles of EEA1 during YHV infection and shrimp mortality in *P. monodon* was investigated.

2. Materials and methods

2.1. The black tiger shrimp

Penaeus monodon or the black tiger shrimps were obtained from Choochai farm in Chonburi province and also from the Shrimp Genetic Improvement Center (SGIC, BIOTEC) in Surat Thani province, Thailand. Shrimps were acclimatized for at least 2 days and maintained in large containers with oxygenated sea water at 10–30 ppt salinity before used. They were fed with commercial feed every day. The water was changed every 2 days.

2.2. Cloning of the full-length PmEEA1

Coding region of EEA1 from *Marsupenaeus japonicus* kindly provided by Dr. Hidehiro Kondo, Tokyo University of Marine Science and Technology, Japan was used to design specific primers to amplify a region of PmEEA1. First, total RNA from ovary was extracted using Tri Reagent (Molecular Research Center) and cDNA was synthesized using Improm-II reverse transcriptase (Promega) according to the manufacturer's protocol. The full-length open reading frame of EEA1 was amplified using Q5 DNA polymerase (New England Biolabs) wtih cdEEA1-F and cdEEA1-R primers (Table 1), with an expected size of approximately 3000 bp. The PCR condition was: denaturation at 98 °C for 30 s, then 35 cycles of 98 °C for 10 s, 55 °C for 20 s, and 72 °C for 3 min. The PCR product was purified and cloned into pGEMT-easy vector and sequenced using T7, SP6, EEA1-Fseq, EEA1-Rseq and asEEA1-R2 primers (Table 1) by First Base Co, Ltd. (Malaysia).

2.3. PmEEA1 nucleotide and protein sequence analysis

The nucleotide sequence of PmEEA1 was confirmed and analyzed by BLASTN program using search under nucleotide database. Predictions of molecular weight and isoelectric point (pI) of the protein were performed by Expert Protein Analysis System (www.expasy.org). Conserved motifs of the deduced amino acids were scanned using ScanProsite tool (http://prosite.expasy.org/scanprosite). EEA1 protein sequences from several organisms were obtained from GenBank database. Phylogenetic analysis was performed using Phylogeny.fr with "A la Carte" mode (http://www.phylogeny.fr) based on neighbor-joining method and 1000 replicates of bootstrap with distance methods [22,23].

2.4. Construction of two dsRNAs targeting PmEEA1 mRNA

Recombinant plasmid containing stem-loop of dsRNA of PmEEA1 was constructed in pET-17b (Novagen) vectors. Two plasmids containing dsRNA-Cter and dsRNA-Nter whose targets were close to the stop and start codons of *PmEEA1* gene, respectively, were constructed. Sense-loop regions of the dsRNAs located near stop and start codons were amplified from the first-strand cDNA using specific primers, sEEA1-F1 and lEEA1-R1 for dsRNA-Cter, and nSLEEA1-F1 and nSLEEA1-R1 for dsRNA-Nter (Table 1). In addition, antisense regions were amplified using asEEA1-F2 and asEEA1-R2 for dsRNA-Cter, and nASEEA1-F2 and nASEEA1-R2 for dsRNA-Nter (Table 1). All PCR fragments were gel-purified and verified by restriction enzyme digestion. The purified fragments of the sense-loop and antisense of the Cter region were digested with *Eco*RI and ligated together using T4 DNA ligase (NEB). Then, the sense fragment was digested by *Xba*I whereas the antisense fragment was cut by *Xho*I. The ligated fragment of the sense and antisense of PmEEA1 was cloned into pET-17b to obtain pET-17b-dsRNA-Cter. In addition, the PCR fragment of sense-loop of the Nter region was cloned into pGEM-3Zf+ at *Xba*I and *Kpn*I sites and then the antisense fragment of the Nter region was subsequently cloned into *Kpn*I and *Eco*RI site of this recombinant plasmid. Then, the sense-loop and antisense fragments of the Nter region in pGEM-3Zf+ was cut and subcloned into pET-17b vector to construct recombinant plasmid named pET-17b-dsRNA-Nter. Both of the recombinant plasmids were used for dsRNA production by *in vivo* bacterial expression.

Table 1
Primer sequences used in this study.

Name	Sequence (5'→ 3')	Purposes
cdEEA1-F	ATGTCAGAGAGAGGAATG	Amplification of full-length cDNA coding region of PmEEA1
cdEEA1-R	TCACATTTTTGAAGTGAG	
T7	TAATACGACTCACTATAGGG	Sequencing of PmEEA1 nucleotides
SP6	ATTTAGGTGACACTATAG	
EEA1-Fseq	GCAGGGTTGAAGGAAGAGATG	
EEA1-Rseq	CCCTTAGCAGCTTCTCTCTCC	
PRT	CCGGAATTCAAGCTTCTAGAGGATCCTT TTTTTTTTTTTTT	The first strand cDNA synthesis
sEEA1-F1	*Xba*I GCTCTAGAACAAAATGAAGCCAAGCAGC	Construction of the recombinant plasmid expressing dsRNA-Cter targeting PmEEA1 mRNA
lEEA1-R1	*Eco*RI GGAATTCTAGCAACCTCAGCCTCCAG	
asEEA1-F2	*Xho*I CCGCTCGAGACAAAATGAAGCCAAGCAGC	
asEEA1-R2	*Eco*RI GGAATTCGGCATCAATTTCAAGCTGG	
nSLEEA1-F1	*Xba*I GCTCTAGAGGGCTTCTTGTGTCCAAC	Construction of the recombinant plasmid expressing dsRNA-Nter targeting PmEEA1 mRNA
nSLEEA1-R1	*Kpn*I GGGGTACCACCTTTTCAGCTTGTAGGG	
nASEEA1-F2	*Eco*RI GGAATTCGGGCTTCTTGTGTCCAAC	
nASEEA1-R2	*Kpn*I GGGGTACCCGCAAGGAACTGTTCAAC	
PmEEA1-F	AGCTTGAAATTGATGCCCAGAAG	Detection of PmEEA1 mRNA level
PmEEA1-R	TTGTTGCAGCTGTGGCAATTTAG	
PmActin-F	GACTCGTACGTGGGCGACGAGG	Detection of PmActin mRNA level
PmActin-R1	AGCAGCGGTGGTCATCTCCTGCTC	
qYHV-F	ATCATCAGCTCACAGGCAAGTTCC	Detection of YHV mRNA level by realtime PCR
qYHV-R	GGGTCTAAATGGAGCTGGAAGACC	
YHV(hel)-F	CAAGGACCACCTGGTACCGGTAAGAC	Detection of YHV mRNA level by RT-PCR
YHV(hel)-R	GCGGAAACGACTGACGGCTACATTCAC	
EF-1α-F	GAACTGCTGACCAAGATCGACAGG	Detection of EF-1α mRNA level by realtime PCR
EF-1α-R	GAGCATACTGTTGGAAGGTCTCCA	

2.5. Production of dsRNAs by in vivo bacterial expression

The recombinant plasmids, pET-17b-dsRNA-Cter and –Nter, were transformed into a RNase III mutant HT115 *E. coli* strain. DsRNAs

expression were induced by 0.1 mM IPTG. Then, they were extracted by using ethanol method [24,25]. The quality of the dsRNAs were characterized by ribonuclease digestion assay using RNase A and RNase III digestions. Concentration of dsRNA was estimated visually using agarose gel electrophoresis by comparing the target band intensity to that of the 100 bp DNA marker.

2.6. Yellow head virus (YHV) preparation

YHV stock was prepared using the hemolymph of YHV-infected moribund black tiger shrimp. The hemolymph was drawn and mixed with anticoagulant (AC-1) solution (27 mM Sodium citrate, 34.33 mM NaCl, 104.5 mM Glucose, 198.17 mM EDTA, pH 7.0), at ratio 1:1, and centrifuged at 20,000 ×g for 20 min at 4 °C to remove hemocyte debris. YHV was separated from the hemolymph by ultracentrifugation at 100,000 ×g for 1 h. YHV contained pellet was then dissolved with 150 mM NaCl and stored at −80 °C until used. The viral titer that caused 100% mortality within 3–4 days was used in this study. For confirmation of YHV infection, total RNA was extracted from the YHV-infected hemolymph that used to prepare the YHV stock and RT-PCR was performed to detect the level of YHV. In addition, the pellet obtained after ultracentrifugation of the hemolymph was dissolved with 150 mM NaCl and injected into shrimp. After 3–4 days of YHV injection, YHV levels can be detected in all dead shrimp, suggesting that the pellet contained YHV.

2.7. Injection of P. monodon with dsRNAs

The efficiency of dsRNA-Cter and dsRNA-Nter were examined by injection of dsRNAs into shrimp hemocoel. Shrimps were injected with 2.5 μg. g^{-1} shrimp of dsRNA-Cter, -Nter, C + Nter or unrelated dsRNA-GFP dissolved in 150 mM NaCl. Injection of 150 mM NaCl was used as control. After 24 h post dsRNA injection, gills of the individual shrimp were collected for total RNA extraction. Suppression effect of dsRNAs was analyzed by reverse-transcription PCR (RT-PCR) to determine PmEEA1 mRNA level.

2.8. Study of the knock down effect by dsRNAs upon YHV infection and shrimp mortality assay

In order to investigate the silencing effect of PmEEA1 upon YHV infection, shrimp were injected with 2.5 μg. g^{-1} shrimp of the combination of dsRNA-C and dsRNA-Nter (1.25 μg. g^{-1} shrimp each) or unrelated dsRNA-GFP, followed by YHV challenged after 24 h post dsRNA injection. For each group, 5 shrimp were used. Twenty-four and 48 h post YHV injection (hpi), gills of individual shrimp were collected and analyzed for PmEEA1 and YHV levels. To determine whether YHV levels could be detected at 60, 72, 84, and 96 hpi, gills from the living shrimp were collected. Moreover, shrimp mortality was also recorded every 12 h post YHV injection (hpi) for 144 hpi. Three replicates of the experiment were performed. Gills from the dead shrimp were also collected to determine YHV and PmEEA1 levels.

2.9. Total RNA extraction and RT-PCR analysis

Total RNA from gill tissue was isolated using Tri Reagent® (Molecular Research Center) following the manufacturer's protocol. Two microgram of the total RNA was used to produce first-strand cDNA using Improm-II™ reverse transcriptase (Promega) with PRT primer (Table 1). PCR products were amplified by using Taq DNA polymerase (New England Biolabs). Multiplex PCR of PmEEA1 (PmEEA1-F and PmEEA1-R1 primers, and PmActin (PmActin-F and PmActin-R1) (Table 1) were amplified under this condition: 95 °C for 5 min, then 30 cycles of 95 °C for 30 s, 61 °C for 30 s, and 68 °C for 45 s, followed by 68 °C for 7 min. YHV mRNA level was amplified using primers, YHV (hel)-F and YHV(hel)-R (Table 1). The multiplex PCR condition for YHV and PmActin was performed according to this condition: 95 °C for 5 min; 25 cycles of 95 °C for 30 s, 55 °C for 30 s, and 72 °C for 45 s; followed by 72 °C for 7 min. The PCR products were analyzed on 1.5% agarose gel. The intensity of each band was quantitated using Scion Image program. Relative mRNA transcript levels of PmEEA1 was normalized with PmActin intensity and recorded as arbitrary unit.

2.10. Detection of YHV mRNA levels by quantitative real time PCR (qPCR)

For qPCR analysis, cDNA template was diluted at 1:4 and mixed with qPCR reaction using KAPA™ SYBR® Fast qPCR master mix (2X) ABI Prism™ (KAPA Biosystems) following manufacturer's protocol. The qPCR was analyzed using Mastercycler RealPlex4 (Eppendorf). qYHV-F and qYHV-R primers (Table 1) were used to amplify YHV mRNA. For internal control, EF1-α, was used (EF1α-F and EF1α-R primers) (Table 1). The qPCR condition was as followed: 95 °C for 3 min; 40 cycles of 95 °C for 5 s, 60 °C for 30 s. The cycle threshold (C_t) values of YHV and EF1-α were compared and calculated using $2^{-\Delta\Delta CT}$ method [26].

2.11. Statistical analysis

The relative transcription levels of PmEEA1 and YHV that were normalized with PmActin or EF1α were presented as mean ± SD. In addition, cumulative percent shrimp mortality was plotted as mean ± SD. A significant difference of the experiment groups was examined by analysis of variance (ANOVA). A probability *(P)* value less than 0.05 was accepted as significant difference.

3. Results

3.1. Cloning and sequence analysis of PmEEA1 coding region

The full-length sequence of PmEEA1 is 3000 bp, including the stop codon (TGA), thus encoded a protein of 999 amino acids (GenBank accession number MK775551; Supplementary Fig. 1). The predicted molecular weight and pI of PmEEA1 protein are 112.6 kDa and 5.04, respectively. Sequence analysis revealed that PmEEA1 protein contains conserved domain of EEA1 which are Zinc finger C_2H_2 type domain at the amino acids 43–64 and 73–94, and the FYVE domain at the amino acids 938–996. These domains are conserved in both invertebrates and vertebrates including CeEEA1, DrEEA1, HsEEA1, LaEEA1, LpEEA1, and RnEEA1 (Fig. 1 and Table 2). Phylogenetic tree analysis revealed that PmEEA1 was closely related to the invertebrate group (Fig. 2).

3.2. Silencing of PmEEA1 mRNA levels by two dsRNAs

Two dsRNAs, dsRNA-Cter and dsRNA-Nter, targeting the PmEEA1 mRNA and dsRNA-GFP that used as unrelated dsRNA control could be cleaved by RNase III but not by RNase A, suggesting that they were of good quality. The expected sizes of these dsRNAs were approximately 400 bp (Supplementary Fig. 2). The effectiveness of dsRNA-Cter and dsRNA-Nter on silencing of PmEEA1 mRNA were investigated. Shrimp were injected with dsRNAs targeting PmEEA1 or unrelated dsRNA-GFP for 24 h. NaCl injection was employed as an experimental control. The result found that shrimp received either dsRNA-Cter or dsRNA-Nter showed a significant reduction of PmEEEA1 mRNA levels at 81% and 76%, respectively. Moreover, in shrimp injected with dsRNA-Cter and dsRNA-Nter (dsRNA-C + Nter), the level of PmEEA1 mRNA could hardly be detected (91% suppression). Interestingly, PmEEA1 mRNA level could be silenced at about 33% in dsRNA-GFP injected shrimp (Fig. 3).

3.3. Knockdown effect of PmEEA1 reduced YHV replication levels

The role of PmEEA1 on YHV level was next investigated during YHV replication. The combination dsRNA-C + Nter was used to silence

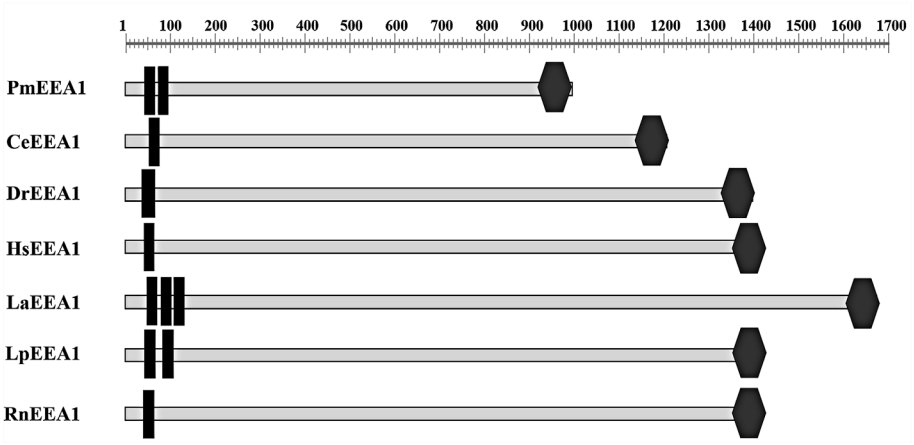

Fig. 1. Schematic of the predicted protein domain of the early endosome antigen 1 (EEA1) from *P. monodon* and other species. The size of EEA1 protein varied among organisms but all contain the signature motifs of Zinc finger C_2H_2 type domain (▮) at the N-terminus and the FYVE domain (⬮) at the C-terminus. *Penaeus monodon* EEA1 (PmEEA1) possess 999 amino acids which compose of two domains of Zinc finger C_2H_2 signature motifs at the position aa 43–64 and aa 73–94 and one FYVE domain at aa 938–996. EEA1 protein from several species including *Penaeus monodon* (PmEEA1; accession number MK_775551), *Caenorhabditis elegans* (CeEEA1; accession number NP_001024127.1), *Danio rerio* (DrEEA1; accession number XP_003200485.1), *Homo sapiens* (HsEEA1; accession number NP_003557.2), *Lingula anatine* (LaEEA1; accession number XP_013419201.1), *Limulus Polyphemus* (LpEEA1; accession number XP_013777228.1), *and Rattus norvegicus* (RnEEA1; accession number NP_001101556.1) were used for domain analysis.

Table 2
Early endosome antigen 1 (EEA1) proteins used for multiple sequence alignment and phylogenetic analysis.

Abbreviations	Species	Accession number
AcEEA1	*Aplysia californica*	XP_005095892.2
BaEEA1	*Balaenoptera acutorostrata scammoni*	XP_007166165.1
BgEEA1	*Biomphalaria glabrata*	XP_013093515.1
CeEEA1	*Caenorhabditis elegans*	NP_001024127.1
DrEEA1	*Danio rerio*	XP_003200485.1
FhEEA1	*Fundulus heteroclitus*	XP_012731526.1
HsEEA1	*Homo sapiens*	NP_003557.2
LaEEA1	*Lingula anatina*	XP_013419201.1
LpEEA1	*Limulus polyphemus*	XP_013777228.1
NgEEA1	*Nannospalax galili*	XP_008822059.1
ObEEA1	*Octopus bimaculoides*	XP_014782058.1
PmEEA1	*Penaeus monodon*	MK_775551
TcEEA1	*Tupaia chinensis*	ELW_61492.1
TrEEA1	*Takifugu rubripes*	XP_003967354.1
RnEEA1	*Rattus norvegicus*	NP_001101556.1
XtEEA1	*Xenopus tropicalis*	XP_002935361.1

PmEEA1 mRNA. Shrimp received the dsRNA after 24 h were challenged with YHV. After 24 and 48 h post YHV injection (hpi), the level of PmEEA1 and YHV mRNAs were determined from the gills. Injected shrimp with dsRNA-C + Nter following YHV challenge showed significant reduction of PmEEA1 at 24 and 48 hpi about 82% and 78% when compared to NaCl→YHV control group, respectively. Moreover, shrimp injected with unrelated dsRNA-GFP → YHV showed no difference in PmEEA1 mRNA levels at both 24 and 48 hpi when compared to the control (Fig. 4A).

The level of YHV mRNAs were determined by real time PCR and expressed as mean ± SD of the fold change of YHV mRNA levels compared to the NaCl injected group at 24 hpi. At 24 hpi, the fold change of YHV mRNA level in the PmEEA1 knock down group injected with dsRNA-C + Nter showed no significant difference when compared to the control groups injected with NaCl or dsRNA-GFP. At 48 hpi, the fold change of the YHV level increased more than 100,000 and 25,000 times for NaCl- and dsRNA-GFP- injected groups, respectively. However, the fold change of the YHV level at 48 hpi (1.28 ± 1.31 fold) remained at very low level and showed no significant difference when compared at 24 hpi (1.16 ± 0.53 fold) of the PmEEA1 knock down group (Fig. 4B). In addition, the expression of YHV mRNA levels were detected in the gills collected from the living shrimp between 48 and 96 hpi. The results showed that knockdown of PmEEA1 resulted in complete inhibition of YHV mRNA levels at 48 hpi. The expression of YHV mRNA levels can be detected at very low levels at 60 hpi and increased from 72 to 96 hpi in living shrimp. High levels of YHV mRNA could be detected in both control groups between 48 and 72 hpi. All shrimp in the control groups died at 72 hpi. These results suggested that knockdown of PmEEA1 restricted the YHV in the early compartment of the endosome. YHV levels could be detected but not high enough to cause shrimp dead between 60 and 96 hpi. Therefore, shrimp mortality was delayed in the dsRNA-C + Nter injected group (Supplementary Fig. 4).

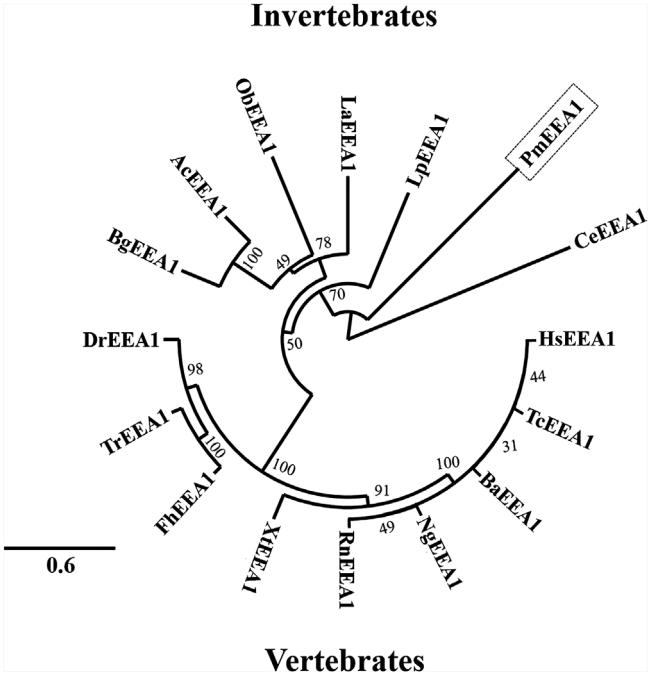

Fig. 2. Phylogenetic analysis of EEA1 protein. The phylogenetic tree was reconstructed using the Neighbor-joining method based on the full amino acid sequences of EEA1 with bootstrap value of 1000. Organisms used for the tree reconstruction were *Aplysia californica* (AcEEA1), *Balaenoptera acutorostrata scammoni* (BaEEA1), *Biomphalaria glabrata* (BgEEA1), *Caenorhabditis elegans* (CeEEA1), *Danio rerio* (DrEEA1), *Fundulus heteroclitus* (FhEEA1), *Homo sapiens* (HsEEA1), *Lingula anatine* (LaEEA1), *Limulus Polyphemus* (LpEEA1), *Nannospalax galili* (NgEEA1), *Octopus bimaculoides* (ObEEA1), *Penaeus monodon* (PmEEA1), *Tupaia chinensis* (TcEEA1), *Takifugu rubripes* (TrEEA1), *Rattus norvegicus* (RnEEA1), *and Xenopus tropicalis* (XtEEA1).

3.4. Silencing of PmEEA1in YHV-infected shrimp decreased shrimp mortality

The shrimp mortality was further observed to investigate the involvement of PmEEA1 on YHV infection. There were 10–15 shrimp per group and the experiments were performed three times. Shrimp

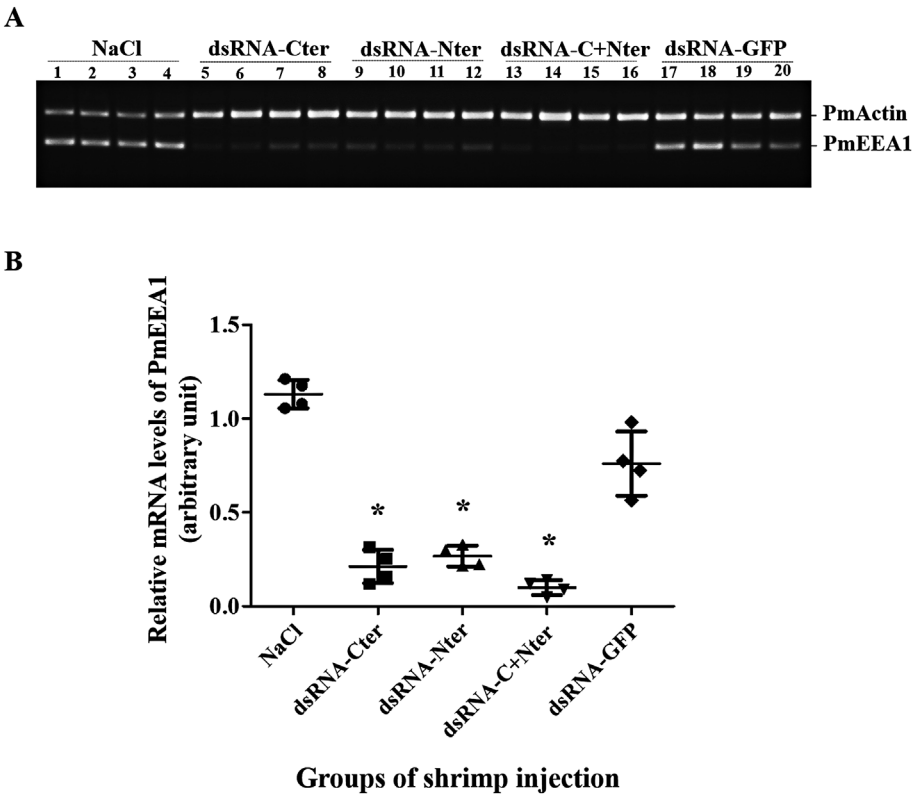

Fig. 3. Effectiveness of two types of dsRNAs targeting PmEEA1 mRNA. A representative gel of RT-PCR products was presented as expression levels of PmEEA1 and PmActin of shrimp injected with NaCl control (lanes 1–4), each dsRNA targeting PmEEA1 which are dsRNA-Cter (lanes 5–8) and dsRNA-Nter (lanes 9–12), the combination between dsRNA-Cter and -Nter (dsRNA-C + Nter) (lanes 13–16) and unrelated dsRNA-GFP (lanes 17–20) at 2.5 μg g^{-1} shrimp at 24 h post dsRNA injection (n = 4) (A). The relative mRNA expression levels of PmEEA1 normalized with PmActin are shown as mean ± SD (n = 4) (B). (*) Statistically significant difference between dsRNA injected shrimp as compared to NaCl injected group ($P < 0.05$).

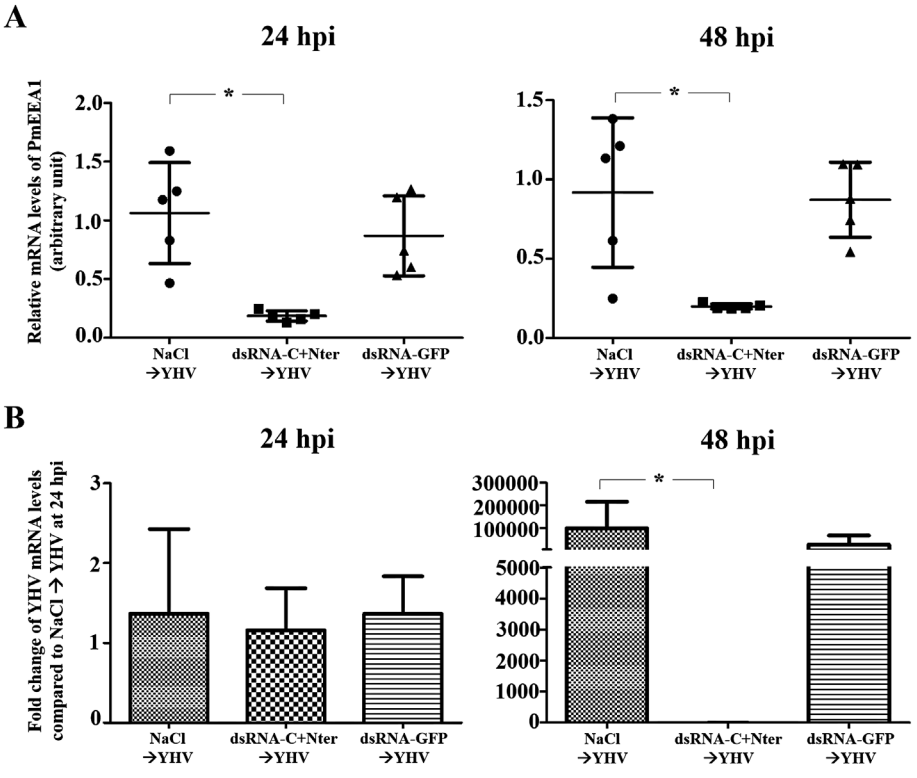

Fig. 4. Effect of PmEEA1 depletion during YHV infection. Shrimp were injected with NaCl alone, dsRNA-C + Nter, and dsRNA-GFP at 2.5 μg g^{-1} shrimp for 24 h followed by YHV challenge and detection at 24 and 48 hpi from gill tissues (n = 5). The relative mRNA levels of PmEEA1 normalized with PmActin are presented as dot graphs of arbitrary unit of mean ± SD (A). Bar graphs represent the quantitative RT-PCR of fold change of YHV mRNA levels compared to NaCl → YHV at 24 hpi. The result was demonstrated as mean ± SD (B). Asterisks indicate significant differences between experimental group and the control group ($P < 0.05$).

received dsRNA-C + Nter followed by YHV challenge showed a significant delay in shrimp mortality as observed in 60 hpi to 168 hpi when compared to NaCl → YHV and unrelated dsRNA-GFP → YHV groups (P value = 0.05). At 60 hpi, no shrimp in dsRNA-C + Nter → YHV group died whereas shrimp in the control groups of NaCl → YHV and unrelated dsRNA-GFP → YHV had 80% and 50% shrimp mortality, respectively. In addition, at 84 hpi, shrimp in both control groups showed 100% mortality while the dsRNA-C + Nter → YHV group demonstrated only 40% mortality (Fig. 5A). In addition, expression of YHV can be detected in all dead shrimp (Fig. 5B).

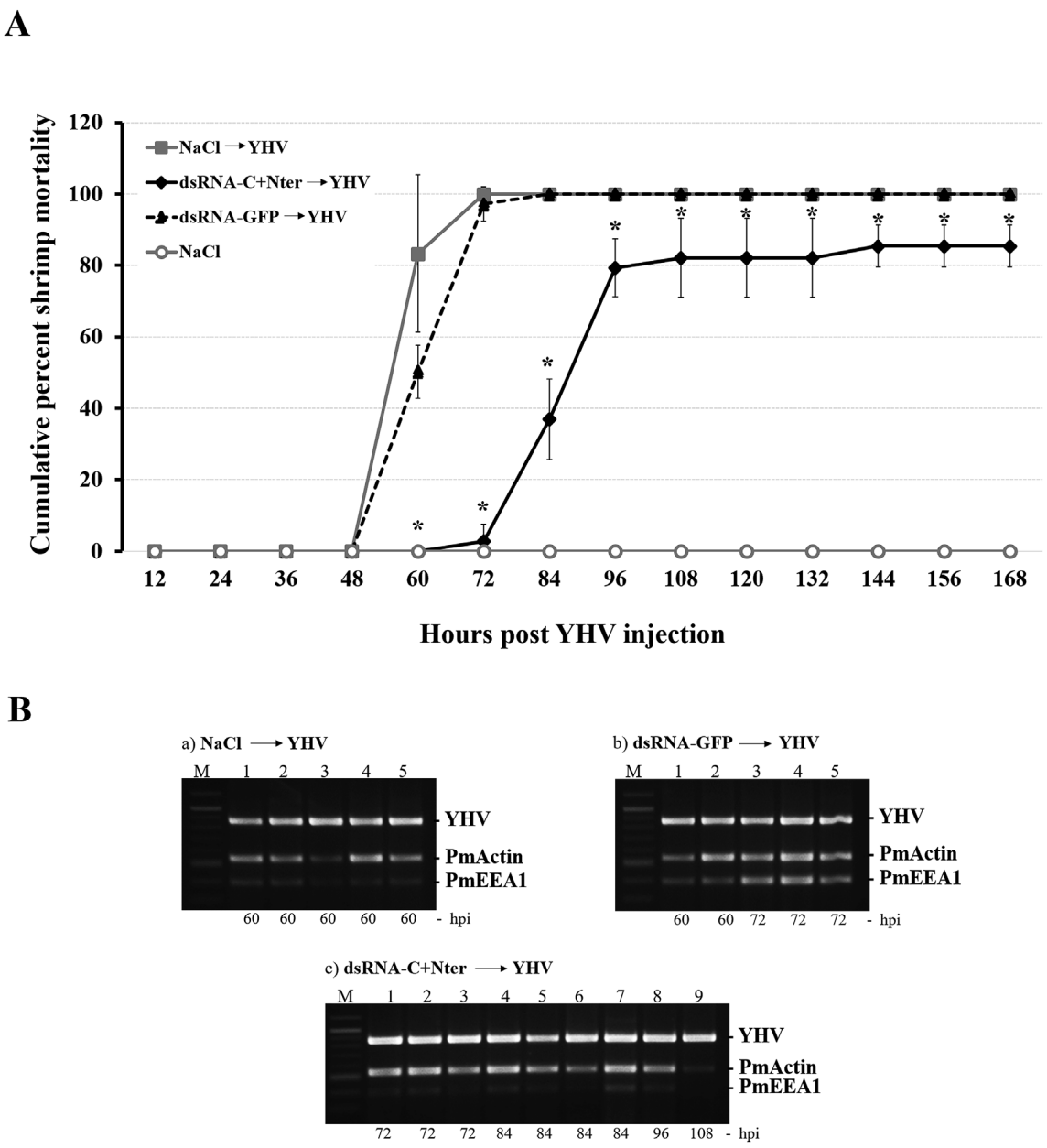

Fig. 5. Silencing of PmEEA1 by the combination dsRNA-C + Nter on YHV infection delayed shrimp mortality. (A) The cumulative percent mortality of shrimp injected with NaCl, dsRNA targeting PmEEA1 (dsRNA-C + Nter), or unrelated dsRNA-GFP at 2.5 μg g^{-1} shrimp followed by YHV injection were observed. Dead shrimp were recorded every 12 hpi. The graph was plotted as mean ± SD from three replicates per group (n = 12–15 shrimp per group). Asterisks represents statistically significant difference between NaCl → YHV and dsRNA-C + Nter → YHV group ($P < 0.05$). (B) A representative gel of RT-PCR products of YHV and PmEEA1 mRNA levels from gill of the dead shrimp in the 3 groups. PmActin was used as an internal control. PmAcin expression level is low in the dead shrimp samples that showed high levels of YHV expression. This result was also. demonstrated in the previous studies [9,15]. The number on the bottom of each lane represents the time (hours of post YHV challenge, hpi) that the shrimp die.

4. Discussion

Clathrin-mediated endocytosis is the major route of YHV penetration inside the shrimp host cell [8,9]. After internalization, YHV requires a small GTPase Rab5 protein to regulate the transportation from plasma membrane to early endosome. Colocalization between YHV and *Penaeus monodon* Rab5 (PmRab5) was observed in the hemocytes from 10 min to 3 h post YHV infection [11]. Rab5 proteins on vesicle membrane are tethered with Rab5 effector early endosome antigen 1 (EEA1) that appeared on the surface of the early endosome to promote the fusion of the two membrane [12,17,18]. Previously under transmission electron microscopy, it was found that YHV particles are inside the early endosomes of shrimp cells [27]. PmEEA1 protein contains 999 amino acids, while other species including CeEEA1, DrEEA1, HsEEA1, LaEEA1, LpEEA1, and RnEEA1 have more than 1200 amino acids (Fig. 1). Although the size of the protein from different species present a wide range of sizes, but they all showed signature characteristics of EEA1, two Zinc finger C_2H_2 domains and FYVE domain of N- and C-terminal sites [14]. Moreover, the function of EEA1 during YHV infection in *P. monodon* was examined. Two dsRNAs targeting N- and C-terminus of PmEEA1 were produced and used to knockdown PmEEA1 transcripts. A combination of two dsRNAs were used to improve the inhibition of YHV infection in shrimp [28]. Since, dsRNA targeting C-terminus of PmEEA1 region (the first construction) was located near 3′ end of the open reading frame (dsRNA-Cter). This dsRNA was first injection into shrimp resulting in inhibition of PmEEA1 mRNA levels only

50–80% compared to the control (data not shown). Local protein factors involving in termination of protein synthesis may cause the positional effect that interrupts the accessibility of RISC-siRNA complex to the local target [29]. After obtaining the full-length coding region of PmEEA1, another dsRNA targeting PmEEA1 mRNA was constructed. This dsRNA was located on near the 5′ end of the open reading frame (dsRNA-Nter). The result demonstrated that injection of the combined two types of dsRNA targeting PmEEA1 could silence the mRNA levels more than using only one type of the dsRNA (Fig. 3). This is probably due to a variety of siRNA population generated from the combined two dsRNAs. It could increase the efficiency of siRNA to bind to the mRNA target. The siRNA could bind with the secondary structure of mRNA as stem and loop structure better than the hairpin structure [30,31].

After testing the effectiveness of the dsRNA, the role of PmEEA1 during YHV infection was investigated. Shrimp that were injected with NaCl → YHV at 48 hpi showed increased YHV replication at about 100,000 times when compared to 24 hpi. On the other hand, injected shrimp with dsRNA targeting PmEEA1 (using the combination between dsRNA-Cter and –Nter (dsRNA-C + Nter)) followed by YHV challenge demonstrated no significant difference of YHV levels at 24 and 48 hpi (Fig. 4B). In addition, dsRNA-C + Nter → YHV group showed a delay in shrimp mortality when compared to the control NaCl → YHV group (Fig. 5). Injection of dsRNA targeting PmEEA1 alone has no effect on shrimp mortality (Supplementary Fig. 3). Shrimp started dying after receiving dsRNA-C + Nter followed by YHV challenge at 84 to 96 hpi (about 108–120 h post dsRNA injection) is probably caused by the loss of the effectiveness of its dsRNA and the increasing number of virus progenies. An increasing levels of YHV expression could be detected between 60 and 96 hpi in gills collected from the living shrimp. However, it did not cause shrimp die (Supplementary Fig. 4). High levels of YHV expression could be detected in all dead shrimp samples (Fig. 5B). Longevity of dsRNA inside the shrimp cells is about five days (120 h) after dsRNA injection and YHV challenge [32]. Therefore, to improve the effectiveness of dsRNA-C + Nter targeting PmEEA1 during YHV infection, multiple injections of dsRNA every 72 h may be performed in order to reduce shrimp mortality. Based on this study, silencing of PmEEA1 which is not lethal is possibly used as an alternative approach to prevent YHV replication. Taken together, this study demonstrated the crucial role of PmEEA1 during YHV transportation inside the cells.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.fsi.2019.10.054.

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Identification and expression of white spot syndrome virus-encoded microRNAs in infected *Penaeus monodon*

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A B S T R A C T

White spot syndrome virus (WSSV) is the most devastating DNA virus that causes shrimp mortality worldwide. To better understand WSSV and *Penaeus monodon* interactions, WSSV-encoded microRNAs (wsv-miRs) were identified by small RNA cloning and next-generation sequencing. Ten wsv-miRs were identified and their expressions can be detected in WSSV-infected tissues only. These wsv-miRs and their flanking sequences can spontaneously form hairpin structure as predicted by Mfold. The expression profiles of 6 wsv-miRs increased dependent on time course of WSSV infection and slightly decreased after 48 hours WSSV challenge. The highest expression was wsv-miR-9 followed by miR-13 and -15. Computational prediction of the candidate targets of wsv-miRs revealed possible functions of wsv-miRs in the controlling of apoptosis, transcription and signaling. This finding provided insights into WSSV-host interaction.

1. Introduction

White spot syndrome virus (WSSV) is a serious causative agent of white spot disease in cultivated shrimp worldwide. Infection of WSSV leads to 100% shrimp mortality within a few days. In addition, this virus showed the highest infection rate in Thailand (Khawsak et al., 2008). WSSV is classified in the *Whispovirus* of the *Nimaviridae* family (Jehle et al., 2006). It has a double-stranded DNA genome of approximately 300 kb, is packed with the nucleocapsid proteins and is surrounded by Envelope proteins such as VP28, VP26 and VP19. Currently, genome sequences of 4 WSSV isolates from the pandemic areas were sequenced including China (WSSV-Ch: AF332093), Taiwan (WSSV-Tw, AF440570), Thailand (WSSV-Th: AF369029) and Korea (WSSV-Kr: JX515788) (Chai et al., 2013). Several strategies are used to control WSSV infection such as environmental control, herbal treatment, recombinant vaccination and RNA interference (RNAi) approach (Sánchez-Paz, 2010). However, effective method to prevent and cure WSSV infection remains limited due to the lack of understanding about WSSV pathogenesis and viral-host interaction. Insights in these areas will drive the therapeutic strategy.

Invertebrates lack adaptive immunity nevertheless they adapt to use the RNAi pathway as a specific immunity. RNAi mechanism plays crucial roles in the regulation of gene expression and antiviral defense by the use of small interference RNA (siRNA) or micro RNA (miRNA). MiRNA is a non-coding single-stranded RNA (ssRNA) of about ~22 nucleotides (nt) in length, which function as regulatory small RNA in the RNAi mechanism. MiRNA is also believed to be involved in post-transcriptional gene regulation in many eukaryotic processes such as development, cell differentiation, apoptosis, and immune response (Dong et al., 2013). The miRNA is transcribed from the genome into a non-perfect matched primary-miRNA (pri-miRNA) and is then cleaved as a precursor-miRNA (pre-miRNA) by Drosha and its cofactor, Pasha (Denli et al., 2004; Gregory et al., 2004). The pre-miRNA is exported to the cytoplasm and is cleaved by Dicer and its partner, Loqs, to become a ~22 bp miRNA duplex (Park et al., 2011; Saito et al., 2005). The miRNA is preferentially selected based on the 5′-end thermostability associated with an argonaute protein (AGO) in an RNA-induced silencing complex (RISC) to become a mature miRNA (Khvorova et al., 2003; Schwarz et al., 2003). For siRNA processing, the perfectly matched dsRNA is the substrate and is directly cleaved by Dicer into a siRNA duplex. The mature miRNA guides the RISC to target mRNA by using complementary base-pairing with the 3′-untranslated region (UTR) of mRNA. Any imperfect match with their target (Pasquinelli, 2012) will result in translational inhibition; whereas, perfectly matched causes mRNA degradation at post-transcriptional levels (Bartel, 2004; Kim et al., 2009).

Recently, a number of miRNAs are found to be encoded by DNA viruses (Grundhoff and Sullivan, 2011) and at least 530 viral-encoded miRNAs are deposited in the miRBase 22 (Kozomara and Griffiths-Jones, 2014) (www.mirbase.org). Virus that can encode miRNA usually has a DNA genome, can invade into the nucleus of the host cell, has long term or persistent infection, and can switch between the lytic and latent

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Table 1
Sequence of primers used in this study.

Primers	Sequence 5′→3′	Purposes
VP28-F	CCGCTCGAGACTCTTTCGGTCGTGTCGGCC	PCR detection of WSSV *vp28*
VP28-R	GGCACCATCTGCATACCAGTG	
YHV-F	CAAGGACCACCTGGTACCGGTAAGAC	PCR detection of YHV
YHV-R	GCGGAAACGACTGACGGCTACATTCAC	
PstDNV-F[a]	TCCAACACTTAGTCAAAACCAA	PCR detection of PstDNV
PstDNV-R[a]	TGTCTGCTACGATGATTATCCA	
EF1α-F	GAACTGCTGACCAAGATCGACAGG	PCR of shrimp's *EF1α*
EF1α-R	GAGCATACTGTTGGAAGGTCTCCA	
PRT	CCGGAATTCAAGCTTCTAGAGGATCCTTTTTTTTTTTTTTTT	Reverse transcription (RT)
SRT-4-5p	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACcatggt	Stem-loop RT of wsv-miR-4-5p
SRT-4-3p	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACttcagg	Stem-loop RT of wsv-miR-4-3p
SRT-5	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACagcaca	Stem-loop RT of wsv-miR-5
SRT-6	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACttagcc	Stem-loop RT of wsv-miR-6
SRT-7-5p	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACagaata	Stem-loop RT of wsv-miR-7-5p
SRT-7-3p	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACgacagc	Stem-loop RT of wsv-miR-7-3p
SRT-8	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACttggcc	Stem-loop RT of wsv-miR-8
SRT-9	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACaggaag	Stem-loop RT of wsv-miR-9
SRT-10	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACtttctt	Stem-loop RT of wsv-miR-10
SRT-11	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACccagcc	Stem-loop RT of wsv-miR-11
SRT-12	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACcgcatc	Stem-loop RT of wsv-miR-12
SRT-13	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACaatgtg	Stem-loop RT of wsv-miR-13
SRT-14	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACgcacga	Stem-loop RT of wsv-miR-14
SRT-15	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACtctcca	Stem-loop RT of wsv-miR-15
SRT-let7	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACaacta	Stem-loop RT of shrimp's let7
SRT-U6	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACaaaatgtggaac	Stem-loop RT of shrimp's U6
SF- 4-5p	CGCCGCCAGGGAAGAAATAG	PCR of wsv-miR-4-5p
SF- 4-3p	CGCCGCTGGAGCATATGTATTC	PCR of wsv-miR-4-3p
SF- 5	GCGTTACCCTTTTCGGTTGGC	PCR of wsv-miR-5
SF-6	CGCCGGTTCGGTTCTTCAAAGA	PCR of wsv-miR-6
SF-7-5p	GCGCTCAGTAGTGTTGTTGCC	PCR of wsv-miR-7-5p
SF-7-3p	CGCCGGCCGCGAAATAATAATAAT	PCR of wsv-miR-7-3p
SF- 8	GATTATTGGACCGCTGGGTCG	PCR of wsv-miR-8
SF- 9	GCCGCAGCCTAAAAATCTCCC	PCR of wsv-miR-9
SF-10	GCCGATCTTCTGGGTTTGGCT	PCR of wsv-miR-10
SF-11	TTATGACTTGGTGCGGCGGG	PCR of wsv-miR-11
SF-12	GCGCCGCTTTTTCCAACACAGAA	PCR of wsv-miR-12
SF-13	GCCGCCAGTCATATCCGTGAT	PCR of wsv-miR-13
SF-14	GCCGTCCAATGTCTTGAAGCTG	PCR of wsv-miR-14
SF-15	CGCCGCAATATTGTCACCGATGT	PCR of wsv-miR-15
SF-let7	GCCGCtGAGGTAGTAGGTTGTA	PCR of shrimp's let7
SF-U6	ACAGAGAAGATTAGCATGGCCCCT	PCR of shrimp's U6
SR	GTGCAGGGTCCGAGGTATT	PCR of every wsv-miR, let-7 and U6

The small characters are nucleotides, specifically designed for each wsv-miRNA.
SRT primers are used for stem-loop reverse transcription of each wsv-miRNA.
SF primers are employed for PCR detection of each wsv-miRNA.
SR primer is a universal primer used for PCR detection of all wsv-miRNAs and shrimp's let-7 and U6.
[a] PstDNV-F and PstDNV-R primers correspond to IHHNV309-F and IHHNV309-R in Kathy et al., 2007.

stages of viral life cycle. Upon viral infection, host cells will encode miRNAs that function in the immune system to protect against the invading viruses. On the other hand, the virus can encode its own miRNAs by using host miRNA machineries and uses them to escape the host defense and also to remodel host gene expression to support the viral life cycle. For example, Epstein-Barr virus (EBV) encodes miR-BART5 which targeted PUMA mRNA to prevent the infected cell from undergoing apoptosis and also to promote latent infection (Choy et al., 2008). Simian virus 40 (SV40) encodes miR-S1 from the late transcripts, which cleaved an antisense transcript that encoded T-antigen, which resulted in infected cells becoming less susceptible to cytotoxic T-cell mediated lysis (Sullivan et al., 2005). Additionally, some viruses also encode miRNAs to control the viral genes itself. For examples, Herpes Simplex Virus 1 and 2 express miR-H2-3p from latency associated transcript (LAT) from its own antisense direction of an immediate early protein, ICP0. MiR-H2-3p is targeted to the viral coding gene and resulted in the switching of virus to the latency stage (Jurak et al., 2010; Tang et al., 2009; Umbach et al., 2008). An insect virus, *Heliothis virescens* ascovirus (HvAC), encodes miR-1 from the major capsid protein gene (MCP) which directly degrades its own DNA polymerase I transcript and thus, regulates its replication (Hussain et al., 2008).

To gain more insights into WSSV pathogenesis and viral-host interaction, this study aimed to identify the WSSV-encoded miRNAs from WSSV-Th during the late stage of viral infection. The results identified 14 candidate WSSV-encoded miRNAs by using next generation Illumina Solexa sequencing. Six of the candidate miRNAs were specifically expressed in viral-infected cells and its expression were up-regulated. In silico analysis identified potential cellular- and viral-gene targets of these candidate WSSV-miRNAs.

2. Materials and methods

2.1. Shrimp culture and WSSV stock

Healthy *P. monodon*, size about 10 g, were purchased from commercial shrimp farms in Nakhon Pathom, Thailand. Shrimps were reared in tanks containing 20 l of continuously aerated saltwater at 10 ppt salinity and maintained at temperature of 28 °C. They were acclimatized a day before WSSV injection and fed with commercial feed every day.

WSSV-Th isolate stock was kindly provided by Dr. Sritunyalucksana, BIOTEC. The viral titer (10^6 virions μl^{-1}) was determined by real-time

PCR (Sritunyalucksana et al., 2006) and maintained at −80 °C until used. For WSSV lysate, it was prepared according to the method of Natividad et al. (2007) (Natividad et al., 2007). Briefly, WSSV-infected gill tissue was homogenized in 10% *w/v* TNE buffer (50 mM Tris, 100 mM NaCl, 1 mM EDTA, pH 7.4) and the tissue debris was removed by centrifugation at 3000 ×*g* for 15 min at 4 °C. The supernatant was filtered through a 0.45 μm membrane (Millipore) and stored at −80 °C until use.

2.2. Sample preparation and RNA extraction

WSSV-infected or uninfected shrimp (control) were intramuscularly injected with 50 μl of diluted purified-WSSV (~10^6 copies) or 150 mM NaCl (control) using tuberculin syringe needle, respectively. After 48 hours post challenge, gill tissues were collected and total RNAs were extracted by using TRIzol Reagent® (Molecular Research Center, Inc.) according to the manufacture's protocol. The quantity and integrity of the total RNAs were determined by Nanodrop spectrophotometer (Thermo Scientific, Wilmington, DE) and RNA agarose gel electrophoresis in Tris-EDTA-acetate (TAE) buffer, respectively.

2.3. Detection of WSSV infection

WSSV infection was confirmed by using reverse transcription PCR (RT-PCR) to amplify viral protein 28 mRNA (*vp28*) (Attasart et al., 2009). Two micrograms of total RNAs were used as templates for complementary DNA (cDNA) synthesis by using reverse transcriptase (ImProm-II™ Reverse Transcriptase, Promega) and PRT primer (Table 1). Elongation factor 1-alpha (EF1α) was used as an internal control gene to normalize for the relative expression of *vp28* mRNA. Stable expression of EF1α can be observed under WSSV (Dhar et al., 2009), YHV and PstDNV infection. Condition of PCR was as followed: 94 °C for 5 min followed by 25 cycles of 94 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s and continued with 72 °C for 7 min to complete the extension. The PCR products of WSSV-VP28 (407 bp) and *EF1α* (140 bp) were separated on 2% agarose gel electrophoresis.

2.4. Construction and sequencing of small RNA libraries

Total RNAs from WSSV-infected and WSSV-free tissues were submitted to Beijing Genome Institute (BGI), China, to construct the small RNAs libraries. Briefly, small RNAs ranged from 18 to 30 nt were purified by polyacrylamide gel electrophoresis before ligation with the 3′ and 5′ adaptors for Solexa sequencing. RT-PCR approach was used to convert the ligation products to DNA and amplified it. The amplicons were used as templates for cluster generation and directly sequenced by Illumina's Solexa sequencer.

2.5. Bioinformatics analysis of small RNAs

Raw small RNAs sequencing data were cleaned by eliminating fragments with sizes shorter than 18 nt, low quality reads, sequences with poly-A and adaptor contamination. Total cleaned reads were blasted against microRNA database (miRbase version 17) to identify the conserved miRNA that matched to mature RNAs in other species. The unannotated sequences were aligned using Rfam 10.1 and GenBank database to get rid of other small RNAs (rRNA, tRNA, snRNAs, and repeat associated RNAs). To identify novel candidate miRNAs derived from shrimp or WSSV, the remaining sequences were blasted against Express Sequence Tag (EST) database of *P. monodon* from the Marine Genomics Project (www.marinegenomics.org) and WSSV genome Thai isolate from GenBank database (accession no.AF369029), respectively. Sequences that perfectly matched to viral genome and not to shrimp's EST were considered for further analysis. To investigate the candidate miRNAs ability to form hairpin structure, flanking sequence of about ~100 nt from each side of the viral genome were used in Mfold prediction with minimum free energy (MFE) less than −20 kcal/mol. The stem-loop structures were analyzed by MIREAP using the following criteria: mature miRNA length 20–24 nt, precursor miRNA has minimum 14 paired and minimum free energy < −18 kcal/mol, to predict the candidate WSSV-encoded miRNAs.

2.6. Stem-loop RT-PCR for validation of candidate miRNAs

Total RNAs from WSSV-infected and uninfected gill tissues at 48 h were extracted and used in the confirmation of WSSV infection by PCR before miRNA validation. Stem-loop primers used to generate cDNA were designed according to Chen (Chen et al., 2005). The primer contained an insertion of the universal sequence binding site of the reverse primer in the stem as described (Varkonyi-Gasic and Hellens, 2010). To set the RT reaction, 250 ng of the total RNA of each sample was mixed with 0.5 μl of 1 μM of stem-loop primers (SRT primers, Table 1) before denaturation at 65 °C for 5 min and quickly cooled on ice. Pre-denatured RNA was mixed with the reaction buffer containing 1× First-strand cDNA buffer, 250 nM of each dATP, dCTP, dGTP and dTTP, 10 mM DTT, 4 unit of RNaseOUT, 25 unit of SuperScript® III RT (Invitrogen) and adjusted to the final volume with sterilized RNase-free water to 10 μl. Reactions were incubated at 16 °C for 30 min, followed by pulsed RT of 60 cycles at 30 °C for 30 s, 42 °C for 30 s and 50 °C for 1 s and terminated by incubation at 85 °C for 5 min. PCR reaction was performed in a total volume of 20 μl; the reaction contained 2 μl of cDNA, 1× *Taq* buffer with $[NH_4]_2SO_4$ (Fermentas), 2.5 mM $MgCl_2$, 0.5 mM dNTPs, 50 nM of specific forward primer (SF) and universal reverse primer (SR) and 1 unit of Taq DNA polymerase. The PCR condition was as followed: 95 °C for 3 min followed by 35 cycles of 95 °C for 10 s, 60 °C for 20 s and cool downed at 20 °C. The expected products of sizes approximately 62–65 bp were analyzed on 15% non-denaturing polyacrylamide gel electrophoresis.

2.7. Profiling of WSSV-encoded miRNAs expression

To prepare WSSV-infected tissues at various time points, shrimps were challenged with WSSV lysate that resulted in shrimp death within 3 days. Gill tissues were collected at 3, 6, 9, 18, 24, 36 and 48 h. At the same time, an uninfected gill tissue injected with 150 mM NaCl was taken at 48 h and used as the control. Three shrimps were used for each time point. Then, total RNAs were extracted and WSSV detection was performed as described above. The expression of the candidate miRNAs were detected by stem-loop RT-PCR. The relative expression levels of the wsv-miRs were determined by semi-quantitative RT-PCR. The intensity of the PCR products was measured using Scion Image 4.0 program and normalized against U6 small nuclear RNA (snRNA) expression.

2.8. Detection of WSSV-encoded miRNAs from other virus infections

To ensure that WSSV-encoded miRNAs identified in this study are specifically derived from the WSSV genome not due to the host immune response against the viral challenge, investigation of the wsv-miRNA expression was performed under various pathogen challenges. Viruses containing the DNA genome such as WSSV or *Penaeus stylirostris* Densovirus (PstDNV, previously name infectious hypodermal and haematopoietic necrosis virus or IHHNV) and the RNA genome such as yellow head virus (YHV) were used in this study. Shrimp were separately injected with 150 mM NaCl solution, WSSV, YHV or IHHNV lysate. The dose of WSSV and YHV that lead to complete mortality within 3 days, IHHNV lysate dilution at 10^{-1} were employed. Based on the high expression level of WSSV-encoded miRNAs at 36 h, viral infected gill tissues were collected at this time. For non-lethal virus as PstDNV, an infected tissue was taken at 72 h which was a time with successful infection of PstDNV (Ho et al., 2011). RT-PCR with specific primers; YHV-F and YHV-R primers (Kongprajug et al., 2017), PstDNV-F and

PstDNV-R (formerly called IHHNV309F and IHHNV309R primers, respectively (Kathy et al., 2007) were used for YHV and PstDNVdetections, respectively. *EF1α* was useded as an internal control. After confirmation of viral infections, expressions of WSSV-encoded miRNAs were detected by stem-loop RT-PCR and the nuclease free water was used as the negative control of PCR reactions.

2.9. Target prediction of the WSSV-encoded miRNAs

To identify potential targets of the candidate miRNAs, miRanda 1.0 webserver was employed (www.microrna.org). The miRanda scores are based on sequence complementarity between miRNA and their target was > 90, the free energy of miRNA:mRNA duplex was < −20 kcal/mol, and a perfect match seed region at the 5′ of miRNA. Due to the lack of the complete genome sequence database for *Penaeus monodon* and other shrimp species, the dataset of identified miRNAs in this study and the EST of *P. monodon* or WSSV-Th genome were used as input. The potential limitation in miRNA target prediction is the EST database which does not equivalent to 3'-UTR of the mRNA target. For viral target genes, WSSV genome sequence was used which may encounter with the problem of short 3'-UTR of some WSSV genes and of polycistronic (encode > 1 gene per mRNA). The target genes that fit with the above criteria were identified by BLASTn against shrimp's EST and nucleotide database or translated into protein using BLASTp against protein database in NCBI.

3. Results

3.1. Solexa sequencing and bioinformatics analysis of the small RNA libraries

In order to identify WSSV-encoded miRNAs, gill tissues from WSSV-infected and non-infected (control) shrimp were used in small RNAs library construction and were sequenced by NGS. The length distribution of raw sequence reads was similar between both small RNA libraries at 18–23 nt (Fig. 1), which are the ideal size of miRNA. A total of 16,257,357 and 16,513,781 raw sequence reads were obtained from control and WSSV-infected library, respectively. After removal of the low quality reads, approximately 15 million clean reads were obtained from each library and 96% of the sequences were shared between the two libraries. Only a few unique sequences were found in the control (0.34%) and WSSV-infected (3.53%) libraries. The repeated sequences and other small RNAs (rRNA, tRNA, snRNA and snoRNA) were removed after analysis with Rfam10.1 and GenBank database. The remaining sequences were compared against miRBase17 to identify known and conserved miRNAs (Table 2). After alignment of the unannotated sequences with expressed sequence tag (EST) of *P. monodon* and the genome of WSSV-Th isolate, the flanking regions of the matching sequences were used for secondary structure prediction of precursor miRNAs by Mfold and analyzed by MIREAP. The results showed that 17 miRNAs were obtained from WSSV-infected library; however, three of them matched with shrimp's EST, pmo-miR-1, -2 and -3. Therefore, 14 candidate miRNAs (wsv-miR-4 to -15) remained that were encoded from WSSV. Notably, the candidate miRNAs, wsv-miR-4 and wsv-miR-7 were predicted to be derived from the 5′- and 3′-arms of pre-miRNAs (wsv-miR-4-5p, wsv-miR-4-3p, wsv-miR-7-5p and wsv-miR-7-3p) (Table 3).

Table 2
Classification of cleaned small RNA sequencing reads.

Small RNAs	Number of reads			
	Control		WSSV-infected	
	Unique[a]	Total reads	Unique	Total reads
Total reads		16,257,357		16,513,781
High_quality		16,219,800		16,467,059
Clean_reads	99,105	15,466,517	343,476	15,158,589
Conserved miRNAs	21,980	14,868,766	52,893	13,448,697
Other small RNAs	14,052	50,739	30,248	250,671
- rRNA	9355	20,542	15,732	121,737
- snoRNA	1184	1513	8214	27,693
- snRNA	237	365	1090	2881
- tRNA	3276	28,319	5212	98,360
Unannotate[b]	63,073	547,012	260,335	1,459,221
Matched shrimp's EST	588	2314	1841	27,880
Matched WSSV-Th genome	122	882	39,195	369,354

[a] They are type of sequence.
[b] Do not match with any-RNA.

3.2. Characterization of candidate WSSV-encoded pre-miRNA

Secondary structure of WSSV pre-miRNAs were predicted using Mfold (Fig. 2). All the flanking sequences of each candidate WSSV-encoded miRNA could form stem-loop structure with the minimum free energy (MFE) ranging from −18.3 to −27 kcal/mol. Hairpin structure of WSSV pre-miRNAs showed characteristics of internal mismatches with bulges in the stem and the terminal loop.

3.3. Mapping of WSSV-encoded miRNAs on WSSV genome

All 12 candidate WSSV-encoded pre-miRNAs were distributed along the WSSV genome. The nucleotides sequences and the genomic position of the candidate wsv-miRs are shown as a schematic diagram (Fig. 3).

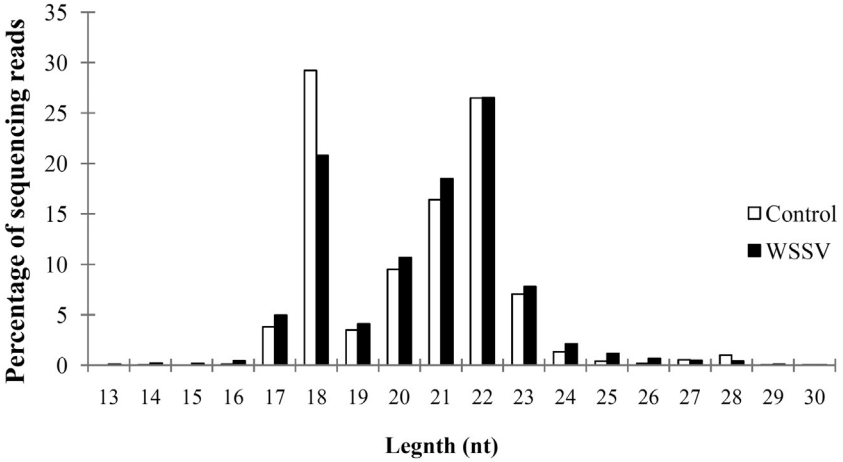

Fig. 1. Length distribution of small RNAs from control (□) and WSSV-infected libraries (■). The highest frequency was around 18–23 nt.

Table 3
Sequence and genomic position of the candidate miRNAs.

miRNA	Location	Strand	Sequence 5′→3′	No. of read	Length (nt)
wsv-mir-4-5p	55,069–55,088	+	cagggaagaaauagaccaug	12	20
wsv-mir-4-3p	55,123–55,144		uggagcauauguauucccugaa	2	22
wsv-mir-5	66,621–66,642	+	acccuuuucgguggcugugcu	5	22
wsv-mir-6	155,594–155,615	+	uucgguucuucaaagaggcuaa	5	22
wsv-mir-7-5p	188,534–188,555	+	caguaguguuguugccuauucu	9	22
wsv-mir-7-3p	188,578–188,597		gaaauaauaauaaugcuguc	1	20
wsv-mir-8	28,262–28,282	−	uggaccgcugggucgggccaa	21	21
wsv-mir-9	38,575–38,596	−	agccuaaaaaucucccuuccu	11	22
wsv-mir-10	58,933–58,954	−	ucuucuggguuuggcuaagaaa	13	22
wsv-mir-11	90,678–90,699	−	gacuuggugcggcgggggcugg	11	22
wsv-mir-12	186,737–186,758	−	uuuuuccaacacagaagaugcg	6	22
wsv-mir-13	209,404–209,425	−	cagucauauccgugaucacauu	12	22
wsv-mir-14	276,164–276,186	−	ccaaugucuugaagcugucgugc	7	22
wsv-mir-15	288,685–288,707	−	aauauugucaccgauguuggaga	6	23

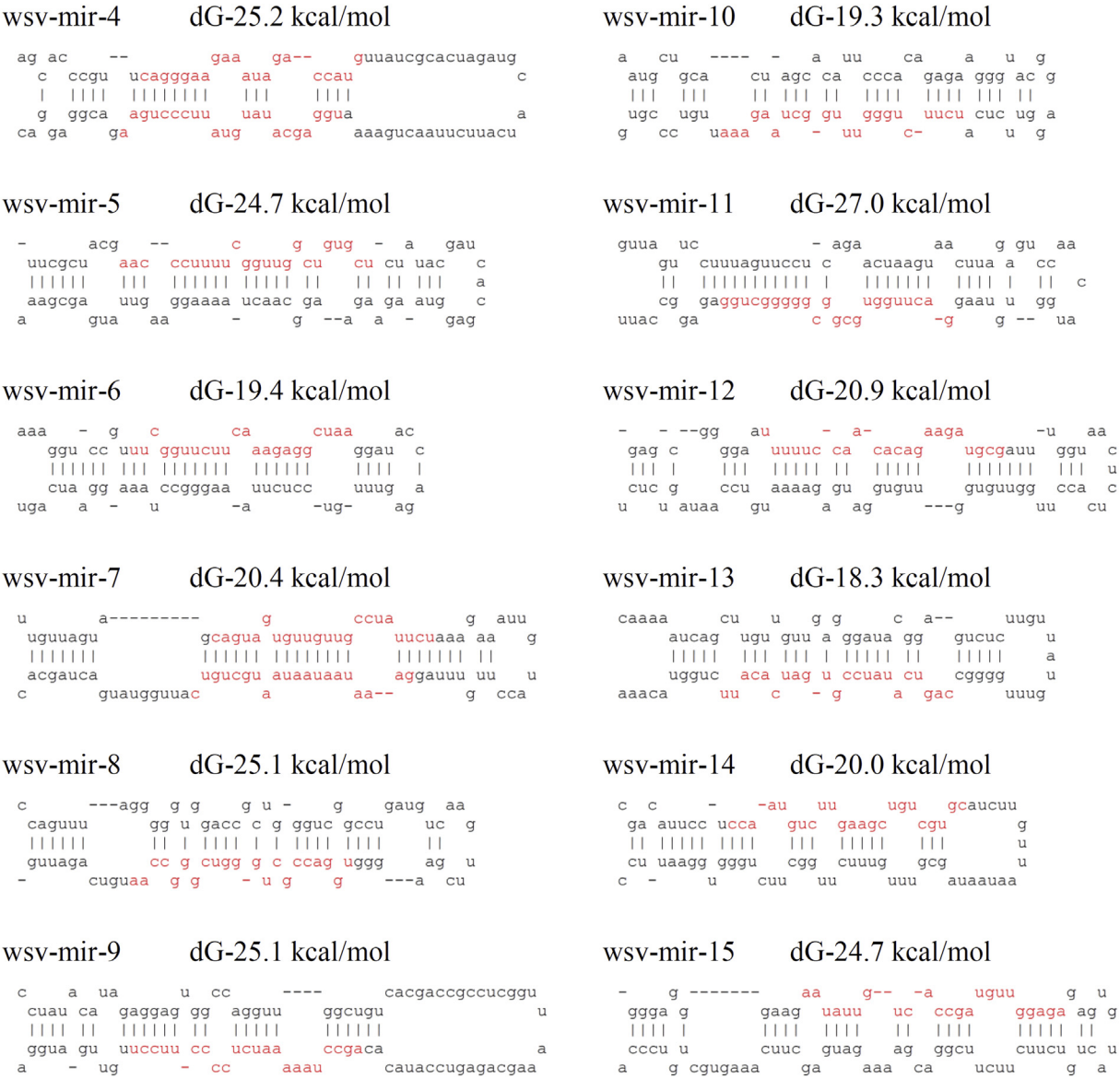

Fig. 2. Secondary structures of the 12 candidate WSSV-encoded pre-miRNAs. The minimum free energy (MFE) was predicted by Mfold program. Red nucleotides indicate mature sequences of miRNAs. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

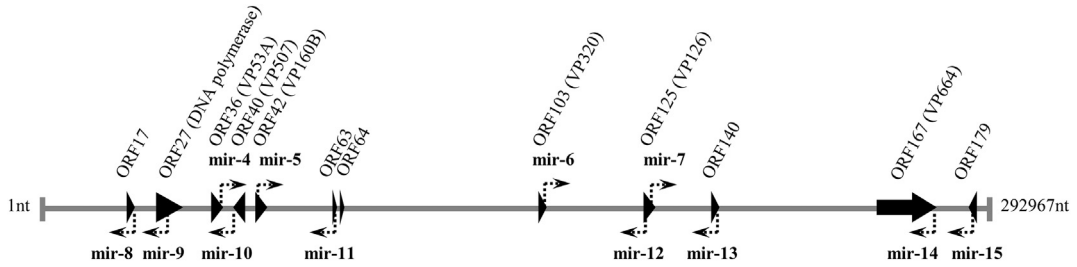

Fig. 3. A schematic diagram of the locations of the candidate WSSV-encoded miRNAs on WSSV genome (GenBank accession number: AF369029). ORFs of WSSV and candidate miRNAs were represented as big and small arrows with the transcriptional direction, respectively.

Candidate wsv-miRs were classified into 4 groups according to the transcriptional direction and location. In the first group, the candidate wsv-miRs (wsv-miR-4, -5, -6 and -7) were located on the sense strand and were encoded in the same direction as the open reading frame (ORFs) of WSSV. The second and third groups were embedded in the antisense strand of the viral genome and were either encoded in the opposite (wsv-miR-8, -9, -12, -13 and -14) or in the same transcriptional orientation with viral ORFs (wsv-miR-10 and -15). The last group which contained only a single candidate, wsv-miR-11, was located in the overlapping sequence between ORF63 and 64 in an antisense direction. Notably, wsv-mir-9 was found located in the antisense strand of the putative WSSV DNA polymerase (ORF27).

3.4. Validation of the candidate WSSV-encoded miRNAs expression

To verify whether the candidate miRNAs were specifically expressed in WSSV-infected tissue, stem-loop RT-PCR technique was performed. Total RNA samples that were used to construct the small RNA libraries were employed as templates. In addition, other sample set which was the control- and WSSV infected- gill samples obtained from different set of shrimp was used to ascertain that the amplification signals of wsv-miRNAs in the WSSV-infected gill tissues were not the artifact. The results showed that most of candidate wsv-miRs can be detected only from WSSV-infected tissues, except for wsv-miR-7-5p, -7-3p, -8 and -11. The same results were obtained from these two independent experiments. MicroRNA let-7 which was used as a positive control was found in all samples (Fig. 4).

3.5. WSSV-encoded miRNAs specifically expressed in shrimp challenging with WSSV but not with YHV and PstDNV

The RT-PCR results confirmed WSSV, YHV and PstDNV replication in the viral challenged shrimp and the individual shrimp was infected with a single virus (Fig. 5A). After performing of SRT-PCR, ten validated wsv-miRs could be detected from WSSV- but not YHV- and PstDNV- infected shrimp. Supporting to the validation of the wsv-miRs expression, wsv-miR-7-5p, -7-3p, -8, and -11 could not be detected (Fig. 5B). These results implied that viral encoded-miRNAs in this study were specifically expressed by WSSV and they were not inducible miRNAs that derived from the immune response to RNA and DNA virus infections.

3.6. Profiling of wsv-miRNA expressions depend on time course of WSSV infection

To investigate the expression profiles of wsv-miRs, the expression

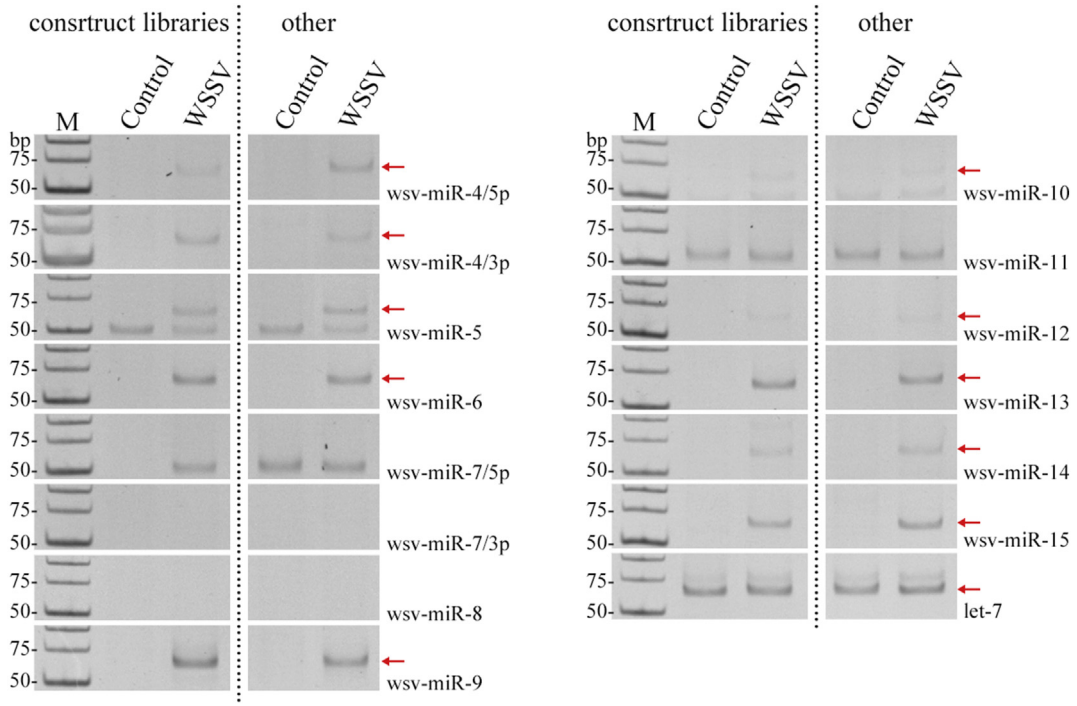

Fig. 4. Validation of the 14 candidate WSSV-encoded miRNAs by stem-loop RT-PCR. The sample that was used to construct the small RNAs libraries (set 1) was compared to the other sample set (set 2). The expressed miRNAs was about 62 bp (red arrow). M is ultra low range DNA ladder. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

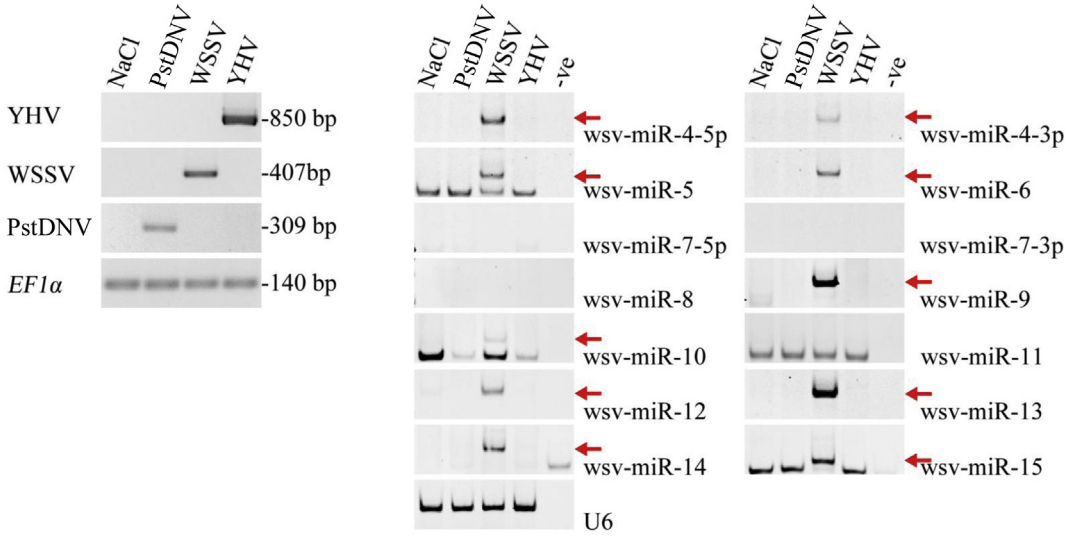

Fig. 5. WSSV-encoded miRNAs specifically expressed in shrimp challenging with WSSV but not with YHV and PstDNV. (A) RT-PCR confirmation of the infectivity of the individual shrimp infected with PstDNV, WSSV or YHV. (B) Expressions of ten WSSV-encoded miRNAs were specifically detected from WSSV infected shrimp (red arrow). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

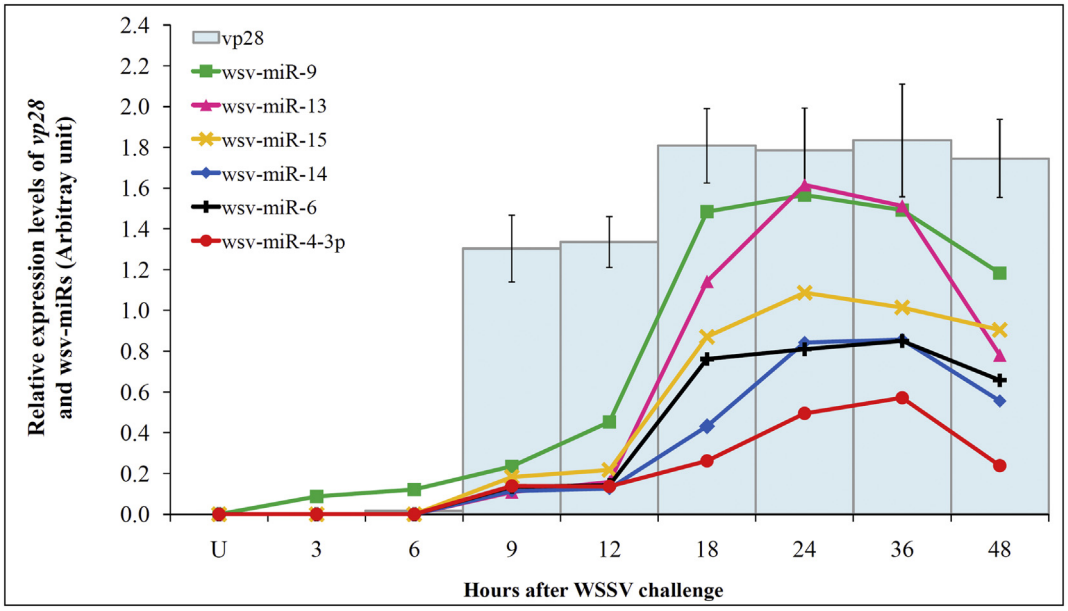

Fig. 6. Expression profiles of wsv-miRs at each time point of WSSV-infection. Uninfected shrimp is marked with U. Semi-quantitative expression of 6 wsv-miRs (colour lines) and *vp28* (blue bars) were normalized with U6 snRNA and *EF1α*, respectively. The result is shown as means from 3 shrimps at each time point. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

levels of wsv-miRs from control and WSSV-infected shrimp at several time points were determined by stem-loop RT-PCR. Six wsv-miRs (wsv-miR-4-3p, -6, -9, -13, -14 and -15) were found to be expressed at different levels and were up-regulated depending on the time course of WSSV infection. Expressions of most wsv-miRs were increased after 12 or 18 hpi and were slightly decreased at 48 hpi. The expression of U6 snRNA in all samples was relatively constant. Detection of *vp28* mRNA confirmed WSSV infection with early at 9 hpi. A representative gel from three sets of experiments is shown in Fig. 6 with the expression level of *vp28* (blue bars). After normalization, wsv-miR-9 showed the highest expression level among all candidate miRNAs, followed by wsv-miR-13 and -15.

3.7. Computational prediction of miRNA targets

Potential targets screening was performed using miRanda software. EST database of *P. monodon* was used for cellular target prediction. After blast search, potential cellular targets were identified and were classified into innate-immune related genes, transporter proteins, proteins involved in translation, and structural proteins (Table 4). The wsv-miR-10 and -13 were predicted to target to just one mRNA which was hemocyanin (HcVn) and *F. chinensis* double WAP domain-containing protein, respectively. Some wsv-miRNAs (miR-4-3p, -5, -6, -14 and -15) were predicted to recognize several mRNA targets for example; wsv-miR-6 was predicted to recognize either anti-lipopolysaccharide factor or cyclophilin. Cellular genes such as anti-lipopolysaccharide factor and elongation factor 1-alpha of *P. monodon* may be recognized by multiple miRNAs. For example, elongation factor 1-alpha of *P. monodon* may be

Table 4
Cellular target prediction of wsv-miRNAs.

wsv-miRs	Potential cellular target genes
	Innate-immune related
wsv-miR-4-3p, -5, -10	*P. monodon* hemocyanin (HcVn) mRNA
wsv-miR-6, -15	*P. monodon* anti-lipopolysaccharide factor
wsv-miR-5	*P. monodon* masquerade-like serine proteinase-like protein 3
wsv-miR-4-3p, -13, -14	*F. chinensis* double WAP domain-containing protein
	Transporter proteins
wsv-miR-15	*P. monodon* putative ligand-gated ion channel-like protein
wsv-miR-15	*P. monodon* NADH dehydrogenase subunit F-like protein
	Protein translation
wsv-miR-5, -14, -15	*P. monodon* elongation factor-1 alpha
wsv-miR-5	*L. vannamei* ribosomal protein L8
	Structural and other proteins
wsv-miR-15	*P. monodon* cathepsin D
wsv-miR-6	*F. paulensis* cyclophilin

Table 5
Viral target prediction of wsv-miRNAs.

wsv-miRs	Potential viral target genes
wsv-miR-4-5p	ORF105, ORF110, ORF154 VP53A, VP15, VP57, VP664, VP544, VP136B ICP11
wsv-miR-4-3p	ORF89, ORF135, ORF142, ORF169, ORF14, ORF38 VP53A, VP300, VP664 TK-TMK, Helicase
wsv-miR-5	ORF18, ORF19, ORF42, ORF43, ORF56, ORF89, ORF96, ORF121, ORF122, ORF125, ORF12, ORF14, ORF25, ORF38, ORF53, ORF82, ORF83, ORF104, ORF108 VP357, VP507, VP387, VP53C P-collagen, CBP, STF[a], class1 cytokine receptor, Helicase, dUTPase, RR1 repeat4
wsv-miR-6	ORF5, ORF73, ORF89, ORF97, ORF47 VP53A, VP320, VP544 STK
wsv-miR-9	ORF121
wsv-miR-10	ORF4, ORF43, ORF63, ORF65, ORF97, ORF122, ORF123, ORF138, ORF67, ORF82, ORF154 VP53B, VP664 P-collagen, E3, AAP-1, STK repeat4, repeat8, repeat7
wsv-miR-12	ORF37, ORF90 VP664
wsv-miR-13	ORF55, ORF3, ORF33, ORF116, ORF159, ORF166 VP38A, VP136B TK-TMK, RR1
wsv-miR-14	ORF4, ORF17, ORF19, ORF49, ORF175, ORF33, ORF111, ORF179 VP53A, VP51A, VP664, VP26 class1 cytokine receptor, RR1
wsv-miR-15	ORF26, ORF136, ORF85, ORF154 VP216, VP136B PK1

TK-TMK: Chimeric Thymidine/Thymidylate kinase, CBP: CREB-binding protein, STF: SOX-transcription factor, RR1: Ribonucleotide reductase I, STK: Putative Serine/Threonine protein kinase, E3: E3 ubiquitin ligase, AAP-1: Anti-apoptotic protein 1, PK1: Protein kinase 1
Marks, 2005; Li et al., 2007[a]; He et al., 2006[b]

the candidate target of wsv-miR-5, −14, and − 15. For viral genes (Table 5), potential targets were distributed on the viral genome encoding either non-structural (helicase, ribonucleotide reductase large subunit (RR1)) or structural proteins (such asVP53A, VP664).

4. Discussion

Several miRNAs have been identified from various organisms and these are conserved in metazoans, including aquatic invertebrates such as *M. japonicus* (Huang et al., 2012; Ruan et al., 2011), *P. monodon* (Kaewkascholkul et al., 2016), *L. vannamei* (Sun et al., 2016) and *F. chinensis* (Li et al., 2017). After viral-encoded miRNAs were first found in the Epstein-Barr virus (EBV) (Pfeffer et al., 2004), a number of viral-encoded miRNAs were identified from other DNA and some RNA viruses (Klase et al., 2013). Here, NGS and small RNAs cloning were used to identify WSSV-encoded miRNAs in *P. monodon*. Fourteen candidate viral-encoded miRNAs were predicted to derive from 12 precursors which can spontaneously form hairpin structure (MFE < -20 kcal/mol) (Fu et al., 2011). Using stem-loop RT-PCR approach, ten candidate wsv-miRs were validated. Most of them could not be detected by northern blot. This might be due to the very low expression level of wsv-miRs which might be below the detection limit of this method. This was not unexpected as other studies also failed to detect viral encoded miRNAs such as HSV-1-5p and MuHV-M1-1, by northern blot (Diebel et al., 2010; Tang et al., 2008).

Different from the eukaryote, the viral-derived miRNAs are less conserved in sequence except for the closely related viruses such as HSV-1 and HSV-2 that show high sequence similarity (Umbach and Cullen, 2009). Novel candidate miRNAs in this study do not appear to share high sequence homology against viral miRNAs in miRNA database. In addition, the number and sequence of our wsv-miRNAs were different from the previously identified 101 WSSV-miRNAs from WSSV-Cn isolate (Huang et al., 2014; Liu et al., 2016). This may be because of the different in viral isolate (WSSV-Th vs WSSV-Cn), stage of WSSV infection (48 h vs 6–24 h), shrimp tissues (gill vs lymphoid) and methods to identify miRNAs (NGS vs microarray). Nonetheless, the stem-loop sequences of pre-miRNAs in this study were conserved among the four WSSV isolates. WSSV-Th genome sequence differs greatly from that of WSSV-Cn isolate as WSSV-Th has a big deletion of 12 kb (Marks et al., 2004). Two WSSV-Cn miRNAs, WSSV-miR197 and -miR201 can be found to be located in the deleted region of WSSV-Th (He and Zhang, 2012). Therefore these miRNAs could not be identified in this study. This suggested that neither WSSV-miR197 nor -miR201 are necessary for WSSV-Th. Moreover, one of our wsv-miRs, wsv-miR-5, showed sequence overlaps with WSSV-miR12 of the previous study (He and Zhang, 2012). The location of WSSV-miR12 is embedded in the wsv-miR-5 precursor, suggesting that they might be conserved in the genomic location similar to the miR-1 of some members in the polyomavirus family: SV-40, JCV and BKV (Lagatie et al., 2013). This study also identified wsv-miRs from the gill tissue in the late stage of WSSV infection at 48 h whereas most of the previously identified WSSV-encoded miRNAs from other study are at the early stage of WSSV infection (He and Zhang, 2012). Some WSSV-miRs were expressed in specific tissues such as hemocyte-specific expression of WSSV-miR-129 and -162 and lymphoid organ-specific expression of WSSV-miR-N30 (Huang et al., 2014). In addition, differences in miRNA expression levels can be observed in lymphoid organ and stomach of WSSV-infected *F. chinensis* (Liu et al., 2016).

WSSV miRNA expression profile showed that 6 wsv-miRs increased upon viral infection at 12–18 h after *vp28*, a viral late gene, expression, suggesting that these wsv-miRs might function at the late stage of viral infection. The viral-encoded miRNA that controls late stage or lytic life cycle of virus is usually up-regulated after late protein expression (Tang et al., 2009). For example, HvAv encoded miR-1 form a major capsid protein (MCP) gene whose expression was increased during the late stage of HvAv infection and targeted its own *DNA polymerase I* mRNA, resulting in the inhibition of viral replication (Hussain et al., 2008). Among wsv-miRs, the expression level of wsv-miR-9 was highest, followed by wsv-miR-13 and -15, when compared to other wsv-miRs at the same time point. MicroRNA-mediated translational inhibition requires an imperfect binding between miRNA and their target at the ratio of at

least 1:1 (tenOever, 2013). Therefore, high expression levels of certain wsv-miRs suggested the abundance of that mRNA targets or that the virus is attempting to quickly suppress the target mRNA. The decreased wsv-miRs expression at 48 h might be caused by WSSV infection that can induce apoptosis after 24 hpi in haematopoietic and gill tissue (Wongprasert et al., 2003).

The potential cellular and viral gene targets were screened by computational prediction. As the complete shrimp genome sequence is not available, this study picked up potential cellular targets from EST of *P. monodon*. Some potential target genes, such as NADH dehydrogenase and elongation factor 1 have been shown to be down-regulated during WSSV-challenged (Wongpanya et al., 2007; Wu et al., 2007). This study used the WSSV genome sequence instead of the WSSV 3'-UTR (Huang et al., 2012) for viral target prediction because some viral mRNAs have an initial ribosome entry site (IRES) and share a poly-A tail (Han and Zhang, 2006; Kang et al., 2009, 2013). Wsv-miRs could target many non-structural genes such as DNA polymerase, anti-apoptotic protein 1 and dUTPase, suggesting that WSSV might use wsv-miRs to control its expression through various mechanisms such as transcription, apoptosis and signaling pathway. Some targets may be recognized by multiple miRNAs, such as the elongation factor 1-alpha and hemocyanin of *P. monodon* or the DNA polymerase and VP664 genes of WSSV. Such event was demonstrated in Kaposi sarcoma-associated herpesvirus (KSHV) as it encoded multiple miRNAs targeting to THBS1 or MAF mRNA (Hansen et al., 2010; Samols et al., 2007). In contrast, the result showed some candidate targets such as wsv-miR-4-3p that recognized *P. monodon* hemocyanin and VP35A. Similarly, WSSV-miR-66, miR-68 (He et al., 2014) and miR-32 (He et al., 2017) each of which binds to two WSSV mRNAs. In addition, this was also demonstrated in *M. japonicus* that encoded *Mj*-miR-12 (Shu and Zhang, 2017) and miR-965 (Shu et al., 2016) to control both shrimp and WSSV genes for down regulation of the virus. Furthermore, wsv-miRs were targeted to WSSV-related sequences such as helicase and putative serine/threonine protein kinase (Huang et al., 2011), suggesting that this wsv-miRs can target either virus or host gene.

Accumulation of wsv-miRNAs in this study and others suggested that WSSV has a lot of miRNAs when compared to other viruses in the miRBase database. The results also suggested that several wsv-miRNAs that were expressed in the late stages of WSSV infection could crosstalk between the host and the virus. Identification of wsv-miRs and their targets revealed the complexity of miRNA-mediated WSSV-host interaction. This knowledge will provide insights into the understanding of WSSV-host interaction and pathogenesis. Understanding of the roles of wsv-miRNAs and their expression pattern during WSSV infection may have potential applicability in applying miRNAs as valuable diagnostic and/or prognostic biomarkers for screening of virus infection and determination of the severity of the disease. Wsv-miRs and their targets may serve as potential therapeutic targets in miRNA-based vaccine development to effectively prevent and control the WSSV infection in shrimp.

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Authors' contributions

1. Thaneeya Nantapojd: design and conduct the experiment, data acquisition, analysis and interpretation, and drafted the manuscript.
2. Sakol Panyim: give comments and suggestion, review and edit the manuscript.
3. Chalermporn Ongvarrasopone: funding acquisition, critically review the design of the experiment, data analysis and interpretation, writing, review and edit the manuscript, and act as corresponding author.

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Functional characterization of a cDNA encoding Piwi protein in *Penaeus monodon* and its potential roles in controlling transposon expression and spermatogenesis

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ABSTRACT

Piwi proteins comprise a subfamily of Argonaute that plays a major role in germline development by association with a distinct class of small RNAs called Piwi interacting RNA (piRNA). Although the functions of Piwi in the development of germline cells as well as transposon regulation were reported in a number of mammalians and insects, developmental expression and function of Piwi subfamily in crustaceans is poorly known. This study is aimed at cloning and characterization of a *Piwi* cDNA in the black tiger shrimp, *Penaeus monodon*. The cDNA encoding a Piwi protein of *P. monodon* (PmPiwi1) was obtained by rapid amplification of cDNA ends (RACE). The *PmPiwi1* coding cDNA contains 2811 nt encoding a putative protein of 936 amino acids, and was specifically expressed in testis and ovary, suggesting its possible function in gametogenesis. RNAi experiment showed that suppression of *PmPiwi1* expression led to a significant up-regulation of retrotransposon *gypsy2* and DNA element transposon *mariner* in shrimp testis. Investigation of the function of *PmPiwi1* in spermatogenesis by sperm count showed significantly lower number of sperms in the spermatophore sac of *PmPiwi1*-knockdown shrimp compared with that in the control shrimp. Our study thus reported for the first time the cDNA encoding a Piwi protein in the shrimp *P. monodon*. Its roles in controlling transposons and spermatogenesis as implied by the results in this study will be important for understanding sperm development and could be useful for the improvement of reproduction in male shrimp in the future.

1. Introduction

Argonaute is a central protein component of an RNA-induced silencing complex (RISC) in a small RNA-mediated gene silencing pathway called RNA interference (RNAi). Argonaute protein family is characterized by the presence of two major conserved domains: the PAZ domain that binds specifically to small non-coding RNAs, and the PIWI domain that forms a catalytic triad Asp-Asp-His (DDH) required for the cleavage of a target mRNA that is complementarily bound to the small RNA (Carmell et al., 2002; Niraj and Leemor, 2006; Olina et al., 2018; Peters and Meister, 2007). Phylogenetic analysis classifies proteins in the Argonaute family into Ago and Piwi subfamilies. The Ago subfamily is ubiquitously expressed and normally functions in association with small interfering RNAs (siRNAs) and/or micro RNAs (miRNAs). In contrast to the Ago subfamily, Piwi proteins exhibit a germline-specific expression pattern and bind to a distinct class of small RNA called PIWI-interacting RNAs or piRNAs in germline cells (Carmell et al., 2002; Peters and Meister, 2007; Seto et al., 2007; Sheu-Gruttadauria and MacRae, 2017).

Piwi proteins and their small RNA partners, piRNAs are implicated in transcriptional gene expression, post-transcriptional gene regulation and transposon silencing that are important during germline development, particularly in spermatogenesis and oogenesis (Akkouche et al., 2017; Marie et al., 2017; Vagin et al., 2006). Loss of *piwi* causes defects in germ cell development in diverse organisms (Houwing et al., 2007; Ma et al., 2017a). Piwi is most studied in *Drosophila*, whose genome codes for three Piwi members; Piwi, Aubergine (Aub) and Argonaute 3 (Ago3). Both Aub and Ago3 are cytoplasmic proteins that are restrictedly expressed in the germline granules called a nuage (Huang et al., 2014; Macdonald, 2001; Nagao et al., 2010). *Aub*-deficient flies displayed male sterility and maternal effect lethality (Ma et al. 2017b; Sahin et al., 2016; Schmidt et al., 1999). By contrast, *Drosophila*'s Piwi seems to be predominantly expressed in the nucleus and is necessary for self-renewing division of germline stem cells in both males and females

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Table 1
Primers used in this study and their nucleotide sequences.

Primer name	Primer sequence (5′ to 3′)	Experiment
oligo dT	CCGGAATTCAAGCTTCTAGAGGATCCTTTTTTTTTTTTTTT	Cloning, mRNA expression and detection of PmPiwi1 knockdown
PM1	CCGGAATTCAAGCTTCTAGAGGATCC	
Actin-F	GACTCGTACGTGGGCGACGAG	
Actin-R	AGCAGCGGTGGTCATCTCCTGCTC	
Piwi-F4	TACCGCGACGGCGTGAGCGAG	
Piwi-R4	CAAAAGCTAGTTTATGTGCAT	
5RACE1	TAACGAGCGTGATGCCGTCGTG	
5RACE2	CGAGTCGAAGTGCTGGAAGA	
5RACE3	AATACCGATCCTCACGCTGG	
5RACE4	ATGGAGCGTGTGACTTGTCG3	
5RACE5	GAGGATCCATTGACATTCCTGAC	
5RACE8	GCCAGATCTCTAGCTTGTGC	
Piwi1-3RACE1	GATCAGCACCAGGATCTT	
Piwi1-3RACE2	TGGCCTCAAGATCTCACTCC	
Coding-F1	ATGAAGGTGATATTCAGGAAGCG	
Coding-F2	ATGGATGGGGACCCAACTCC	
Coding-R	TCAGAGGAAGAAGAGCTTGTCA	
Sense-*Xba*I-F	GCTCTAGACCACGTGATTAAGGCTCTGG	dsRNA-PmPiwi1 synthesis
Sense-*Hin*dIII-R	CCCAAGCTTGGATCCATTGACATTCCTGAC	
dsPAZ-anti-*Xho*I-F	CCGCTCGAGCCACGTGATTAAGGCTCTGG	
dsPAZ-anti-Hind-R	CCCAAGCTTTGTCATGTAGCATAGCTCTGG	
MarinerF	CGGTTGGGAGAATAGGCAAATCA	Transposable elements expression
MarinerR	CCTTACAAACTGACGTTGATGGC	
GyPemo1bF	CTACAGCACCAACAACGTCCAA	
GyPemo1bR	CGTTTCCTCAAGCTGTATGAGGTG	
GyPemo2F	GATGCCTCAAACCTCGGGCT	
GyPemo2R	AGTGACGGAGGGCCCATGTG	
EF1αF	GAACTGCTGACCAAGATCGACAGG	
EF1αR	GAGCATACTGTTGGAGGTCTCCA	

(Cox et al., 1998, 2000; Gonzalez et al., 2015). The depletion of Piwi led to infertility and axis specification defects in the developing egg chambers (Cox et al., 1998). In the mouse, *Mus musculus,* three members of Piwi have been identified namely Miwi, Mili and Miwi2. Miwi and Mili are expressed in both testis and oocyte. They are involved in meiotic regulation of spermatogenesis and oocyte development (Ding et al., 2013; Kabayama et al., 2017; Kuramochi-Miyagawa et al., 2001; Kuramochi-Miyagawa et al., 2004). On the other hand, Miwi2 is expressed in both germ cells and somatic cells, and is essential for maintaining germ-line stem cells (Carmell et al., 2007; Wasserman et al., 2017). Similarly, the two Piwi proteins of zebrafish, Ziwi and Zili, are essential for germ line maintenance. Ziwi is abundantly expressed during both mitotic and early meiotic stages of germ cell differentiation, while Zili is involved in germ cell differentiation similar to the mouse Miwi2 (Houwing et al., 2007; Saskia Houwing, 2008). Like in other organisms, the expression of two Piwi proteins in the silkworm *Bombyx mori*, Siwi and BmAgo3, was found in germline cells. Both of them are abundantly expressed in testes and ovaries indicating that they might be involved in spermatogenesis and oogenesis in *B. Mori* (Kawaoka et al., 2008). Similarly, the regulation of spermatogenesis and oogenesis in the honey bee, *Apis mellifera* is regulated by two *piwi*-like genes, Am-*aub* and Am-*ago3* (Liao et al., 2010). Recently, genes encoding three crustacean Piwi proteins have been first identified in the crab *Portunus trituberculatus*. All of *P. trituberculatus*' *piwi* genes were expressed in adult testis, thus suggesting their functions during spermiogenesis (Xiang et al., 2014).

Recent studies have shown that piRNAs are central players in transposon silencing, which is particularly important for germ cell differentiation and genome maintenance during germline developmental process (Chambeyron et al., 2008; De Fazio et al., 2011; Teixeira et al., 2017). The piRNAs are primarily derived from transposons and other repeated elements by a proposed ping-pong model that involves the three Piwi proteins in *Drosophila* (Saito et al., 2006; Wang and Elgin, 2011; Wang et al., 2015; Webster et al., 2015). The Piwi proteins are important for controlling transposon mobilization in germ cells. For examples, loss-of-*miwi*,-*mili* and -*miwi2* mice exhibited transposon activation in germline that consequently resulted in germ cells deficiency (Carmell et al., 2007; Kabayama et al., 2017). In *Drosophila*, Piwi controlled expression and mobilization of retrotransposons. Mutation of *piwi* deregulates retrotransposon expression in the germline that finally led to embryonic defects (Akkouche et al., 2017; Kalmykova et al., 2005; Teixeira et al., 2017). Although Piwi proteins have been extensively studied in diverse organisms, but Piwi in crustacean is less known. To help fulfill our knowledge in the control of gonad development in this large subphylum of arthropods, we cloned and characterized a cDNA encoding a member of Piwi proteins from the black tiger shrimp, *Penaeus monodon*. The expression of *PmPiwi* during gonad developmental stage, its function in controlling transposon expression and regulating spermatogenesis in the male germline of *P. monodon* were also investigated.

2. Materials and methods

2.1. Penaeus monodon samples

P. monodon were kindly provided by Shrimp Genetic Improvement Center, Surat Thani, Thailand. Male shrimps at three different maturation stages were used in this study: adolescent or immature shrimp about 4 months old or approximately 20 g bodyweight (bw) were defined as those forming spermatophores without sperm inside; sub-adult male shrimp were about 6 months of age with approximately 40 g bw; and adult male shrimp were over 10 months old. Female shrimp were divided into five reproductive maturation stages based on histochemical staining with hematoxylin and eosin according to Tan-Fermin and Pudadera (1989). The experiments involving animals were carried out in accordance with animal and use protocol of the Mahidol University-Institute Animal Care and Use Committee.

2.2. Cloning of a full-length Piwi cDNA of P. monodon (PmPiwi1)

Total RNA was extracted from the testis of *P. monodon* by TriSolution Plus Reagent (GMbiolab) as described in the manufacturer's

protocol. Approximately 2 µg of total RNA were used for cDNA synthesis by incubating with 0.5 µM of oligo dT primer in a volume of 5 µl followed by incubating at 70 °C for 5 min and cooling on ice for 5 min. Then, the mixture containing 5× Impromt II™ reaction buffer, 3 mM $MgCl_2$, 0.5 mM each dNTP, and 1 µl of Impromt II™ reverse transcriptase (Promega) was added, and the reaction was continued at 42 °C for 60 min, then at 70 °C for 15 min. One microliter of the cDNA was used as a template for amplification of the partial *Piwi* cDNA with specific primers PIWI-F4 and PIWI-R4 (Table 1) at 95 °C for 5 min followed by 35 cycles of 95 °C for 30 s, 57 °C for 30 s, and 68 °C for 30 s.

The 3′ end of *PmPiwi1* cDNA were obtained from the oligo-dT-primed first strand cDNA by 3′ RACE. The first amplification was performed with 3RACE1 primer designed from the partial Piwi cDNA obtained above and oligo-dT reverse primer. Subsequently, the nested PCR was performed using 3′ inner primer 3RACE2 and PM1 primer. The PCR profile for 3'RACE was as follows; initial denaturation at 95 °C for 5 min, annealing at 55 °C for 30 s and extension at 68 °C for 2 min 30 s for 35 cycles using *Taq* DNA polymerase (NEB® Inc.).

For 5′ RACE, the first strand cDNA was synthesized using specific reverse primer of PmPiwi1 (5RACE-R1), followed by tailing of poly A at its 3′ end using terminal deoxynucleotidyl transferase (Promega). The 5′ cDNA of *PmPiwi1* was obtained by three rounds of 5'RACE using the following temperature profile: initial denaturation at 95 °C for 5 min, annealing at 55 °C for 30 s and extension at 68 °C for 2 min 30 s for 35 cycles using *Taq* DNA polymerase (NEB® Inc.). Schematic diagrams of 3′ and 5′ RACE amplification are shown in Fig. 1, and all primers together with their nucleotide sequences are shown in Table 1.

The entire coding region of *PmPiwi1* was obtained by amplification with coding-F and coding-R primers using Expand High Fidelity enzyme (Roche) in a 25 µl reaction containing 1× Expand High Fidelity buffer with $MgSO_4$, 0.352 mM dNTP and 0.3 µM each primer. The amplification was carried out using the following temperature profile; denaturation at 94 °C for 10 s, annealing at 50 °C for 30 s and extension at 68 °C for 2 min for 10 cycles, followed by the second round of amplification with 25 cycles of denaturation at 94 °C for 15 s, annealing at 50 °C for 30 s and extension at 68 °C for 2 min 20 s. All the primers used and their nucleotide sequences are listed in Table 1. The amplified fragments were purified and cloned into pGEM®-T easy (Promega). The nucleotide sequences were determined by automated DNA sequencing (1st BASE DNA Sequencing Services, Singapore) and analyzed by Blast program (http://www.ncbi.nlm.nih.gov/blast).

2.3. 2.3 Determination of PmPiwi1 expression in P. monodon

Adult male and female *P. monodon* (approximately 100 g bw) were used for tissue distribution determination. Several tissues such as brain, gill, hepatopancreas, heart lymphoid, throracic ganglia, testis, vas deferens, spermatophore and ovary were dissected and sliced into small pieces. About 100 mg of each tissue were homogenized in Trisolution Plus Reagent (GMbiolab), Approximately 2 µg of total RNA from each tissue were used for cDNA synthesis with oligo dT as described above. The *PmPiwi1* mRNA expression was determined by cDNA amplification with Coding-F1 and 5RACE-R5 primers by *Taq* DNA polymerase (NEB® Inc.) in a 25 µl PCR reaction using the PCR profile as previously described for the amplification of *PmPiwi1* coding cDNA. Actin was used as an internal control. All primers were shown in Table 1.

The mRNA expression levels of *PmPiwi1* in the ovary and testis at different developmental stages were determined by real-time PCR using KAPA SYBR® FAST qPCR kit (Kapa Biosystems) according to the manufacturer's protocol. The fluorescent signal was detected by Eppendorf Realplex (Eppendorf) machine. Relative expression level of *PmPiwi1* was compared with that of the reference gene (elongation factor 1 alpha: *Ef1α*), and the data was analyzed by $2^{-\Delta\Delta CT}$ method.

2.4. Double-stranded RNA preparation

The recombinant plasmid harboring the PAZ domain region of *PmPiwi1* cDNA was used as a template for *PmPiwi1* dsRNA production. The dsRNA was synthesized as a stem-loop precursor in *Escherichia coli* expression system. The template of the sense (stem) strand was amplified with sense-*Xba* I–F and sense-*Hind* III-R primers, whereas the anti-sense (stem-loop) strand template was amplified with anti-*Xho* I–F and anti-*Hind* -R primers. The reaction was performed by 30 cycles of denaturation at 95 °C for 2 min, annealing at 55 °C for 30 min and extension at 72 °C for 1 min using *Pfu* DNA polymerase (Thermo scientific). The sense and anti-sense template fragments were sequentially cloned into pET17b vector at the restriction sites corresponding to their termini. The pET17b vector harboring *PmPiwi1* dsRNA template was expressed in *E. coli* strain HT115 with 0.4 mM IPTG induction at 37 °C for 4 h. The *PmPiwi1* dsRNA was extracted by TriSolution Plus Reagent with the addition of 5 ng RNaseA to digest host single strand RNA and the loop region of the stem-loop dsRNA precursor. The quality of dsRNA was determined by RNase digestion assay with RNaseA and RNaseIII.

2.5. In vivo silencing of PmPiwi1

In order to investigate the function of *PmPiwi1*, its expression was first suppressed by dsRNA-mediated silencing. To demonstrate the potency of dsRNA to knockdown *PmPiwi1* expression in the shrimp, male *P. monodon* approximately 50 g bw (approximately 8 months old) were injected with *PmPiwi1*-dsRNA (dsPiwi1) at 2.5 $\mu g \cdot g^{-1}$ shrimp bw in a volume of 100 µl. Shrimp injected with 150 mM NaCl were used as a control group. The shrimp were injected twice on day 0 and day 7. Testes were collected on day14 after the first injection to determine silencing effect of dsRNA by detecting transcript levels of *PmPiwi1* in the testis by RT-PCR with specific primers as shown in Table 1.

2.6. Effect of PmPiwi1 silencing on transposon expression level

The consequence of *PmPiwi1* silencing on transposon expression was determined in the testis of *PmPiwi1*-silenced shrimp on day 14 after the first dsRNA injection. Three types of transposon elements i.e. two LTR-retrotransposons; *gypsy1* (Accession no. HF548819), *gypsy2* (Accession no. HF548820.1) and DNA element transposon *mariner* (partially cloned in our laboratory, unpublished data) were examined. The expression level of each transposon was determined by real-time PCR with

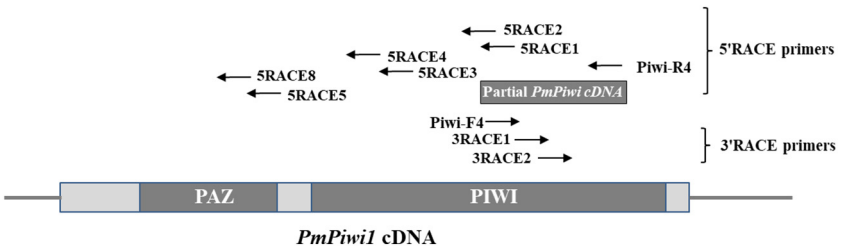

Fig. 1. A schematic diagram for 3′ and 5' RACE of *PmPiwi1* cDNA amplification.
Specific primers were designed from the partial Piwi cDNA sequence. A diagram represents the structure of *PmPiwi1* cDNA and primers for cloning.

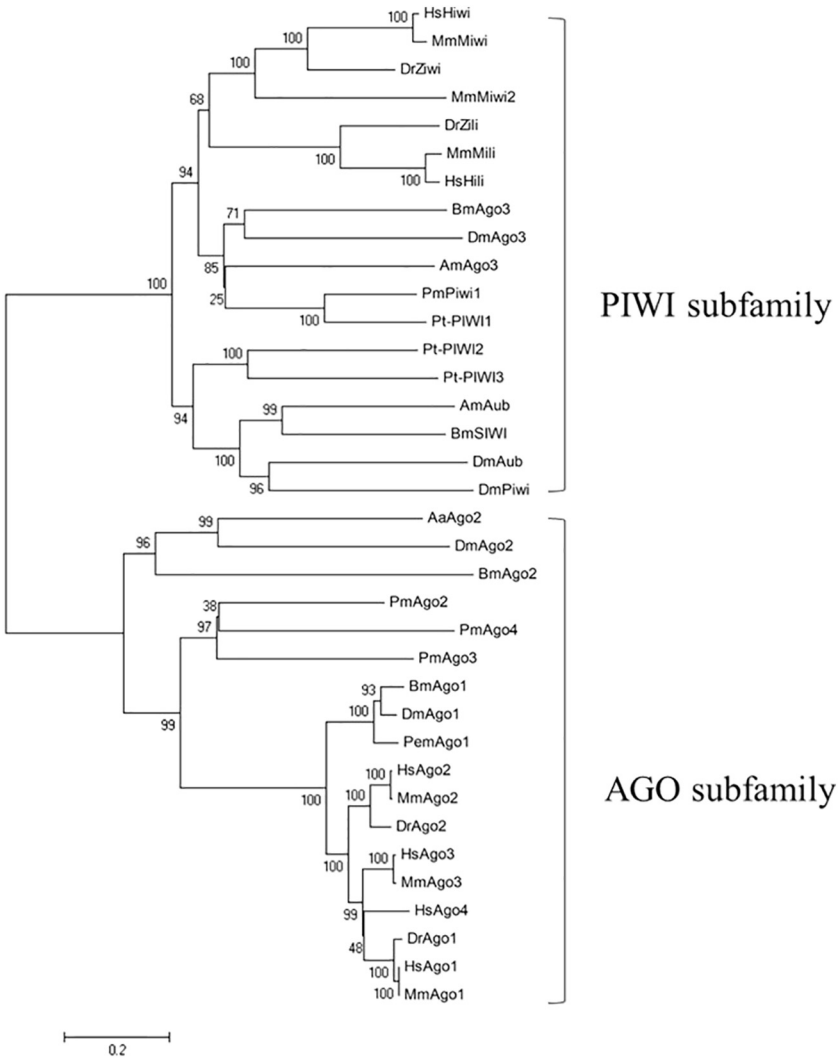

Fig. 2. Phylogenetic relationship among Piwi and Argonaute proteins.

Phylogenetic tree was constructed by Mega4 Program using the neighbor-joining distance analysis. The amino acid sequences analyzed include Piwi and Argonaute proteins of *P. monodon*: PemAgo1 (ABG66640.1), PmAgo2 (AHB63227.1), PmAgo3 (AGC95229.1), PmAgo4 (AIE15914.1), PmPiwi1 (MH279567); *B. mori*: SIWI (AB372006), BmAgo1 (BAF73719.1) BmAgo2, (BAD91160.2), BmAgo3 (AB372007); *D. melanogaster*: DmPiwi (AAF53043.1), DmAub (AG18944.1), DmAgo1 (AAF58314.1), DmAgo2 (AAF49620.2), DmAgo3 (ABO27430.1); *Aedes aegypti*: AaAgo2 (ACR56327.1); *A. mellifera*: AmAub (GQ444142), AmAgo3 (GQ444137); *P. trituberculatus*: Pt-PIW1 (KC203335), Pt-PIWI2 (KC203336), Pt-PIWI3 (KC203337); *D. rerio*: Ziwi (NP899181.1), Zili (NP001073668.2), DrAgo1 (AFU66007.1), DrAgo2 (AFU66008.1); *M. musculus*: Miwi (AAL3104.1), Mili (BAA93706.1), Miwi2 (AAN75583.1), MmAgo1 (NP_700452.2), MmAgo2 (NP_694818.3), MmAgo3 (NP_700451.2); *Homo sapiens*: HsAgo1 (NP_036331.1), HsAgo2 (NP_036286.2), HsAgo3 (NP_079128.2), HsAgo4 (NP_060099.2), HsHiwi (AAC97371.2), HsHili (NP_001129193.1). Bootstrap values from 1000 replicates are indicated at the nodes.

specific primers for each element as shown in Table 1 using KAPA SYBR® FAST qPCR kit (Kapa Biosystems) according to the manufacturer's protocol. The fluorescent signal was detected by Eppendorf Realplex (Eppendorf) machine. All samples were analyzed in duplicate. *Ef1α* was used as reference gene, and the data was analyzed by $2^{-\Delta\Delta CT}$ method.

2.7. Determination of sperm numbers in PmPiwi1-silenced shrimp

According to Jiang et al. (2009), spermatophores and sperms in male *P. monodon* were first detected at 157 days of age or about 21.7 g bw. To ensure the formation of spermatophore, adult male shrimp approximately 11 months old was used to determine the function *PmPiwi1* in spermatogenesis. The shrimp were divided into 2 groups; the first group was injected with *GFP*-dsRNA (dsGFP) as a control group, and the second group was injected with dsPiwi1 ($n = 4$ each). The dsRNA was injected at a dose of 2.5 μg·g^{-1} shrimp bw into the hemocoel at the base of the fifth pleopod. Previous study reported that spermatogenesis was related to molting cycle in *P. monodon*, and the newly formed spermatophores could be observed around day 3 after molt. Therefore, to investigate the function of *PmPiwi1*, male shrimps were injected on day 3 after molting (molting stage C-D0), and tissues (testes and spermatophores) were collected on day 3 after the next molt. One of the two spermatophores (the left one) was collected and homogenized in 1 ml of Ca^{2+}-free seawater (370 mM NaCl, 15 mM KCl, 8.5 mM H_3BO_3, 4.75 mM NaOH, 20 mM $MgSO_4.7H_2O$, pH 7.4) at 4 °C. Then, 25 μl of sperm suspension were mixed with 0.4% trypan blue and incubated at room temperature for 5 min. After that, 15 μl of the mixture were dropped on a hemacytometer, and the number of sperms were counted under light microscope. Data were analyzed using SPSS program. Differences between groups was analyzed by *t*-test at $P < .05$ as statistical significance. All experiments were repeated in triplicate.

3. Results

3.1. Cloning and characterization of Piwi1 cDNA in P. monodon

The full-length nucleotide sequence of *PmPiwi1* cDNA was obtained by RACE strategy. The combined *PmPiwi1* cDNA fragment is 2988 bp in length with a 66 bp 5′UTR, a putative 2811 bp coding region and a 111 bp 3′ UTR (GenBank accession no. MH279567). The continuous reading frame of *PmPiwi1* was verified by RT-PCR. The deduced amino acid sequence of PmPiwi1 contains 936 residues with a predicted molecular weight of 105.31 kDa and a theoretical isoelectric point of 9.36. Identification of conserved domains by ScanProsite program (prosite.expazy.org/scanprosite) revealed that PmPiwi1 contains the signature PAZ and PIWI domains of the Argonaute family (Supplementary Fig. S1). The predicted catalytic residues Asp-Asp-His (DDH) were also present at the C-terminal PIWI domain of PmPiwi1 similar to other members of the Argonaute family.

Comparison of similarity among PmPiwi1 and their homologues in other species shows that most of the similarities lay in the conserved

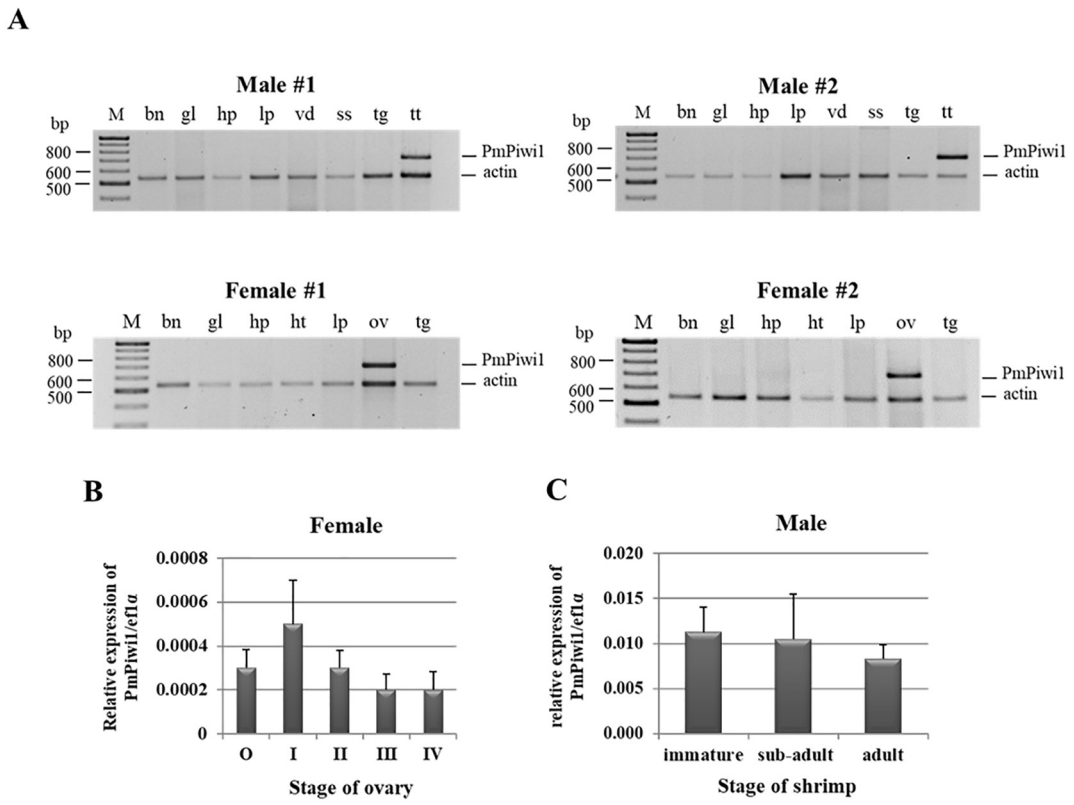

Fig. 3. Expression profile of *PmPiwi1* in *P. monodon*.
A) Tissue distribution of *PmPiwi1* expression in *P. monodon*. The mRNA transcript levels of PmPiwi1 in eyestalk ganglia (Es), brain (Bn), gill (Gl), haemolymph (Hl), hepatopancreas (Hp), lymphoid organ (Lp), throracic ganglia (Tg), testis (Tt), sperm duct or vas deferens (Vd), spermatophore sac (Ss) and ovary (Ov) were detected by semi-quantitative RT-PCR. The level of actin transcript (550 bp) was also detected as an internal control. The pictures show the inverted images of ethidium bromide stained agarose gels of *PmPiwi1* transcript in two male and two female shrimp. B) The expression levels of *PmPiw1* in shrimp ovaries at different stages of ovarian development i.e. undeveloped stage (stage O), pre-developed stage (stage I), early-developed stage (stage II), late developed stage (stage III) and mature stage (stage IV) were determined by real-time PCR (n = 4 each). Expression levels of *PmPiwi1* relative to that of *EF1α* were analyzed by $2^{-\Delta\Delta Ct}$ method and presented as mean ± SEM. C) The expression levels of *PmPiwi1* in the testis of adolescent or immature, sub-adult and adult *P. monodon* (n = 4 each) were determined by RT-PCR and analyzed as mentioned above.

PAZ and PIWI domains. Phylogenetic tree analysis revealed that PmPiwi1 was classified into the PIWI subfamily of Argonaute proteins and clustered in the same group as insect Ago3 with the closet relatedness to Piwi1 of the crab *P. trituberculatus* (Fig. 2).

3.2. Expression of PmPiwi1 in P. monodon

The expression of *PmPiwi1* mRNA in *P. monodon* tissues was determined by RT-PCR. High levels of *PmPiwi1* transcript were detected in the testis and, at a lower level, in the ovary but was not detected in other tissues (Fig. 3A).

In order to investigate further whether or not the expression of *PmPiwi1* in the ovary changes upon ovarian development, the levels of *PmPiwi1* transcript in the ovary at different developmental stages were determined by real-time PCR. The result in Fig. 3B showed that the expression levels of *PmPiwi1*were not significantly different throughout ovarian development from stage 0 to stage IV. In male shrimp, the expression levels of *PmPiwi1* in the testis was rather constant from immature to adult shrimp (Fig. 3C).

3.3. Function of PmPiwi1 in transposon suppression

The efficiency of *PmPiwi1* silencing by specific dsRNA was investigated in the testis of *P. monodon*. The injection with double dosages of dsPiwi1 at 2.5 $\mu g \cdot g^{-1}$ bw on day 0 and day 7 showed the highest suppression of *PmPiwi1*, approximately 96%, at 14 days post-injection (dpi.) (Fig. 4A). The expression of other *Agos* of *P. monodon* was not affected by dsPiwi1 (Fig. 4B), indicating the specificity of dsPiwi1 to knockdown its target transcript.

To determine the influence of *PmPiwi1* silencing on transposon expression in shrimp testis, the expression of *PmPiwi1* was suppressed by dsPiwi1 for 14 days as described above. The transcript levels of three types of transposons including two *gypsy*-like elements and a *mariner*-like element in *PmPiwi1*-knockdown shrimp were determined by real-time PCR. The results showed that the expression level of *gypsy1* was slightly increased, while *gypsy2* and *mariner*-like elements were significantly up-regulated in *PmPiwi1*-knockdown shrimp when compared with the control (Fig. 5).

3.4. Effect of PmPiwi1-knockdown on spermatogenesis in P. monodon

To investigate the function of *PmPiwi1* in sperm production, male shrimp were injected with dsPiwi1 at 2.5 $\mu g \cdot g^{-1}$ bw on day 3 after molt, and the testes and spermatophores were collected on day 3 after the next molting. The efficiencies of *PmPiwi1* knockdown in this experiment (Fig. 6A) were comparable to the previous experiment. The numbers of sperm deposited in the spermatophores of *PmPiwi1*-knockdown shrimp were significantly reduced when compared with that in the dsGFP-injected and the control group (Fig. 6B). Moreover, the spermatophores of *PmPiwi1*-knockdown shrimp were apparently smaller than that of the control groups (Fig. 6C).

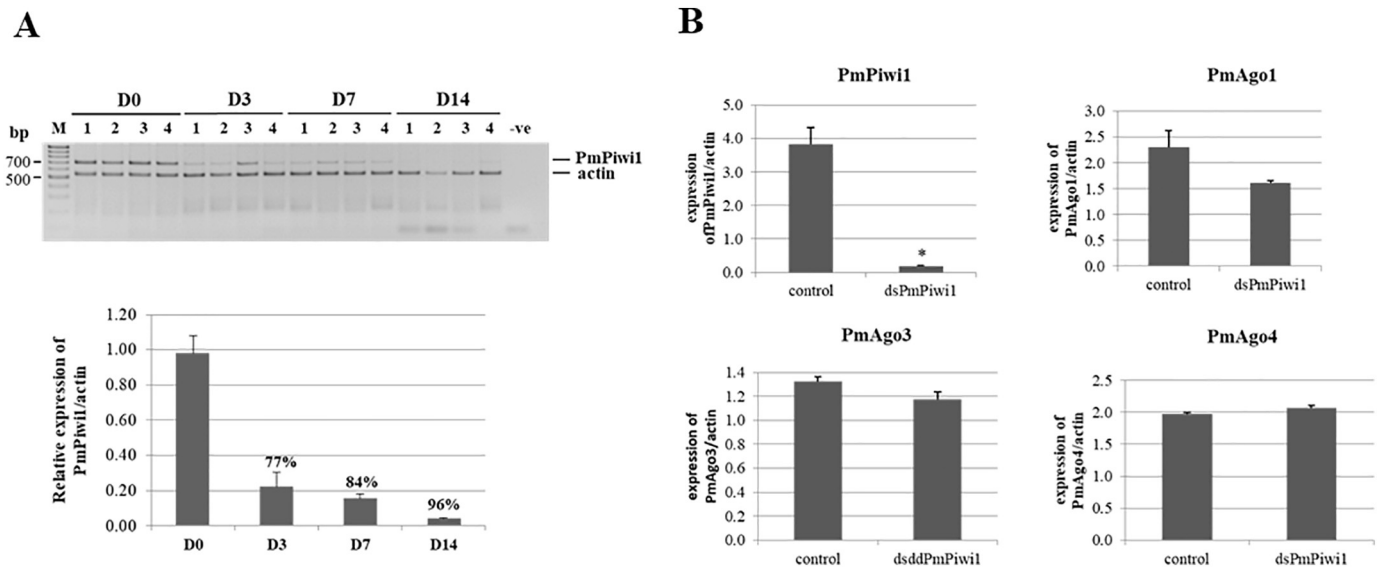

Fig. 4. Efficiency of *PmPiwi1* suppression by dsPiwi1.
A) The *PmPiwi1* transcript levels in the testis of dsPiwi1-injected *P. monodon* at 14 dpi were determined by RT-PCR comparing to that of the control (NaCl injected shrimp). *Actin* transcript was amplified as an internal control. The intensity of each band of *PmPiwi1* and *actin* transcripts on the ethidium bromide-stained agarose gel (upper panel) was determined by Scion-Image program and used for the calculation of the relative expression levels of *PmPiwi1* and *actin* as shown in bar graph (lower panel). B) Specificity of *PmPiwi1* suppression by dsPiwi1 is demonstrated by determination of the expression levels of *PmAgo1*, *PmAgo3* and *PmAgo4* cDNAs in dsPiwi1-injected shrimp compared with the control. An asterisk indicates statistical difference between groups as determined by Turkey's test of independent sample *t*-test from SPSS program ($p < .05$).

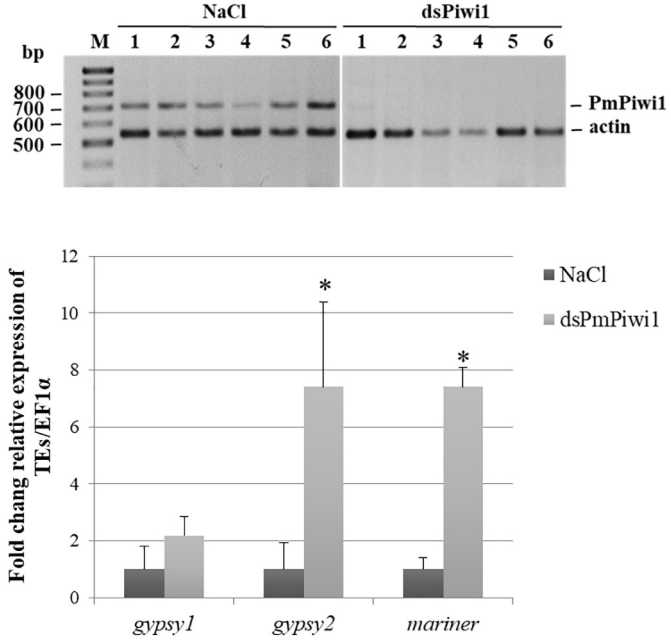

Fig. 5. Transposon expression in the testis of *PmPiwi1*-knockdown *P. monodon*. The expression of *PmPiwi1* in the testis of *P. monodon* was suppressed by the injection of dsPiwi1 as determined by RT-PCR compared to that of the control (NaCl injected shrimp). Actin transcript was amplified as an internal control (upper panel). The expression levels of three types of transposons (*gypsy1*, *gypsy2* and *mariner*-like elements) in the testis of *PmPiwi1*-knockdown shrimp and the control (NaCl-injected shrimp) were determined by real-time PCR (lower panel). Expression level of each transposon relative to that of *Ef1α* was analyzed by $2^{-\Delta\Delta Ct}$ method and shown as mean ± SEM ($n = 6$). Asterisk indicates statistical difference between the *PmPiwi1*-knockdown and NaCl-injected groups as analyzed by *t*-test from SPSS program ($p < .05$).

4. Discussion

A cDNA encoding Piwi protein in the black tiger shrimp, *P. monodon* was identified and characterized. The alignment of the deduced amino acid sequences revealed that PmPiwi1 contained the conserved PAZ and PIWI domains, which are signature of the Argonaute family. Similarly to the PAZ domain of the Ago subfamily that forms a specific binding module for the 2-nt 3′ overhang of small RNAs generated by RNase III-like enzyme such as Dicer, the PAZ domain of the PIWI subfamily forms a binding pocket that anchors the exonuclease-trimmed 3′ end of piRNAs (Matsumoto et al., 2016). The PIWI domain has similar fold to RNaseH with the catalytic triad DDH that is essential for slicing activity of the Ago subfamily (Niraj and Leemor, 2006; Olina et al., 2018; Peters and Meister, 2007). In *Drosophila*, all three members of the PIWI subfamily (Ago3, Aub and Piwi) also possess the conserved DDH residues in their PIWI domain. Whereas the nuclease catalytic triad of Ago3 and Aub was essential for the piRNA biogenesis pathway via the ping-pong cycle, it did not seem to be required for the function of *Drosophila*'s Piwi in repressing transcription of its targets (Rozhkov et al., 2013). The PIWI domain of PmPiwi1 also contained the conserved DDH residues, indicating that PmPiwi1 could form a nuclease catalytic triad, possibly for cleavage of the substrate RNA complementary to the bound piRNAs.

One feature that distinguishes Piwi proteins from the Ago subfamily proteins is the presence of putative asymmetric dimethylated arginine residues (arginine-glycine/RG, arginine-alanine/RA) or symmetrically dimethylated arginine (sDMA) composing of arginine flanked by glycine (GRG) or alanine (GRA or ARG) repeats at the N-terminal region (Kirino et al., 2009; Vagin et al., 2009). Arginine methylation is an important post-transcriptional modification that mediates protein-protein interaction. Piwi proteins were reported to associate with multiple members of the Tudor protein family through sDMA methylation, which are necessary for piRNA function in transposon silencing and gametogenesis in both flies and mice (Kirino et al., 2010; Mathioudakis et al., 2012; Nishida et al., 2009; Vagin et al., 2009). The deduced PmPiwi1possesses multi-arginine methylation sites at the N-terminus, suggesting the potential to form heterodimeric complex with Tudor

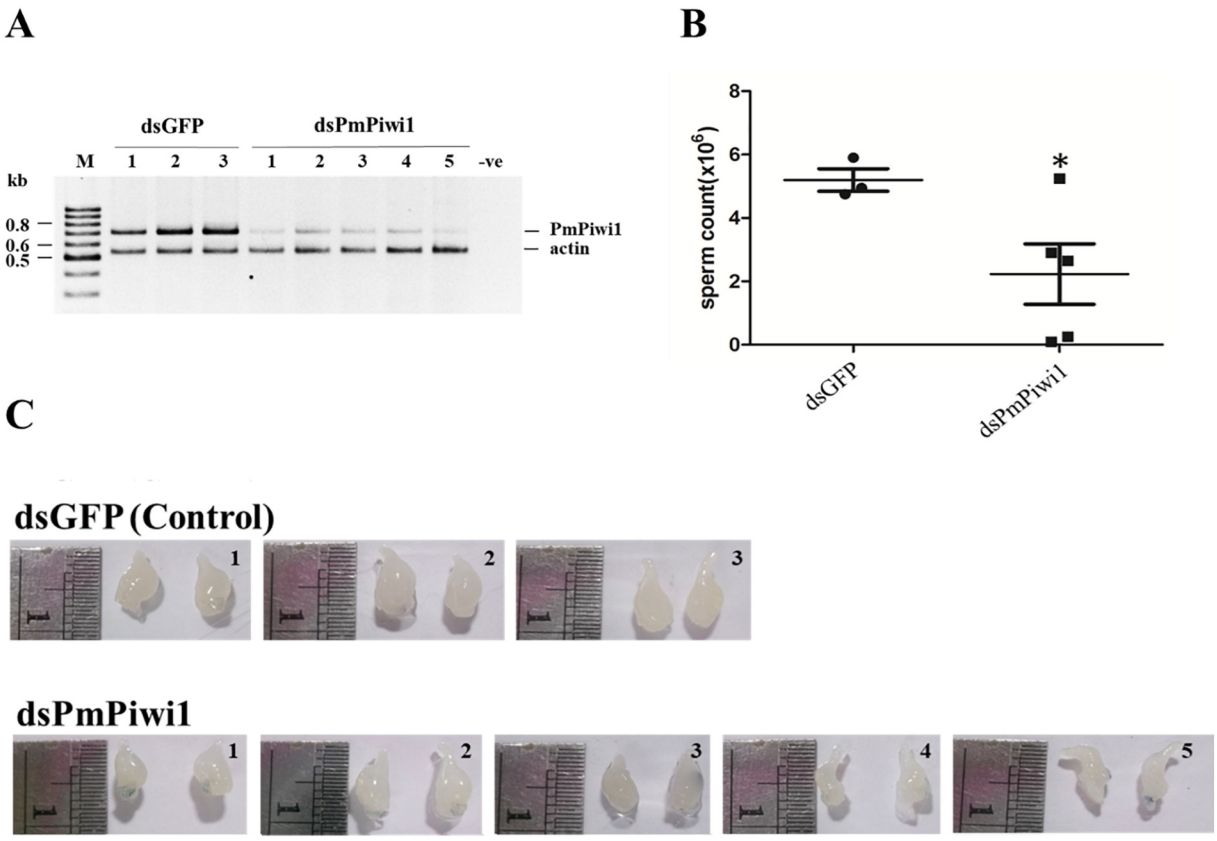

Fig. 6. Numbers of sperms in *PmPiwi1*-knockdown *P. monodon*.
DsPiwi1 was injected into male *P. monodon* at 2.5 μg.g^{-1} bw on day 3 after molt, and the testes and spermatophores were collected on day 3 after the next molt. Shrimp injected with dsGFP were used as a control group. A) The efficiency of dsPiwi1 to knockdown *PmPiwi1*expression in the testis was determined by RT-PCR compared to the control shrimp. B) The numbers of sperms in the spermatophore of *PmPiwi1*-knockdown and the control shrimp were counted using the hemacytometer under microscope. Asterisk indicates statistical difference of sperm numbers between both groups as determined by One-way ANOVA from SPSS program ($\rho < 0.05$). C) Morphology of spermatophore of the *PmPiwi1*-knockdown shrimp (dsPmPiwi1) and dsGFP-injected shrimp (control) was compared.

proteins and play role in the operation of piRNA pathway during germline development of the shrimp.

The restricted gonad expression of *PmPiwi1* conforms to the expression and the role in germline development, a conserved function of Piwi proteins across species. Different types of Piwi may display distinct expression profiles during sperm development suggesting that they have diverse functions in different phases of spermatogenesis. For example, in the murine *Mus musculus*, Miwi2 was restricted expressed only in the testis (Carmell et al., 2007) whereas Miwi and Mili were detected in both testis and oocyte (Deng, 2002; Ding et al., 2013; Kabayama et al., 2017). Miwi is expressed from meiotic spermatocytes to elongating spermatids (Deng, 2002), whereas Mili is expressed from 3 dpp mitotically arrested prenatal germline stem cell to round spermatids (Kuramochi-Miyagawa et al., 2004; Unhavaithaya et al., 2009). *Miwi*-deficient mice show spermatogenesis arrest at early spermiogenic stage while *Mili*-deficient mice are terminally blocked at zygotene or early pachytene stages of meiotic prophase I (Beyret and Lin, 2011; Deng, 2002; Grivna et al., 2006; Kuramochi-Miyagawa et al., 2004). Miwi2 is detected from day 15.5 dpc to 3 dpp in mitotically arrested prenatal germline stem cells (Aravin et al.; Aravin et al., 2008). Miwi2 was also found in Sertoli cells, which are somatic supporting cells within seminiferous tubules (Carmell et al., 2007). *Miwi2* mutants not only displayed a meiotic progression defect in early prophase of meiosis I but also seemed to affect mitotic germ cell maintenance (Wasserman et al., 2017). In addition, Miwi and Mili proteins were detected in mouse oocyte, implicating that it may also function in oocyte development (Ding et al., 2013; Kabayama et al., 2017). The function of Piwi was also required for germline stem cell maintenance and differentiation in *Drosophila*. The *piwi* mutant female showed ovarioles that are deficient in germline cells, whereas *piwi* mutant testis contained much fewer bundles of mature sperm. A novel group of *pumilio* mutations affects the asymmetric division of germline stem cells in the *Drosophila* ovary (Lin and Spradling, 1997). A mutation in *aubergine*, one of *Drosophila*'s *piwi* genes also affected the mitotic cycle during oogenesis and led to loss of germline cells. *Cutoff* and *aubergine* mutations result in retrotransposon upregulation and checkpoint activation in *Drosophila* (Chen et al., 2007).

In *P. monodon*, the significant decrease in the number of sperms in spermatophore of *PmPiwi1*-knockdown shrimp compared with that in the control shrimp indicated the function of *PmPiwi1* during spermatogenesis. Recent report in the crab, *P. trituberculatus*, showed the expression of three *piwi* genes at different stages of spermtid and mature spermatozoon suggesting their roles in spermiogenesis (Xiang et al., 2014). Since *PmPiwi1* transcript was detected in the testis but not in vas deferens and spermatophore, PmPiwi1 might be directly involved in meiotic regulation in spermatogenesis but not in sperm differentiation or sperm maturation. Although the gonad-specific expression of *PmPiwi1* suggests its function in both sperm and oocyte development, the detail at which steps PmPiwi1 play a role in gametogenesis control in the shrimp remains to be elucidated. Moreover, other *Piwi* proteins in *P. monodon* that participate in piRNA biogenesis and reproductive regulation still await identification.

Piwi proteins have important function in the control of transposon in animal germline. *Piwi* knockout resulted in transposon activation, which led to germline defects. For example, derepression and up-regulation of endogenous retrotransposon *copia* was found in *loss-of-Piwi*

Drosophila testes. Similarly, *Drosophila Piwi* mutant caused accumulation of *mdg1* transcripts at the apical tip of testes where Piwi protein was not detected (Brennecke et al., 2007; Kalmykova et al., 2005). In the zebrafish, *Zili* mutant resulted in up-regulation of both retrotransposons and DNA transposable element (Saskia Houwing, 2008). The increased expression levels of *gypsy* LTR-retrotransposons and DNA element *mariner* in the *PmPiwi1*-knockdown testis of *P. monodon* in this study suggested the function of *PmPiwi1* in the control of transposable elements in shrimp testis. Another member of Argonaute proteins, namely PmAgo4, that is highly expressed in *P. monodon*'s germline was also demonstrated to regulate transposable elements in shrimp testis (Leebonoi et al., 2015). Whether or not PmPiwi1 works in cooperation with PmAgo4 to protect shrimp germ cells from deleterious effects of excessive movement of transposable elements during gamete development needs further investigation. In addition, piRNA biogenesis and transposable elements activation in *Drosophila* and mice are known to be regulated by three members of Piwi proteins (Brennecke et al., 2007; Manakov et al., 2015; Rozhkov et al., 2013; Saito et al., 2006). Three types of Piwi transcripts were also identified in the crab, *P. trituberculatus* (Xiang et al., 2014). Therefore, identification of additional members of Piwi in *P. monodon* still awaits exploration.

In conclusion, a novel cDNA encoding *PmPiwi1* in *P. monodon* was identified. Its gonad-specific expression was correlated with potential roles in sperm production and regulation of transposable elements in shrimp testis. The possibility that PmPiwi1 functions together with PmAgo4 and other Piwi members to maintain integrity of shrimp germ cells from transposition effects as has been demonstrated in a number of organisms needs to be elucidated.

Supplementary data to this article can be found online at https://doi.org/10.1016/j.cbpa.2018.11.022.

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Regulation of vitellogenin gene expression under the negative modulator, gonad-inhibiting hormone in *Penaeus monodon*

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ABSTRACT

Vitellogenesis is a principal process during ovarian maturation in crustaceans. This process is negatively regulated by gonad-inhibiting hormone (GIH), a neuronal peptide hormone from eyestalks. However, the detailed mechanism through which GIH regulates *Vg* expression is still ambiguous. In this study, suppression subtractive hybridization (SSH) under specific *GIH*-knockdown condition was utilized to determine the expression of genes in the ovary that may act downstream of GIH to control vitellogenin synthesis in *Penaeus monodon*. The total of 102 and 82 positive clones of up-regulated and down-regulated genes in *GIH*- knockdown shrimp were identified from the forward and reverse SSH libraries, respectively. Determination of the expression profiles of these reproduction-related genes during ovarian development revealed that the expression of *calreticulin* (*CALR*) was significantly reduced in vitellogenic ovary suggesting its role in vitellogenesis. Suppression of *CALR* by specific dsRNA showed elevated *vitellogenin* (*Vg*) transcript level in the ovary at day 7 post-dsRNA injection. Since CALR can bind to steroid hormone receptors and prevents the binding of the receptor to its responsive element to regulate gene expression, it is possible that CALR is an inhibitory mediator of vitellogenin synthesis via steroidal pathway. Our results posted a possible novel pathway of GIH signaling that might interfere the steroid signaling cascade to mediate *Vg* synthesis in the shrimp.

1. Introduction

Vitellogenesis is essential for ovarian maturation in crustaceans. This process can be divided into two phases: the synthesis of a yolk precursor, vitellogenin (Vg) and the accumulation of a yolk protein or vitellin (Vn) into oocytes. In the black tiger shrimp *Penaeaus monodon*, Vg is synthesized in both the ovary and hepatopancreas like in other penaeid shrimps (Tiu et al., 2006). Following its synthesis, the Vg precursor is proteolytically cleaved into smaller subunits by enzymes of the subtilisin family in the hemolymph. The processed Vg is subsequently deposited into developing oocytes before undergoing further biochemical modifications into vitellin that is a major source of nutrient during embryogenesis (Tiu et al., 2008; Wilder et al., 2010). Vitellogenesis in crustaceans is negatively influenced by a gonad-inhibiting hormone (GIH), which is well characterized in a number of crustaceans (Yang and Rao, 2001; Edomi et al., 2002; Treerattrakool et al., 2008; Chen et al., 2014). GIH is a member of type II crustacean hyperglycemic hormone family that is synthesized and stored in the X-organ-sinus gland complex in the eyestalks. The mature peptide of GIH consists of 78–83 amino acid residues with the predicted molecular weight of 8–9 KDa (Treerattrakool et al., 2008; Webster et al., 2012). Detection of GIH peptide in the hemolymph revealed high levels of GIH during immature stage before rapidly declined in later stages of ovarian maturation cycle (de Kleijn et al., 1998; Okumura et al., 2007; Urtgam et al., 2015). Oppositely, Vg levels in the hemolymph as well as *Vg* mRNA levels in both hepatopancreas and ovary were almost undetectable at the immature stage, then sharply increased in vitellogenic stage and maintained at relatively high levels throughout the rest of ovarian maturation cycle (Longyant et al., 2003; Kang et al., 2014).

Recent studies demonstrated that, ovarian maturation in *P. monodon* could be induced when the *GIH* expression was suppressed by a specific double-stranded RNA (Treerattrakool et al., 2011), and neutralization of GIH peptide by monoclonal antibody against the recombinant GIH (Treerattrakool et al., 2014) also gave rise to ovarian maturation. These results suggest that GIH retards ovarian maturation via inhibition of *Vg* expression. However, the detailed mechanism through which GIH regulates *Vg* expression is not well studied.

In order to understand the molecular basis underlying vitellogenesis regulation in the shrimp, we investigated differential gene expression in the ovary of *P. monodon* under GIH silencing by suppression subtractive

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hybridization. The expression pattern during ovarian maturation of calreticulin (CALR), one of the genes that were significantly down-regulated upon GIH deprivation, and its possible involvement in the control of *Vg* expression were determined. The understanding of the control mechanism of vitellogenesis via GIH-mediated pathway will be useful for hormonal manipulation methods to achieve efficient improvement of shrimp reproductive performance in the future.

2. Materials and methods

2.1. Shrimp sample

Immature and previtellogenic female shrimp were kindly provided by the Shrimp Genetic Improvement Center, Suratthani, Thailand. Vitellogenic shrimp were caught from the Andaman sea in the southern part of Thailand. The shrimp were acclimatized in 30 ppt sea water at 28 °C at the aquaculture unit, Institute of Molecular Biosciences, Mahidol University until used.

2.2. Silencing of PmGIH using dsRNA interference

To investigate the differential ovarian gene expression under specific *GIH*-knock down condition in female shrimp, the *GIH*-specific double-stranded RNA (*GIH*-dsRNA) was synthesized in *Escherichia coli* as described earlier (Treerattrakool et al., 2008). Previtellogenic female shrimp (approximately 85–120 g) were injected with 0.3 $\mu g.g^{-1}$ shrimp bodyweight (bw.) at the base of eyestalks. Shrimp injected with *GFP*-dsRNA were used as the control group ($n = 3$). The shrimp were cultured in 30 ppt sea water at 28 °C for 5 days. Then, the expression of *GIH* in the eyestalk and *Vg* in the ovary of the shrimp in each group were determined by RT-PCR.

2.3. Detection of transcript levels by RT-PCR

Shrimp eyestalk ganglia and ovaries were freshly dissected and homogenized in TRI-Reagent® (Molecular Research Center). The RNA was extracted according to the manufacturer's protocol, and analyzed by NanoDropTM 1000 Spectrophotometer and 2% agarose gel electrophoresis.

The first strand cDNA was synthesized from 1.5 μg of total RNA sample with PRT-oligo-dT_{12} primer, and reverse transcriptase using the following condition: 25 °C for 5 min, 42 °C for 60 min, and 70 °C for 15 min. The suppression of *GIH* transcript in the eyestalk ganglia was determined by PCR in a 25 μl-reaction containing 1 μl of the first strand cDNA, 0.5 μM each of GIH1-F and 3UTR-PmGIHR1 primers, 0.5 mM of dNTPs, 1× Taq buffer, and 1.25 U of Taq DNA polymerase (New England BioLab). The PCR reaction was subjected to the following temperature profile: 94 °C for 2 min; 35 cycles of 94 °C for 15 s; 55 °C for 15 s; 68 °C for 2 min, and a final extension at 72 °C for 3 min. The transcript of *Vg* gene in the ovary of *GIH*-dsRNA treated shrimp and *GFP*-dsRNA treated shrimp was also determined by RT-PCR using the above condition except that Vg-F1 and Vg-R1 primers were used instead. The *actin* transcript was amplified as an internal control using PmActin-F and PmActin-R primers with 21 cycles of 94 °C for 30 s, 55 °C for 30 s and 74 °C for 1 min followed by 74 °C for 7 min. The amplicons of *GIH*, *Vg*, and *actin* with the expected sizes of 360, 380 and 550 bp, respectively were analyzed by 1.5% agarose gel electrophoresis.

2.4. Construction of suppression subtractive hybridization (SSH) library

To determine genes in the ovary whose expression alters under dsRNA-mediated *GIH* silencing, changes in gene expression in the ovary of the *GIH*-knockdown shrimp were determined by suppression subtractive hybridization (SSH). One milligram of total RNA from three individual shrimp in either *GIH*-dsRNA or *GFP*-dsRNA treated group were pooled, and poly A^+ RNA was isolated using poly A^+ Spin™ mRNA isolation kit (New England Biolabs) according to manufacturer's protocol. Then, 1.5 μg of the poly A^+ RNA from each group were used to construct forward and reverse cDNA libraries using a PCR-select™ cDNA subtraction kit (Clonetech). Briefly, the cDNA synthesized from the poly A^+ RNA of the *GFP*-dsRNA treated and *GIH*-dsRNA treated shrimps were digested with *Rsa* I to generate the blunt-ended cDNA fragments. In order to obtain the genes that were up-regulated upon *GIH*-knockdown condition, the *Rsa* I-digested cDNA from *GFP*-dsRNA treated shrimp was used as a driver, while the *Rsa* I-digested cDNA from *GIH*-dsRNA treated shrimp was ligated to adaptors and used as the tester. After hybridization and amplification as mentioned in the manufacturer's protocol, this library was referred to as a forward library. Vice versa, the reverse library was constructed by using the *Rsa* I-digested cDNA from GIH-dsRNA treated shrimp as a driver and the *Rsa* I-digested cDNA from *GFP*-dsRNA treated shrimp as a tester to determine the genes that were down-regulated upon *GIH*-knockdown condition. The efficiency of SSH was analyzed using *actin* gene amplification.

The subtracted mixture was nested amplified, cloned into the pGEM-T Easy vector (Promega), and introduced into *E. coli* strain DH5α by transformation. All the transformants were selected on X-gal/IPTG agar plates and screened by *Eco*R I digestion. The nucleotide sequences of the subtracted libraries were determined by automated DNA sequencing at 1st BASE Laboratories Sdn Bhd, Malaysia.

2.5. Analysis of cDNA from SSH libraries by bioinformatics

The cDNA fragments obtained from subtractive libraries were analyzed and processed by removing the unwanted vector and primer sequences using the Bio-Edit program and NCBI VecScreen. Homologs of known sequences were searched by the blastn and blastx programs against NCBI GenBank database (http://www.ncbi.nlm.nih.gov/BLAST) for clone annotation. The significant matches were accepted at *E*-values lower than 1×10^{-7}.

2.6. Validation of the expression of responsive genes upon GIH suppression

The expression of the genes of interest from forward and reverse SSH libraries were verified by quantitative reverse transcription PCR (RT-qPCR). The dilution of 1:5 of cDNA from the ovary of either *GIH*-dsRNA-injected shrimp or *GFP*-dsRNA-injected shrimp were used in the amplification of gene transcripts with 0.2 pmol of each gene specific primer, (Table 1) using KAPA SYBR® FAST qPCR kit (KAPABIOSYSTEMS, USA) according to the manufacture's protocol. The reactions were subjected to ABI® Prism 7500 with the following temperature profile; 95 °C for 3 min then 40 cycles of 95 °C for 5 s and 60 °C for 30 s. The *EF-1α* gene was amplified with 0.1 pmol of each gene-specific primer, and used as an internal control. The melting curve of the amplification products was analyzed by subsequent dissociation process at 95 °C for 15 s, followed by annealing at 60 °C for 15 s, then gradually increased for 10 s each at 0.2 °C increment to 95 °C (Fig. A.1). The amplification of each gene was done in triplicate. The amount of relative gene transcript levels was calculated using $2^{-\Delta\Delta Ct}$ method according to Livak and Schmittgen (2001). The efficiency of each primer pair was analyzed by the standard curve generated in triplicate with 5 different cDNA concentrations prepared by 2-fold serial dilution. The relative expression was calculated using a mathematic model of Pfaffl (2001).

2.7. Relative quantification of gene expression levels in the ovary during ovarian maturation

Ovarian maturation was divided into four stages as determined by ovarian size and color, gonado-somatic index (GSI) as well as by histochemical staining with hematoxylin and eosin based on Tan-Fermin and Pudadera (1989). Ovary from the shrimp at each stage of ovarian

Table 1
Primers use in this study.

Primer	Sequences (5′-3′)	size	Usage
PRT	CCGGAATTCAAGCTTCTAGAGGATCCTTTTTTTTTTTTTTTT		cDNA synthesis
GIH1-F	GTGGTGGGAGCGCAGCTTAGCT	360	GIH gene silencing and Vg expression
3UTR-PmGIHR1	TCT CCCCCCTGCGCTAGGATCCCG		
Vg-F1	CTAAGGCAATTATCACTGCTGCT	380	
Vg-R1	AAGCTTGGCAATGTATTCCTTTT		
PmActin-F	GACTCGTACGTCGGGCGACGAGG	550	
PmActin-R	AGCAGCGGTGGTCATCACCTGCTC		
TSP-F	GGCAGCACTGCTTTGGCATGA	114	The genes obtained by SSH and validation
TSP-R	ACCCTGGTACAAGTAGAACCTAATGG		
Per1-F	GCTTGGTGGCGTGTTGCAG	160	
Per1-R	GGCCTGGACACAAGTTATCAGGG		
qVg-F	TCCATCTGCAGCACCAATCTTCGC	174	
qVgR	GCAACAGCCTTCATTCTGATGCCA		
CALR-F	CCAGACTGGACAGGATGCCC	187	
CALR-R	GGTATGGCGACTCTCCGTGC		
Sap-F	CGTCCCTTTCCAACAGGTGC	236	
Sap-R	GGAGAGCATCCAGCTTGGAC		
ANT-F	CGAGCGAAGTCAAGGGGGTAG	177	
ANT-R	CCGATATTTCCCCACCCAGGC		
EF1α-F	GAACTGCTGACCAAGATCGACAGG	140	
EF1α-R	GAGCATACTGTTGGAAGGTCTCCA		
PmCALR-F	ATGAAGACCTGGGTTTTTCTTGCC	1221	CALR-dsRNA construction and CALR gene silencing
PmCALR-R	TTACAGCTCGTCATGTTCAAGATCATTATCAAG		
SL-NCALR F-*Xba*I	GCTCTAGACGACAGCCCAGATTGGGAG	511	
SL-NCALR R-*Bam*HI	CGGGATCCCTCGAGTTCACCAGACTGAGC		
ST-NCALR F-*Xho*I	CGCTCGAGCGACAGCCCAGATTGGGAG	431	
ST-NCALR R-*Bam*HI	CGGGATCCGATGGGAAAATACGTCATCCTTGC		
3CALR-F	GGGTGAATGGAAGCCTAAGCAG		

development (n = 3–5) was dissected for total RNA isolation by Tri Reagent® (Molecular Research Center). Approximately 1.5 μg of the total RNA was subjected to reverse transcription reaction with oligo-dT primer as described in 2.3. The cDNA from shrimp at each ovarian maturation stage was used for amplification of the selected genes by RT-qPCR as described in 2.6.

2.8. Production of calreticulin specific double-stranded RNA (CALR-dsRNA)

Calreticulin (PmCALR) is probably involved in the regulation of Vg synthesis because its expression was down-regulated under *GIH*-knockdown condition. The RNA interference (RNAi) gene silencing was chosen as an approach to investigate the function of PmCALR in this study. The *PmCALR* cDNA was amplified from shrimp ovary using specific primers designed from the ORF of *PmCALR* (Visudtiphole et al., 2010) in a reaction containing 1 μl of first-stranded cDNA from shrimp ovary, 0.3 mM of dNTPs, 1 × long range buffer, 1.75 mM $MgCl_2$, 0.5 μM PmCALR-F primer, 0.5 μM PmCALR-R primer and 1.25 U KAPA Long-Range DNA polymerase in a total volume of 25 μl. The PCR reaction was carried out with the following temperature profile: 94 °C for 2 min; then 35 cycles of 94 °C for 15 s; 55 °C for 15 s; 68 °C for 2 min, and a final extension at 72 °C for 3 min.

After verification of the nucleotide sequence, the plasmid harboring *PmCALR* cDNA was used as a template to design specific dsRNA targeting the N-terminal domain, and produced in a bacterial expression system. Briefly, a DNA template for the 511 bp stem-loop template of dsRNA was amplified with primers SL-NCALR F-*Xba* I, and SL-NCALR R-*Bam*H I, while the DNA template for the 431 bp stem of dsRNA was amplified with primers ST-NCALR F-*Eco*R I and ST-NCALR R-*Bam*H I. The stem-loop fragment was first cloned into pET17b vector at *Xba* I and *Bam*H I sites, following by the stem fragment at *Eco*R I and *Bam*H I site. Then, the recombinant NCALR-pET17b expression cassette was used to transform *E. coli* strain DH5α. After verification of the nucleotide sequence, the plasmid of the correct clone was transformed to *E. coli* strain HT115. The expression of a stem-loop *CALR*-dsRNA was carried out by 0.4 mM IPTG induction in 2XYT medium for 4 h at 37 °C with shaking. The stem-loop *CALR*-dsRNA was extracted by Tri-solution and dissolved in 150 mM NaCl and stored at −30 °C until used. The concentration and purity of the dsRNA was determined by agarose gel electrophoresis. The quality of the dsRNA was verified by RNAse digestion assay.

2.9. In vivo silencing of CALR

To investigate the role of CALR in regulating *Vg* gene, the expression of *Vg* was determined upon *CALR*-knockdown in *P. monodon*. Vitellogenic female shrimp (approximately 250 g) were divided into two groups; shrimp injected with *GFP*-dsRNA as a negative control and shrimp injected with *CALR*-dsRNA at 2.5 $\mu g.g^{-1}$ body weight of shrimp (bw) (n = 5). The expression level of *CALR* and *Vg* in the ovary of shrimp in each group were determined on day 7 after injection by semi-quantitative RT-PCR. The *CALR* transcript was amplified using multiplex PCR reaction containing 0.5 μM of 3CALR-F and CALR-R primers, 0.1 μM actin-F and actin-R primers with 25 cycles of 94 °C for 30 s, 55 °C for 30 s and 74 °C for 1 min followed by 74 °C for 7 min. The transcript levels of *Vg* in the ovary of both groups were also determined by semi-quantitative RT-PCR using Vg-F1 and Vg-R1 primers as previously mentioned.

2.10. Statistical analysis

All statistical analyses were performed using SPSS 18.0 Software. The statistically significant differences among treatments ($p < .05$) was analyzed by One-way ANOVA and Student's t-test. Before the comparison, Kolmogorov–Smirnov and Levene's test were used to test the normality and homogeneity of variances, respectively.

3. Results

3.1. Differential gene expression in the ovary of P. monodon under GIH-knockdown condition

In order to identify genes that may play roles in vitellogenesis,

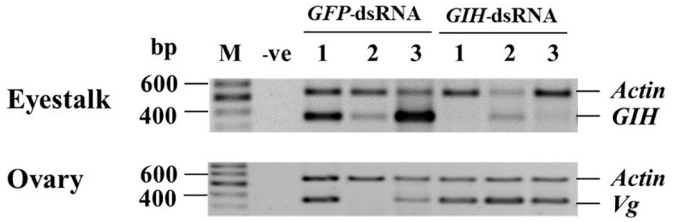

Fig. 1. Silencing of *PmGIH* by dsRNA. Previtellogenic *P. monodon* (approximately 85–120 g) were injected with *GIH*-dsRNA and a negative control *GFP*-dsRNA at 0.3 $\mu g.g^{-1}$ shrimp b.w. at the basal of eyestalk. On day 5 post-injection, the eyestalk and ovary were collected and processed for RT-PCR analysis of *PmGIH* and *Vg* expression, respectively. The expression of *actin* was used as an internal control. The amplification products were analyzed on 1.5% agarose gel along with the 100 bp ladder DNA size marker (M). The number above each lane represents individual shrimp in each group; −ve is a negative control of PCR.

changes in global gene expression in the ovary of *GIH*-knockdown shrimp were determined by SSH. SSH libraries were constructed from a pool of ovary cDNA of three individual *GIH*-dsRNA-injected *P. monodon* in which the expression levels of *Vg* was confirmed to be up-regulated (Fig. 1).

The efficiency of SSH was shown by the successful subtraction of the actin transcript (Fig. A.2). After nucleotide sequence determination and processing by removing the unwanted vector and primer sequences, 102 and 82 high-quality sequences were obtained from the forward and reverse subtraction libraries, respectively. The homology search against the GenBank database by blastn and blastx programs at NCBI revealed that 63 cDNA sequences from the forward library (representing genes that were up-regulated upon *GIH*-knockdown) were annotated to 37 different known genes, and 39 were hypothetical or unknown genes. Whereas the reverse library contained 45 down-regulated sequence that could be annotated to 32 different genes, and the remaining 37 cDNA sequences were hypothetical or unknown genes (Fig. 2).

3.2. Verification of reproduction-related genes under GIH deprivation

The genes that were up-regulated upon *GIH*-knockdown were categorized based on their functions as shown in Table 2. These include ribosomal RNA genes, hypothetical and unknown genes, genes encoding proteins in several pathways such as ovarian development, focal adhesion, energy/lipid metabolism, signaling transduction pathway, cell cycle/transcription factor/DNA repair, and protein folding. The RT-qPCR analysis of three ovarian development related genes namely *peritrophine I* (*Per I*), *thrombospondin II* (*TSP II*), and *Vg* with the efficiency of 97.7%, 98.0% and 99.9%, respectively confirmed their up-regulated expression under *GIH*-suppressed condition (Fig. 3).

The 32 down-regulated genes upon *GIH*-knockdown from the reverse library were categorized into ribosomal RNA genes, hypothetical and unknown genes, and genes that are involved in ovarian development, energy/lipid metabolism, calcium signaling pathway, protein trafficking/protein folding, and protein synthesis (Table 3). The validation of expression levels of genes involving in reproductive system i.e. *calreticulin* (*CALR*) and energy metabolism such as *saposin* (*Sap*), and *Adenine nucleotide translocate* (*ANT*) with RT-qPCR efficiency of 98.4%, 99.0% and 99.8%, respectively revealed the reduced expression levels under *GIH*-suppressed condition (Fig. 3).

3.3. Expression of reproduction-related genes at different ovarian developmental stages in P. monodon

In order to investigate whether the genes that were expressed responsively to *GIH*-knockdown have function in ovarian development or not, the relative expression of six candidate genes during different stages of ovarian development in the shrimp was determined by RT-qPCR. The result showed that all of the genes from the forward library i.e. *Per I, TSP II* and *Vg* exhibited similar expression profile during ovarian development. Their expression levels were elevated from previtellogenic stage through late-vitellogenic stage, and declined when the ovary entered the ripe stage (Fig. 4A-C). By contrast, the candidate genes from the reverse library (*CALR*, *Sap*, and *ANT*) were highly expressed in the pre-vitellogenic stage and decreased to the lowest levels at early-vitellogenic or late- vitellogenic stages before rising again when the ovary entered the ripe stage (Fig. 4D-F). The ovarian development-related patterns of the expression of these up- or down-regulated genes are consistent with their relative expression in the *GIH*-knockdown shrimp, and suggests the importance of these gene products in early-vitellogenic development of the ovary.

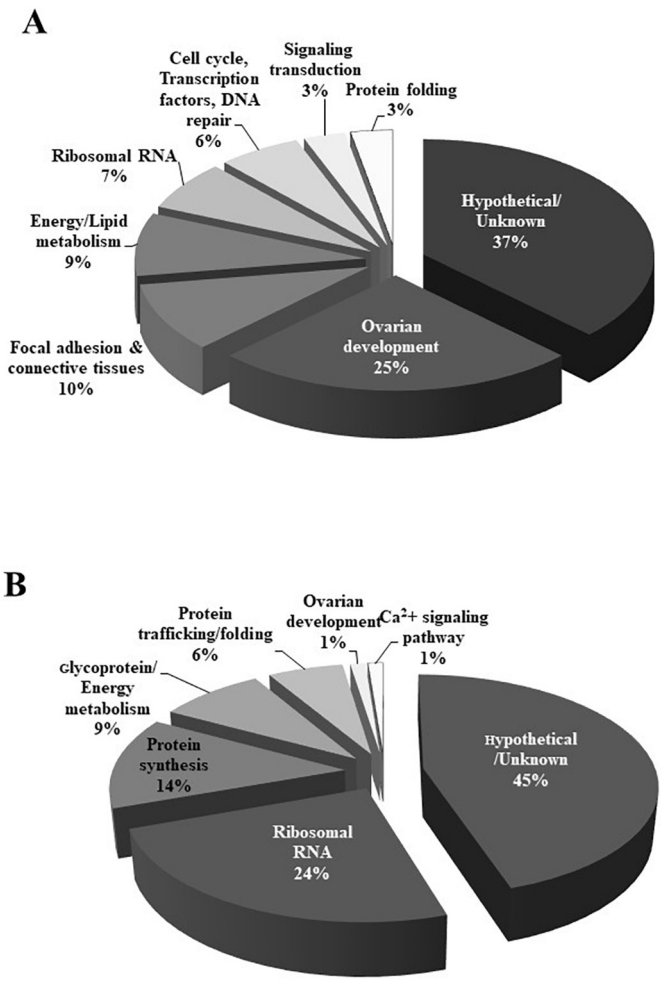

Fig. 2. Percentage of genes identified from SSH libraries according to the functional annotation. A total of 102 and 82 sequences of clones from forward (A) and reverse (B) SSH libraries, respectively, were annotated and categorized into each functional group of genes using BLAST analysis at NCBI.

3.4. Functional study of PmCALR in regulating the expression of Vg gene

The possible function of *PmCALR* in regulating the expression of *Vg* gene was studied by RNA interference experiment. The *CALR*-dsRNA was produced in the *E. coli* expression system, and verified by RNase digestion assay (Fig. A.3). The result in Fig. 5 showed that injection of the *CALR*-dsRNA at 2.5 $\mu g.g^{-1}$ shrimp bw could suppress the expression level of *PmCALR* by approximately 54% on day 7 after dsRNA injection, and the *Vg* expression level in the ovary of *CALR*-knockdown shrimp was increased by approximately 2.7-fold when compared with that in *GFP*-dsRNA treated group. This result suggests that *PmCALR* possibly

Table 2
Candidate genes from the forward SSH library that were up-regulated upon GIH-knockdown.

Highest homology	Accession no	*E*-value	Closet species	Assigned accession no	No of clones
Ovarian development					
Ovarian peritrophin I	AF510331.1	0	*Penaeus monodon*	MN639222–25	4
Ovarian peritrophin II	AF510332.1	$1.00E^{-85}$	*Penaeus monodon*	MN639226	1
Ovarian peritrophin III	EF153270.1	$4.00E^{-98}$	*Penaeus monodon*	MN639227–32	6
Peritrophin-44-like isoform X1	XP_027222433.1	$3.00E^{-44}$	*Litopenaeus vannamei*	MN639233	1
Thrombospondin II	AGI56293.1	0	*Penaeus monodon*	MN639234–44	11
Vitellogenin	DQ288843.1	0	*Penaeus monodon*	MN639245	2
Polehole-like protein	ACV60547.1	$2.00E^{-91}$	*Penaeus monodon*	MN639246	1
Focal adhesion					
Connectin	XM_027363872.1	0	*Litopenaeus vannamei*	MN639247	2
Paxillin	NG_029820.1	$3.00E^{-50}$	*Homo sapiens*	MN639248	1
Myosin light chain kinase var. x1	XR_003475463.1	$2.00E^{-107}$	*Litopenaeus vannamei*	MN639249	1
Myosin light chain kinase var. x5	XM_027353508.1	$2.00E^{-73}$	*Litopenaeus vannamei*	MN639250	1
Actin1	AF100986.1	$5.00E^{-149}$	*Penaeus monodon*	MN639251	2
Actin2	AF100987.1	$4.00E^{-104}$	*Penaeus monodon*	MN639252	1
Tubulin	AEI88096.1	$2.00E^{-73}$	*Scylla paramamosain*	MN639253–4	2
Energy/Lipid metabolism					
Glutaryl-CoA dehydrogenase	XM_027376212.1	$3.00E^{-99}$	*Litopenaeus vannamei*	MN639255	1
GAPDH	MG787341.1	$8.00E^{-146}$	*Litopenaeus vannamei*	MN639256	1
Glycogen phosphorylase	MK721970.1	0	*Litopenaeus vannamei*	MN639257	1
Cytochrome c oxidase IV	JQ828862.1	$9.00E^{-99}$	*Litopenaeus vannamei*	MN639258	1
Nitric oxide synthase	GQ429217.1	0	*Litopenaeus vannamei*	MN639259	1
Thioredoxin reductase 2	AAF21431.1	$2.00E^{-116}$	*Homo sapiens*	MN639260	1
Glutamine synthetase	AMD09631.1	$6.00E^{-94}$	*Penaeus monodon*	MN639261	2
NADH dehydrogenase 1 alpha subunit 11-like	XP_027210098.1	$2.00E^{-42}$	*Litopenaeus vannamei*	MN639262	1
Signaling transduction pathway					
Serum deprivation response	NM_004657.5	$5.00E^{-27}$	*Homo sapiens*	MN639263	1
Calpain-1-like	XM_027378586.1	0	*Litopenaeus vannamei*	MN639264	1
Arrestin	XM_027382709.1	0	*Litopenaeus vannamei*	MN639265	1
Cell cycle, Transcription factors, DNA repair					
CDK5 regulatory subunit associated 1	XM_027382438.1	0	*Litopenaeus vannamei*	MN639266	1
Origin recognition complex subunit 3	XM_027380864.1	$3.00E^{-111}$	*Litopenaeus vannamei*	MN639267	1
Ku protein	XP_012363148.1	$2.00E^{-59}$	*Nomascus leucogenys*	MN639268	2
Protein bicaudal C homolog 1 isoform X5	ROT69835.1	$7.00E^{-44}$	*Litopenaeus vannamei*	MN639269	1
Protein folding					
Ubiquitin-conjugating enzyme E2	KR106186.1	$3.00E^{-110}$	*Penaeus monodon*	MN639270	1
Ubiquitin/ribosomal S27 fusion protein	KR106186.1	$4.00E^{-107}$	*Penaeus monodon*	MN639271	1
Cold shock Y-box protein	XM_027378572.1	$7.00E^{-38}$	*Litopenaeus vannamei*	MN639272	1
Ribosomal genes				MN639273–77	7
Hypothetical & unknown genes					39

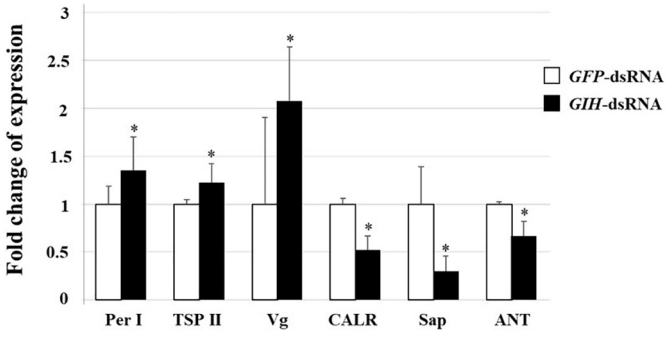

Fig. 3. Verification of the expression of selected genes from SSH libraries in the ovary of *GIH*-knockdown *P. monodon*. The cDNA from *GIH*-dsRNA-injected shrimp were analyzed for the transcription level of genes from the forward library (*peritrophine I*, *Per I*; *thrombospondin II*, *TSP II*; *vitellogenin*, *Vg*) and genes from the reverse library (*calreticulin*, *CALR*; *saposin*, *Sap*; *Adenine nucleotide translocate*, *ANT*). The expression levels of each gene were calculated relatively to that of the control shrimp injected with *GFP*-dsRNA. The results from three independent experiments were present as mean ± SEM ($n = 3$). Asterisks indicates statistically significant differences from the control at $P < .05$.

controls vitellogenesis by inhibiting *Vg* gene expression in the ovary.

4. Discussion

Ovarian maturation in shrimp is reliant on successful vitellogenesis, which is known to be mediated by an eyestalk peptide hormone GIH. Eyestalk ablation destroys the synthesis and storage site of GIH, and thus is a powerful technique that has been widely used in the hatcheries to induce ovarian maturation of the female broodstock. Although eyestalk ablation gives predictable and reliable shrimp production, it also has adverse effects on the broodstock (Benzie, 1998; Racotta et al., 2003; Sainz-Hernández et al., 2008). We have shown previously that suppression of *GIH* expression by specific double-stranded RNA (*GIH*-dsRNA) could induce the expression level of *Vg* gene as well as the successful maturation of shrimp ovary. (Treerattrakool et al., 2008; Treerattrakool et al., 2011). Since *GIH*-dsRNA provided specific suppression on *GIH* gene, the dsRNA-mediated *GIH* suppression was therefore used in this study to determine genes in the ovary that may act downstream of GIH to regulate *Vg* gene expression.

With the use of suppression subtractive hybridization (SSH), 102 up-regulated and 82 down-regulated sequences in the ovary upon *GIH* suppression were obtained from the forward library and reverse library, respectively. Gene annotation revealed that ovarian development-related genes were found in both libraries. Among these, *Per I*, *TSP II* and *Vg* genes were validated to be up-regulated under *GIH* suppressed

Table 3
Candidate genes from the reverse SSH library that were down-regulated upon GIH-knockdown.

Highest homology	Accession no	*E*-value	Closet species	Assigned accession no	No of clones
Ovarian development					
QM protein	ROT74357.1	$2.00E^{-67}$	*Litopenaeus vannamei*	MN639286	1
Energy/Lipid metabolism					
Saposin	ADK94870.1	$1.00E^{-157}$	*Penaeus monodon*	MN639287	1
Transketolase	XP_623196.3	$3.00E^{-160}$	*Apis mellifera*	MN639288	1
Glyceraldehyde-3-phosphate-dehydrogenase	AWH12534.1	$4.00E^{-128}$	*Litopenaeus vannamei*	MN639289	1
Adenine nucleotide translocase	AFK93891.1	$9.00E^{-153}$	*Penaeus monodon*	MN639290	1
Metallothionein	ADQ28316.1	$8.00E^{-19}$	*Penaeus monodon*	MN639291–2	2
NADH dehydrogenese	XP_027237828.1	$1.00E^{-105}$	*Litopenaeus vannamei*	MN639293	1
Ca^{2+} signaling pathway					
Calreticulin	ADO00927.1	$1.00E^{-179}$	*Penaeus monodon*	MN639294	1
Protein trafficking/ Protein folding					
Rab GDP dissociation inhibitor alpha-like	XP_018016172.1	$6.00E^{-19}$	*Hyalella azteca*	MN639295–6	2
Coatomer subunit delta-like isoform X2	XP_018026409.1	$2.00E^{-51}$	*Hyalella azteca*	MN639297	1
Prefoldin subunit 6	XM_027379965.1	$9.00E^{-81}$	*Litopenaeus vannamei*	MN639298	2
Protein synthesis					
Elongation factor 1α	MG775229.1	$1.00E^{-107}$	*Penaeus monodon*	MN639299	1
Elongation factor 2	ABR01223.1	$1.00E^{-113}$	*Penaeus monodon*	MN639300	1
Eukaryotic translation initiation factor 3	AEI88048.1	$2.00E^{-92}$	*Scylla paramamosain*	MN639301	1
Arginine kinase	C7E3T4.1	$2.00E^{-131}$	*Penaeus monodon*	MN639302–4	4
Beta-actin	ACZ60616.1	$1.00E^{-106}$	*Panulirus argus*	MN639305	2
nm23 protein	AFL02665.1	$4.00E^{-27}$	*Penaeus monodon*	MN639306	1
Nucleolar protein 58	XP_027208389.1	$5.00E^{-131}$	*Litopenaeus vannamei*	MN639307	1
Ribosomal genes				MN639308–22	20
Hypothetical& unknown gene					37

condition. In addition, the high expression levels throughout vitellogenic stages suggest that these genes are required for ovarian development in the shrimp. These dynamic expression profiles are consistent with previous reports (Khayat et al., 2001; Yamano et al., 2004; Urtgam et al., 2015).

A majority of negatively regulated genes under *GIH* deprivation in the reverse library includes *Sap*, which codes for a lysosomal lipid-degrading enzyme (Kishimoto et al., 1992) and a gene involving in ATP synthesis, *ANT* (Liu et al., 2016). The verification of expression levels revealed the up-regulation of these two genes during ovarian development in female shrimp. This event suggests the reservation of energy for yolk lipoprotein synthesis in the maturating ovary.

One of the interesting genes is a gene in the calcium signaling cascade, calreticulin (*CALR*). CALR is a multifunctional endoplasmic reticulum (ER) luminal resident protein that plays roles in Ca^{2+} homeostasis, molecular chaperoning, and stress responses (Michalak et al., 1999; Dey and Matsunami, 2011; Jeffery et al., 2011). It is located mainly in the ER lumen and the nuclear envelope (Roderick et al., 1997; Michalak et al., 2009). CALR is a major Ca^{2+} binding protein in the lumen of the ER. *CALR* deficient cells have substantially reduced capacity of ER Ca^{2+} storage and impaired agonist-induced Ca^{2+} release as well as delayed store-operated Ca^{2+} entry (Nakamura et al., 2001; Wang et al., 2017).

In this study, *CALR* expression was significantly down-regulated upon *GIH*-knockdown. The expression of *CALR* during ovarian maturation was declined in early vitellogenic stage, corresponding to the expression pattern of *GIH* that was previously reported (Urtgam et al., 2015). Further study of a possible function of CALR in the regulation of *Vg* gene in *P. monodon* by *CALR*-specific dsRNA revealed an elevated *Vg* expression level in the ovary of *CALR*-knockdown shrimp. This result suggest that *Vg* regulation is a calreticulin-dependent process.

The *Vg* synthesis in insects such as *Drosophila melanogaster* and *Aedes aegypti* was reported to be controlled by the activation of the heterodimer of ecdysone-ultraspiracle nuclear receptor by ecdysteroids that enables the direct binding of the heterodimeric receptor to its responsive element on the regulatory region of *Vg* gene in insect adipose tissue (Antoniewski et al., 1996; Martin et al., 2001). In crustacean, several clusters of heat shock factor binding site (HSE), and estrogen responsive element were identified within the 5′-upstream region (5'UPS) of *MeVg2* gene of the shrimp *Metapenaeus ensis*. The expression of *MeVg2* was negatively regulated by the heat shock cognate 70 (Hsc70) through the formation of a repression complex with heat shock factor (Chan et al., 2014). Moreover, the study of Wu, 2008 demonstrated that another molecular chaperone Hsp90 could be induced by estradiol -17β in the immature *M. ensis*, suggesting that *Vg* expression in shrimp is probably regulated by estrogen-related hormone similar to that in vertebrates. In addition, previous studies by Nagaraju et al., 2011 and Gong et al., 2015 indicated that ecdysone receptor (EcR) and retinoid X receptor (RxR) could promote ovarian development in the crabs *Scylla paramamosain* and *Carcinus maenas*, respectively.

Calreticulin can bind to the DNA binding motif (KXGFFKR) of a steroid nuclear protein receptor, and prevents the binding of the receptor to its responsive element to regulate gene expression in vertebrate (Dedhar et al., 1994). Taken together, our present study suggests that calreticulin is a potential mediator of Vg synthesis in *P. monodon*, possibly by interfering the binding of steroid nuclear receptor to its binding site on *Vg* 5' UPS. Further investigation on the regulatory sequences of the *Vg* gene and the effect of CALR-steroid receptor complex on the regulation of *Vg* expression will help unravel the molecular mechanism modulating vitellogenin synthesis via GIH mediated pathway in shrimp ovary.

5. Conclusion

This study utilized suppression subtractive hybridization technique to determine genes in the ovary of *P. monodon* whose expression was altered under specific-dsRNA mediated *GIH* suppression. The expression of *calreticulin* (*CALR*) gene was significantly down-regulated in response to *GIH* suppression. Silencing of *CALR* led to the elevated *Vg* expression in shrimp ovary. Since CALR can bind to a steroid receptor, and prevents the binding of the receptor to its responsive element to regulate gene expression, it is possible that CALR is an inhibitory mediator of Vg synthesis via the steroidal pathway. Further studies on the influence of this mechanism on ovarian development will shed light on the molecular mechanism of reproductive modulation in female shrimp.

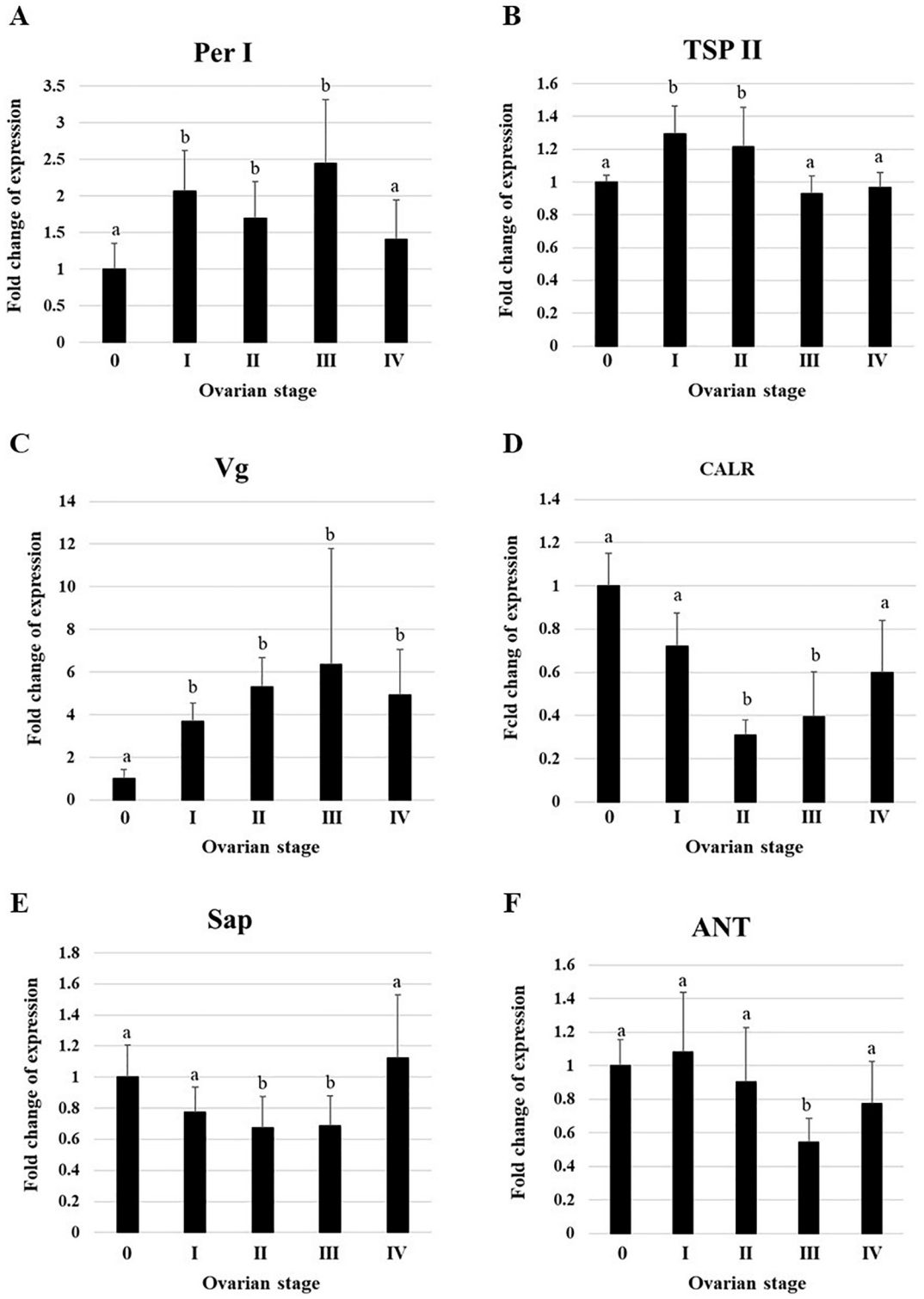

Fig. 4. Expression of candidate genes in the ovary of female *P. monodon* during ovarian development. The expression levels of six selected genes; *Per I* (A), TSP II (B), *Vg* (C), *CALR* (D), *Sap* (E), and *ANT* (F) in the ovary of female *P. monodon* at the immature stage (0), previtellogenic stage (I), early vitellogenic stage (II), late vitellogenic stage (III) and ripe stage (IV) were determined by RT-qPCR. The amounts of gene transcripts in relation to that of *EF1-α* were analyzed by $2^{-\Delta\Delta Ct}$ method. The expression level of each gene at each ovarian stage was calculated relatively to that of the shrimp at stage 0. The results from three independent experiments were presented as mean ± SEM (n = 3–5). Different letter indicates statistically significant differences from the control at $P < .05$.

Declaration of Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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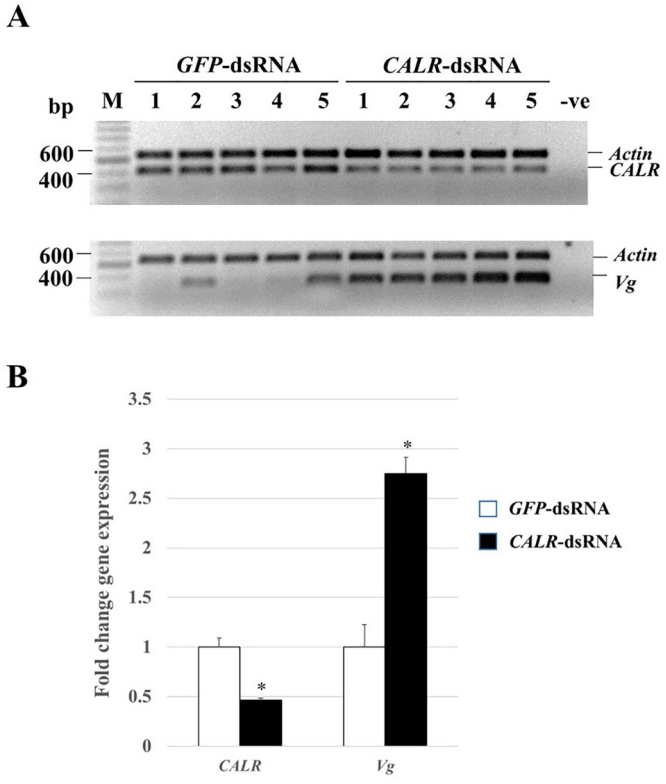

Fig. 5. Determination of *CALR* and *Vg* transcript in the ovary of *CALR*-dsRNA-injected vitellogenic female *P. monodon.*
(A) The expression of *CALR* and *Vg* in the ovary of *CALR*-dsRNA-injected vitellogenic female *P. monodon* was determined by RT-PCR compared to the expression *of CALR* in *GFP*-dsRNA treated control shrimp on day 7 after dsRNA injection. The number above each lane represents individual shrimp in each group. (B) The relative amounts of *CALR* and *Vg* transcripts to the actin transcript in individual shrimp were quantitated by Scion-image program. The data of the relative expression of *CALR* and *Vg* was presented as bar graphs comparing between that of the *CALR*-dsRNA-injected shrimp and the control shrimp injected with *GFP*-dsRNA. Asterisks indicate statistically significant difference from the control ($P < .05$).

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.cbpa.2020.110682.

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