RESEARCH ARTICLE



Adenosine monophosphate-activated protein kinase from the mud crab, *Scylla paramamosain*: cDNA cloning and profiles under cold stress

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Abstract

Adenosine monophosphate-activated protein kinase (AMPK), an important energy sensor, is crucial for organism survival under adverse conditions. In this study, the roles of this gene under cold stress in a warm-water mud crab, *Scylla paramamosain* was investigated. The full-length cDNA (*SpAMPK*) was 1884 bp and its open reading frame of 1566 bp was isolated and characterized. The expressions of *SpAMPK* detected by quantitative real-time PCR (qRT-PCR) in various tissues revealed that the highest expression was in the hepatopancreas. The profiles of *SpAMPK* gene in the hepatopancreas, chela muscle and gill were detected when the subadult crabs were exposed to the four temperature conditions of 10, 15, 20 and 25°C. The results showed that the expression patterns of *SpAMPK* mRNA in the three tissues were significantly higher when crabs were exposed to 15° C than the other three temperature treatments, while at 10° C treatment, the *SpAMPK* mRNA was lowest among the four temperature treatments. These findings suggested that the high expression of *SpAMPK* mRNA might initiate ATP-producing pathways to generate energy to cope with cold stress at 15° C treatment, which was slightly below the range of optimum temperatures; while treatment at 10° C, far lower than optima, the low expression of *SpAMPK* mRNA could reduce the energy expenditure and thus induce the crabs into cold anesthesia. The results of *SpAMPK* in this study might contribute to the understanding of the molecular mechanism of acclimation to cold hardiness in *S. paramamosain*.

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Introduction

For poikilotherms, such as crustaceans, one of environmentally relevant stressors is temperature change, which has been discovered to impact on multiple physiological processes, such as growth, development and reproduction (Aguilar-Alberola and Mesquita-Joanes 2014; Thongda *et al.* 2015), and even survival (Hochachka and Somero 2002). Especially, cold temperature can lead to the destruction of tissues. For example, cold stress could cause damnification to the balance of oxidation–antioxidant in tissues, and bring about the oxidation damage of DNA (Jia *et al.* 2009). Moreover, studies have shown that the stress associated with cold temperature affects the inflammatory response, neuroendocrine regulation and energy metabolism (Hangalapura *et al.* 2004; van den Brand *et al.* 2010). When exposed to cold stress, poikilotherms initiate adaptive tactics, such as mechanisms to compensation for energy (Hochachka and Somero 2002). Other protective mechanisms, such as antioxidant defense, heat shock response and an increase in mitochondrial density are also important for organisms to maintain cellular homeostasis at low temperatures (Wang *et al.* 2007; Kong *et al.* 2008; De Gobba *et al.* 2014; Zhang *et al.* 2014). It is well known that cold stress would lead to disturbance of aerobic metabolism and reduction of ATP (Hochachka and Somero 2002). Therefore, some animals have to initiate anaerobic metabolism to meet part of energy needs (Costanzo *et al.* 2004; Colson-Proch *et al.* 2009).

Adenosine monophosphate-activated protein kinase (AMPK), a highly conserved serine/threonine kinase, plays a pivotal role in regulating cellular energy metabolism (Hardie 2004). ATP-generating catabolic pathways, such as oxidations of amino acid, fatty acid and glycolysis are

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switched on by AMPK. Synchronously, AMPK shuts off ATP-consuming anabolic processes, such as the synthesis of lipids, proteins and glycogen (Hardie and Sakamoto 2006). Due to its function in energy metabolism regulations, AMPK has become an increasingly important research object in thermal stress, including high and cold temperature stresses. In vertebrates, such as fish (Olsvik et al. 2013), common frog (Bartrons et al. 2004), chicken (Zhang et al. 2014), rat (Hardie and Sakamoto 2006), mouse (Mulligan et al. 2007) and pig (Faure et al. 2013), the expressions of AMPK were upregulated during heat or cold exposure. In invertebrates, the effects of heat temperature stress on the expression of AMPK have been carried out, in the brine shrimp, Artemia franciscana (Zhu et al. 2007); rock crab, Cancer irroratus (Frederich et al. 2009); intertidal limpet, Cellana toreuma (Han et al. 2013). However, the effects of cold temperature stress on the expression of AMPK in invertebrates are still indefinite.

The mud crab, Scylla paramamosain is widely distributed in intertidal and subtidal unstructured soft sediments in the coastal area of southeast China, and has been a commercially important species in aquaculture (Le Vay et al. 2008; Ye et al. 2011). Although it can survive between 7 and 37°C, the optimum temperature for its growth and development are approximately 18-30°C (Shelley and Lovatelli 2012). It was reported that the biological zero of S. paramamosain is 12.19°C, and the embryos cannot complete its development below this temperature (Hamasaki 2002). Cold temperatures in winter generally brings about large-scale mortality in this species, in aquaculture. In consideration of its important economic value, the effects of cold temperatures on diversely physiological adaptations for sustaining metabolism in mud crab have been valued increasingly (Kong et al. 2012; Yu et al. 2014b).

In the present study, the full-length cDNA of *S. para-mamosain AMPK* (*SpAMPK*) was identified and characterized. The effects of cold temperature on *SpAMPK* in the three tissues of subadult crabs were detected by quantitative real-time PCR (qRT-PCR) and revealed the potential of *SpAMPK* to be applied as a biomarker for stress responses in *S. paramamosain*.

Material and methods

Experimental animals

The experimental, *S. paramamosain* were obtained from a commercial source located in Xiang'an, Xiamen, Fujian, China. Three female adult crabs with carapace length of 8.5 ± 0.6 cm and body weight of 370 ± 35 g were selected for the acquisition of full-length *SpAMPK* and analysis of tissue distribution. Besides, 105 subadult crabs, averaging 5.1 ± 0.7 cm in carapace length and 90 ± 8 g in body weight were chosen for cold stress experiments. All crabs in this study were healthy with both claws and appendages intact. Soon after the crabs were transported to the laboratory, they

were acclimated to common aquaculture conditions (salinity 25, $28 \pm 0.5^{\circ}$ C) for two days, during which the crabs were fed with live clam, *Ruditapes philippinarum*.

Low temperature stress and sample preparation

We assigned five temperature regimes 5, 10, 15, 20 and 25° C, by using five temperature-controlled incubators. Subadult crabs were randomly placed into these incubators. Each crab was placed in an individual round plastic culture vessel (diameter 10 cm; height 12 cm). Filled with about one third of volume of filtering seawater (salinity 25), each vessel was kept in the controlled temperature for 24 h to achieve the desire levels, respectively. After that, the subadult crabs were transferred into the vessels at random. At 0, 1, 3, 6, 12, 24 and 48 h of cold exposure, for each cold exposure, three crabs were selected, respectively. The hepatopancreas, chela muscle and gill were dissected from each crab and frozen immediately in liquid nitrogen and stored in -80° C.

Nucleic acid extraction and cDNA synthesis

Total RNA was isolated from the samples of *S. paramamo-sain* by using RNAizol reagent (Invitrogen, Carlsbad, USA) based on the manufacturer's protocol. The RNA integrity and concentration were detected by 1.5% agarose gel electrophoresis and by using a NanoDrop 2000 spectrophotometer (NanoDrop Technologies, Wilmington, USA), respectively.

For first-strand cDNA synthesis, 2 μ g total RNA was treated with RNase-free DNase I (TaKaRa, Kyoto, Japan) to remove genomic DNA, then reversely transcribed by using the Revert AidTM. First-strand cDNA synthesis kit (Fermentas) and random primers were used for cDNA synthesis.

Cloning of SpAMPK from S. paramamosain

Based on expressed sequence tags (ESTs) from cDNA libraries of S. paramamosain, which was homologous to AMPK of the rock crab Cancer irroratus, the brine shrimp Artemia franciscana and some other species, specific primers SpAMPK-F1 and SpAMPK-R1 (table 1) were designed to verify it. By using rapid amplification of cDNA ends (RACE), the 3'- and 5'-end cDNA sequences of SpAMPK were acquired. The 5' SpAMPK-R1 and 5' RACE primer F, 3' SpAMPK-F1 (table 1) and 5' RACE primer R were used for the first round 5'-end and 3'-RACE-PCR. The RACE-PCR performed as follows: initial denaturation at 94°C for 3 min, 11 cycles of 94°C for 30 s, 65°C for 30 s (decreasing by 1°C per cycle) and 72°C for 1.5 min, followed by 20 cycles of 94°C for 30 s, 55°C for 30 s, 72°C for 1.5 min and final elongation at 72°C for 10 min. The conditions for the second round 5'-end and 3'-RACE-PCR using 5' SpAMPK-R2 and 5' RACE primer F, 3' SpAMPK-F2 and 5' RACE primer R (table 1) were the same as the first round. Finally, the full-length cDNA of SpAMPK was verified by specific primers SpAMPK-F2 and SpAMPK-R2.

Table 1. Primers u	used in cloning and	l characterizing the	gene of SpAMPK.
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Name	Sequence $(5'-3')$	PCR objective
SpAMPK-F1	CTTTTCCGTCATCCCCACATC	Sequence verifying
SpAMPK-R1	GCTTCCCAGGAGTTCCTTTCG	Sequence verifying
3' SpAMPK-F1	GAAGCGAGCCACCATTGAAGA	Genomic cloning
3' SpAMPK-F2	GTGGAATGCCGAAAGGAACTCC	Genomic cloning
5' SpAMPK-R1	AATGCGTTCTGGATGTGGTTT	Genomic cloning
5' SpAMPK-R2	CGCTTCATTGGGTCCACCAT	Genomic cloning
SpAMPK-F2	GCACATTCTCACAGGCACCA	Validation of full-length cDNA
SpAMPK-R2	ACAGGGTAGTGCTGAGGTTAGGC	Validation of full-length cDNA
SpAMPK-F3	AAAGTGGCACCTCGGTATTCG	Real-time PCR
SpAMPK-R3	CTCCTGTTATCGGGTTCTTGC	Real-time PCR
<i>18S</i> rRNA-F	CAGACAAATCGCTCCACCAAC	Internal control
18S rRNA-R	GACTCAACACGGGGAACCTCA	Internal control
GAPDH-F	AATGCCATCACAATAGAAAAATC	Internal control
GAPDH-R	GGAACAATCAACACTACCACACC	Internal control
<i>β-actin-</i> F	GAGCGAGAAATCGTTCGTGAC	Internal control
β -actin-R	GGAAGGAAGGCTGGAAGAGAG	Internal control

Bioinformatics analysis

After the open reading frame (ORF) was gained by the ORF finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html), the coding region sequences were translated into amino acid sequences. The AMPK protein sequences from other species were determined using a GenBank database search with basic local alignment search tool (BLAST) program (http://blast. ncbi.nlm.nih.gov/Blast.cgi). ClustalW program was used for performing the multiple sequence alignment. According to the deduced amino acid sequences of *Sp*AMPK and other known AMPK proteins, a phylogenic tree was constructed by the neighbour-joining (NJ) method using the software of MEGA 5.0. To determine the confidence of tree branch positions, bootstrap analysis of 1000 replicates was carried out.

qRT-PCR analysis

At present studies have shown that the housekeeping genes could be influenced by several factors such as different tissues and development stages, leading a potential discrepancy to the results. In view of these factors, it is necessary to select two or three appropriate housekeeping genes for the analysis of gene expression (Radonić et al. 2004; Czechowski et al. 2005; Yang et al. 2013). Thus, three housekeeping genes: 18S rRNA (GenBank ID: FJ774906), *β-actin* (GenBank ID: GU992421) and GAPDH (GenBank ID: JX268543) were used as control for normalizing SpAMPK mRNA transcripts. The qRT-PCR was employed to detect the SpAMPK mRNA levels in various tissues (cerebral ganglion, eyestalk ganglion, heart, stomach, gill, hepatopancreas, thoracic ganglion, chela muscle, epidermis and hemocytes). While crabs were exposed to the four low temperature treatments, SpAMPK mRNA levels in the three tissues (hepatopancreas, chela muscle and gill) were detected by qRT-PCR. Gene-specific primers (table 1) were designed to amplify a 101 bp fragment of coding sequence. The reaction mixture of 20 μ L in total, contained 10 μ L of 2 × SYBR Premix Ex TaqTM (TaKaRa), 1.2 μ L of diluted cDNA template, 0.8 μ L of each 10 μ M primers, and 6.4 μ L of ddH₂O. Real-time PCR conditions were 95°C for 10 min, 40 cycles of 95°C for 20 s, 54°C for 30 s, 72°C for 30 s. The sample was carried out for three replicates and normalized by the average of *18S* rRNA, β -actin and GAPDH (Yang et al. 2013). The gene expression levels were calculated by the 2^{- $\Delta\Delta$ Ct} comparative threshold cycle (Ct) method.

Statistical analysis

The data were determined using one-way ANOVA followed by Duncan's multiple range tests, and statistical analysis was performed on SPSS 16.0 software (SPSS, Chicago, USA). Differences were considered as significant, when P value <0.05.

Results

Cloning and identification of SpAMPK cDNA

The full-length cDNA of *SpAMPK* was successfully cloned by 5'-RACE and 3'-RACE. *SpAMPK* cDNA (GenBank accession no. KP161206) was 1884 bp, containing an ORF which encoded a putative protein with 521 amino acids, a 29 bp 5'-untranslated region (UTR) and a 289 bp 3'-UTR with a polyadenylation signal sequence 'aataa' and a poly(A) tail (figure 1). Molecular weight and theoretical isoelectric point (pI) of *SpAMPK* were 58.89 and 7.31 kDa, respectively.

Homology analysis of cDNA

We investigated identities of AMPK α subunit amino acid sequences of *S. paramamosain* and several other species derived from the NCBI GenBank database through multiple sequence alignment on ClustalW. As shown in figure 2,

1	ACAGCTGACGGACGGACGCAGCAGCAGCAGCCA TG GATACACCAGTCCAAGGACAAGCGCCTGGCTCCCAGACCATTACCTTAATGAAAATAG
	M D T P V Q G Q A P G S Q T I T L M K I
91	GCCATTATCAGATTGGTAATACATTTGGTGCTGGAACCTTCGGAAAAGTGAAAATATGGGGAGCACATTCTCACAGGCACCAAAGTTGCCA
	G H Y Q I G N T F G A G T F G K V K Y G E H I L T G T K V A
181	TAAAAATCCTCAACCGCAAGACCATTAAAAACTTGGACATGGTCAGTAAAATAAAGCGAGAGATTACCAACCTCGAGCTTTTCCGTCATC
	I K I L N R K T I K N L D M V S K I K R E I T N L E L F R H
271	CCCACATCATCAAGTTATATCAAGTGATCAGTACACCAACAGACATTTTCATGGTGATGGAATATGCTTCTGGAGGAGAACTGTTTGATT
	PHIIKLYQVISTPTDIFMVMEYASGGELFD
361	ACATCAAGCAGAAAAGCAAGCTCAAAGAATCAGAAGCACGGAGGTTCTTCCAGCAGATTATCTCTGGTGTGGATTATTGCCATAGACATA
	Y I K Q K S K L K E S E A R R F F Q Q I I S G V D Y C H R H
451	TGGTGGTTCACCGGGACCTTAAGCCAGAAAACCTCCTCCTGGATCACAACTTGCATGTCAAGATTGCAGACTTTGGTTTGTCAAACATAA
	M V V H R D L K P E N L L L D H N L H V K I A D F G L S N I
541	TGGTTGATGGAGAAATTCCTTCGTACTAGTTGTGGATCTCCTAATTATGCTGCTCCTGAAGTCATATCTGGAAAGCTGTATGCTGGTCCAG
	M V D G E F L R T S C G S P N Y A A P E V I S G K L Y A G P
631	AGGTGGATGTGGGGTCTTGTGGGTATTATCCTGTATGCCCTACTATGTGGCACACTTCCTTTTGATGATGAGCACGTCCCATCACTTTTCC
	E V D V W S C G I I L Y A L L C G T L P F D D E H V P S L F
721	GCAAGATAAAATCGGGTGTGTTTCCAGATCCCAGACTACCTTAATCAGAGTGTAGTACGCCTGCTATTGCACATGTTGATGGTGGACCCAA
	R K T K S G V F Q T P D Y L N Q S V V R L L H M L M V D P
811	TGAAGCGAGCCACCATTGAAGATATCAAGAAGCATGAATGGTTCCAGAAAGACCTACCAGCATATCTCTTCCCTCCACCATATGATCATG
011	M K R A T I E D I K K H E W F Q K D L P A Y L F P P P Y D H
901	ACAATTCTGTGATAGATCAAGAGGCAATAACTGAAGTTGGGAGAAATTCCCAAGTTGAAAACAGCAGAAGTTCAGAGTGCCATTCTGTCAG
001	D N S V I D Q E A I T E V C E K E Q V E T A E V Q S A I L S
991	AAGATCAGCATAACCAACTAAAAAATTGCCTACAATCTGATTGTTGACAAACGTTTTGCTGATGCCGGTGCCATGTACAGTATATCTG
001	F D Q H N Q I K T A Y N I T V D N K R F A D A S A M Y S T S
1081	CTTTCTATACTGGTGTGTCCCCCCCCCCCCGCTGCGTGCCCCCCCC
1001	A F V T G V S P P P A V P T P A F S P S D S S P S P F K P H
1171	
1111	P F R T A P I R F R A I S C D R C M P K C T P C K R A K W H
1261	
1201	
1351	
1001	
1441	
1441	
1591	S IL L D F K I I C N E G D I A Q Y E K K G L E E E E I G F
1931	
1621	$I \circ \Pi = \Pi$
1711	tgatgtatactgtgcattctccaccacaaaccatttacaagcaag
1801	tagtgcctatgggtcagtgacaacattttttgctgcctcattgca <u>aataa</u> tgaaaactttgtaaaaaaaaaaaaaaaaaaaaaa

Figure 1. The full-length cDNA sequence of *SpAMPK* and deduced amino acid sequence. The nucleotide sequence is numbered from the 5' end and the single-letter amino acid code is shown above each corresponding codon. Uppercase letters indicate the translated region and lowercase letters indicate the untranslated region. The start code ATG and the termination code TGA are shown in bold. The polyadenylation signal 'aataa' is underlined.

*Sp*AMPK had the typical conserved domains of AMPKs: a catatytic domain, a USA-like autoinhibitory domain and ATP-binding sites. The major site on AMPK phosphorylated by upstream kinases was found to be Thr-172, and it was conserved. Compared with other arthropods and vertebrates, *Sp*AMPK exhibited relatively a high degree of identity: 71% with *A. franciscana*, 63% with the insect *D. melanogaster*, and 60% with *D. rerio* and *M. musculus*.

The NJ phylogenic tree (figure 3) was constructed according to the reported AMPK α amino acid sequences from some vertebrate and invertebrate species, by the software of MEGA 5.0. On the whole, the phylogenic tree of AMPK included two large clades: vertebrates and invertebrates groups. In the invertebrate clade, *Sp*AMPK clustered first with *C. irroratus* to form an independent clade, and was close to the clade of insects.

Tissue distributions of SpAMPK

The qRT-PCR was carried out to determine the expression levels of *SpAMPK* in various tissues. Compared with the control tissue (chela muscle), *SpAMPK* mRNA was abundantly expressed in the hepatopancreas, and moderately distributed in the eyestalk ganglion, thoracic ganglion and heart (figure 4).

Expression of SpAMPK mRNA in the hepatopancreas, chela muscle and gill under low temperatures

In this study, we observed that the mud crabs could move freely at 25 and 20°C, slightly at 15°C and could only move when they were disturbed at 10°C. At 5°C, they were already in the state of cold anesthesia and became motionless, and died after the 12 h cold stress.

SpAMPK mRNA under cold stress

Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	MDTPVQGQAPGS-QTITLMKIGHYQIGNTFGAGTFGKVKYGEHILTGTKVAIKILNRKTIKNLDMVSKIKREITNLELFRHPHIIK MDTPVQGQAPGS-QTITLMKIGHYUGETLGVGTFGKVKIGEHQLTKHKVAIKILNRQKIKNLDVVGKIRREIQNLKLFRHPHIIK MPQMRAAAAEAVAAGSANGQPLVKIGHYLGATLGTGTFGKVKIGEHQITRVKVAVKILNRQKIKSLDVVGKIRREIQNLKLFRHPHIIK MAEKQKHEGRVKIGHYILGDTLGVGTFGKVKIGEHQLTGHKVAVKILNRQKIRSLDVVGKIKREIQNLKLFRHPHIIK MAEKQKHDGRVKIGHYULGDTLGVGTFGKVKIGEHQLTGHKVAVKILNRQKIRSLDVVGKIKREIQNLKLFRHPHIIK CD	85 76 90 78 78
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	LYQVISTPTDIFMVMEYASGGELFDYIKQKSKLKESEARRFFQQIISGVDYCHRHMVVHRDLKPENLLLDHNLHVKIADFGLSNIMVDGE LYQVISTPTDIFMIMEYVSGGELFDYIVKHGKLKEHEARRFFQQIISGVDYCHRHMVVHRDLKPENLLLDSNLHVKIADFGLSNMMSDGE LYQVISTPSDIFMIMEYVSGGELFDYIVKHGKLQEHQARRFFQQIISGVDYCHRHMIVHRDLKPENLLLDHNMHVKIADFGLSNMMSDGE LYQVISTPTDFFMVMEYVSGGELFDYICKHGRVEDAEARRLFQQIISAVDYCHRHMVVHRDLKPENVLLDGNMNAKIADFGLSNMMSDGE LYQVISTPTDFFMVMEYVSGGELFDYICKHGRVEEVEARRLFQQILSAVDYCHRHMVVHRDLKPENVLLDAQMNAKIADFGLSNMMSDGE CD AAA A AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	175 166 180 168 168
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	FLRTSCGSPNYAAPEVISGKLYAGPEVDVWSCGIILYALLCGTLPFDDEHVPSLFRKIKSGVFQIPDYLNQSVVRLLLHMLMVDPMKRAT FLRTSCGSPNYAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFDDEHVPTLFRKIKSGVFPIPDYLNKSTVNLLCHMLQVDPMKRAT FLRTSCGSPNYAAPEVISGKLYAGPEVDIWSCGVILYALLCGTLPFDDEHVPTLFRKIKSGIFPIPEYLNKQVVNLVCQMLQVDPLKRAN FLRTSCGSPNYAAPEVISGRLYAGPEVDIWSCGVILYALLCGTLPFDDEHVPTLFKKIRGGVFYIPEYLNRSVASLLMLMLQVDPLKRAT FLRTSCGSPNYAAPEVISGRLYAGPEVDIWSCGVILYALLCGTLPFDDEHVPTLFKKIRGGVFYIPDYLNRSVASLLMLMLQVDPLKRAT CD	265 256 270 258 258
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	IEDIKKHEWFQKDLPAYLFPPPYDHDNSVIDQEAITEVCEKFQVETAEVQSAILSEDQHNQLKIAYNLIVDNKRFADASAM—YSISAFY LDDIKKHEWFQKDLPAYLFPSPVEQDTSVIDTVAVQEVCDKFGVREQEVHSALLSGDPHEQLAIAYHLVIDNKRIADEAAK—AQIKDFY IEEIKKHEWFQKDLPAYLFPSSIEQDSNVIDTYAVAEVCTKFGVKETEVHNSLLSGDPHDQLAIAYHLIIDNKRFADDAANQINEINNFF IKDIREHEWFKQDLPGYLFPEDPSYDATVVDEEAVREVCEKFECTEAEVLSSLYSGDPQDQLAVAYHLIIDNRRIMNQASEFY IKDIREHEWFKQDLPSYLFPEDPSYDANVIDDEAVKEVCEKFECTESEVMNSLYSGDPQDQLAVAYHLIIDNRRIMNQASEFY CD AID	353 344 360 341 341
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	TGVSPPPALSGDRGMPK VAGSPPPVGVGPNIPYPPDTSSSSPTSRPHPERIAPRGGDKVVPAAQIR VAGSPPPPPPPPVQSSMDHQAPLATVTVGGGTSASSGTATPVPPVAGGTPSSTIPIRPHPERIAPMRDRQLAMSVQTSGGGAFPEKTAR LASSPPTSPKARCPLDALNTTRP LASSPPSSPKARCPLDALNTTKP	400 391 450 391 392
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	-GTPGKRAKWHLGIRSQSKPLDIMSEVYKAMKVLGFEWKVVNPFHVRVRRKNPITGGCVQMALQLYQVDYRSHLLDFKIICNEGD -AAPMKRAKWHLGIRSQSKPHDIMYEVYRAMKALSFEWKTVNAYHVRVRKTNSVTGKHVKMSLQLYQVDHRSYLLDFKSLCTEEHEG GGTPIKRAKWHLGIRSQSKPNDIMLEVYRAMKALSYEWKIINPYHVRVRRQNVKTGKFSKMSLQLYQVDAKSYLLDFKSLTNDEVEQGDD KPLAVKKAKWHLGIRSQSKPYDIMAEVYRAMKQLEYEWKVVNPYHLRVRRKNPVTGNFVKMSLQLYQVDNRSYLLDFKSIDDDIMEHKSG KSLAVKKAKWHLGIRSQSKACDIMAEVYRAMKQLGFEWKVVNAYHLRVRRKNPVTGNYVKMSLQLYLVDSRSYLLDFKSIDDEVVEQRSG	484 477 540 481 482
Scylla paramamosain Artemia franciscana Drosophila melanogas Danio rerio Mus musculus	IAQVEPTSHHVMEFFEMCAALITELAR 521 -LMTSLSGSALSSSGAHQGGHHTMEFFEMCAALITQLAK 515 VIMESLTPPPLSVSGVMPLQPTGHHTMEFFEMCAALIIQLAR 582 SSTPQRSGSTAGLLRPRLSIDSASVVAMEMPQLSSSLPGSLTGSTP-LLTPRQGSHTMDFFEMCASLITTLAR 553 SSTPQRSCSAAGLHRARSSFDSSTAENHSLSGSLTGSLTGSTLSSASPRLGSHTMDFFEMCASLITALAR 552	

Figure 2. ClustalW alignment of AMPK α amino acid sequences for some vertebrate and invertebrate species. The sequence for *S. paramamosain* is from this study, and others were obtained from GenBank (*Artemia franciscana* ABI13783.1, *Drosophila melanogaster* NP_726730.1, *Danio rerio* XP_700831.4, *Mus musculus* NP_835279.2). The shaded regions indicate conservative residues. The flanking areas indicate the large conservative region T172 that activates the AMPK protein. \blacktriangle , ATP-binding site; CD, catalytic domain; AID, autoinhibitory domain.

In the hepatopancreas (figure 5a), the expression of *SpAMPK* mRNA at each point did not markedly change at both 25 and 20°C (P > 0.05), similar to that of control temperature (28°C) at 0 h. While at 15°C treatment, the abundance of *SpAMPK* mRNA increased dramatically (P < 0.05) from 0 to 6 h, reaching a peak of approximately 2.2-fold at 0 h, then decreased from 6 to 12 h, followed by stable expressions lasting till the end of the experiment. The

SpAMPK mRNA at 15°C treatment was obviously higher than other three treatments (P < 0.05) at each time of sampling. At 10°C treatment, the expression of *SpAMPK* mRNA declined rapidly and was significantly lower than other temperature regimes at 6–48 h (P < 0.05).

In the chela muscle (figure 5b), compared with 25°C treatment, the expression levels of *SpAMPK* mRNA at 6 and 24 h were higher at 20°C, and no obvious variation was detected

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Figure 3. NJ phylogenetic tree of representative vertebrate and invertebrate *Sp*AMPK amino acid sequences. Bootstrap values supporting branch points are expressed as the percentage of 1000 replicates. The following organisms with AMPK GenBank-reported sequences were included in the analysis: *Danaus plexippus* (EHJ71225.1), *Bombyx mori* (NP_001093315.1), *Musca domestica* (XP_005180024.1), *Culex quinquefasciatus* (XP_001844429.1), *Megachile rotundata* (XP_003707119.1), *Solenopsis invicta* (EFZ13258.1), *Daphnia pulex* (EFX87591.1), *Artemia franciscana* (ABI13783.1), *Cancer irroratus* (ACL13568.1), *Scylla paramamosain* (KP161206), *Danio rerio* (XP_700831.4), *Callorhinchus milii* (XP_007901898.1), *Xenopus tropicalis* (NP_001135554.1), *Mus musculus* (NP_835279.2), *Erinaceus europaeus* (XP_007518085.1), *Pongo abelii* (NP_001125173.1) and *Homo sapiens* (NP_006243.2).



Figure 4. Expression levels of *SpAMPK* gene normalized to *18S* rRNA, β -*actin* and *GAPDH* in the chela muscle, epidermis, gill, hemocytes, stomach, cerebral ganglion, heart, thoracic ganglion, eyestalk ganglion and hepatopancreas of *S. paramamosain*. Gene expression levels are relative to *SpAMPK* expression in chela muscle, values are the mean \pm SE (n = 3).

at any other time at 20°C treatment. At 15°C treatment, however, it showed significantly higher *SpAMPK* mRNA levels than other treatments (P < 0.05): *SpAMPK* mRNA level was rapidly and significantly upregulated and reached a peak at 1 h after cold challenge, with expression level about 2.3-fold than at 0 h. At 10°C treatment, the expression of *SpAMPK* mRNA markedly decreased at 1 h (P < 0.05), and increased slightly from 1 to 6 h, then no distinctive changes took place till the end. On the whole, the expression of *SpAMPK* mRNA at each time at 10°C treatment was lower than the other treatments (P < 0.05).

In the gill (figure 5c), except a transient increase at 3 h at 20°C (P < 0.05), *SpAMPK* expressions at 20°C treatment were not significantly different from those at 25°C treatment.



Figure 5. The relative expression of *SpAMPK* in three tissues of *S. paramamosain* at four temperatures. Each point represents the mean value from three determinations with standard error. Significant differences in different low temperature groups are indicated by different small letters on the top of break-points (P < 0.05): one-way ANOVA, N = 3. (a) Relative expression of *SpAMPK* mRNA in the hepatopancreas. (b) Relative expression of *SpAMPK* mRNA in the chela muscle. (c) Relative expression of *SpAMPK* mRNA in the gill.

At 15°C treatment, obviously higher expression levels were observed at 3 h (P < 0.05), and the mRNA expression reached maximum at 6 h, and then dropped slightly at 12 h, which showed much higher than other temperatures (P < 0.05). In contrast to 25, 20 and 15°C treatments, the 10°C

group crabs showed significantly lower *SpAMPK* mRNA levels (P < 0.05).

In short, the expression of *SpAMPK* mRNA in three tissues (hepatopancreas, chela muscle and gill) during four temperature treatments had a similar pattern. The *SpAMPK* mRNA level was not obviously affected by 25°C treatment, and it happened to be transiently upregulated at 20°C treatment. While at slightly colder temperature of 15°C, *SpAMPK* mRNA showed a markedly higher level than the other temperatures. However, at 10°C treatment, the *SpAMPK* mRNA expression was significantly lower than the other three (15, 20 and 25°C) treatments.

Discussion

In this study, the AMPK genes were isolated and characterized from the mud crab, S. paramamosain. The full-length SpAMPK cDNA encoded a deduced protein with 521 amino acids, which was similar to that of the brine shrimp, A. franciscana (Zhu et al. 2007) and the mouse, M. musculus (Stapleton et al. 1996). The putative protein of SpAMPK displayed a high similarity to some vertebrate and invertebrate sequences (60–71%). Like its mammalian counterparts ($\alpha 2$), SpAMPK contained an N-terminal catalytic domain and a C-terminal region combining with β -subunits and γ -subunits to form an active and stable complex (Hardie 2004). The protein sequence of SpAMPK showed that it had all the conserved domains necessary for kinase activity, such as the conserved threonine residue, Thr172 in the activation loop of the catalytic domain. In this study, the phylogenetic analysis supported the result that vertebrate AMPKs were paralogous to invertebrate AMPKs.

Tissue distribution detected by qRT-PCR revealed that SpAMPK mRNA was present in all the examined tissues in the present study. The highest level of SpAMPK transcript in the hepatopancreas signified the importance of this gene in energy regulation. This finding was consistent with the reports of high abundance in the liver of mouse, where AMPK was believed to play a significant role in controlling fat and glucose metabolisms (Davies et al. 1989; Mulligan et al. 2007). In mammals, AMPK $\alpha 2$ is expressed abundantly in tissues mainly involving high energy demand, such as liver, pancreas, neurons and skeletal muscles (Towler and Hardie 2007). In mud crab, metabolic enzymes are rich in the hepatopancreas, and the process of synthesis and secretion of enzymes are mainly in hepatopancreas. It is considered as a main organ in modelling physiological metabolism and responsible for the nutrient supplies of the ovary and food digestion, as well as the metabolism centre of lipid and carbohydrate (Kong et al. 2008; Zeng et al. 2010). Therefore, the hepatopancreas plays a strong role in metabolism process in S. paramamosain.

In this study, we observed that the subadult crabs died after 12 h at 5°C stress. Previous studies have showed that the Ca²⁺-ATPase and Ca²⁺/Mg²⁺-ATPase activities in the mud crabs decreased sharply at this temperature (Kong

et al. 2012). Treatments with 5°C were considered to be beyond the critical range of adaptive low temperature, so it caused physiological disturbance in *S. paramamosain*, and the subadult crabs died at last.

At 25°C treatment, the patterns of SpAMPK mRNA level in all the three tissues (hepatopancreas, chela muscle and gill) did not change obviously, and they were all similar to that of control temperature (28°C). The optimum temperatures for feeding and growing of the mud crabs are approximately 18-30°C (Shelley and Lovatelli 2012), within which small-scale temperature fluctuations show little influence on the physiological progress of the mud crabs (Yu et al. 2014a). The stable expressions of SpAMPK mRNA in all the three tissues at 25°C revealed that the physiological metabolism in S. paramamosain was unaffected at this temperature. When the temperature dropped to 20°C, the expression of SpAMPK significantly upregulated in the gill (3 h) and chela muscle (6, 24 h) and only slightly changed in the hepatopancreas. This might suggest that the gill and chela muscle are more sensitive to temperature changes than the hepatopancreas. As both a respiratory and osmoregulation organ, gill directly in contact with aquatic environment, leading to prompt heatchange between gill and water. Under low temperatures, gill raises metabolism to sustain its physiological functions (Xu and Qin 2012). Chela muscle is just beneath the carapace, acutely sensing the fluctuation of temperature, with burning energy to generate heat under low temperatures (Atwood and Cooper 1995). It was reported that cold temperatures would improve aerobic metabolism in muscle by inducing AMPK (Jäger et al. 2007). Thus, when the subadult crabs were exposed to 20°C environment, a transient upregulation of SpAMPK mRNA was observed in both gill and chela muscle, which indicated that more energy was required to maintain the respiratory metabolism of gill and heat production of chela muscle.

Preliminary data showed that AMPK was elicited by cold stress in mouse and chicken hepatocytes to restore cellular energy homeostasis, which is a compensatory response for ATP-consuming processes (Corton et al. 1994; Zhang et al. 2014). It was found that AMPK could induce lot of metabolic changes, such as an increase in intake and oxidation of plasma fatty acids and glucose, besides enhancing the expressions of glucose transporter 4 (GLUT4) and hexokinase II (HKII) (Hardie and Sakamoto 2006). Further, low temperature could increase generation of reactive oxygen species (ROS) in the swimming crab P. trituberculatus and lead to oxidative stress (Meng et al. 2014). Intriguingly, recent studies showed that ROS produced by cold stress could arouse the AMPK, and then resulted in the increase of glycolysis and mitochondrial biogenesis, which in turn reduced deleterious effects caused by oxidative stress (Wu et al. 2014). Briefly, low temperatures induce AMPK for two purposes: one to meet energy demand, and the other to reduce deleterious effects caused by ROS.

Temperature 15°C is just below the range of optimum temperatures (18–30°C) (Shelley and Lovatelli 2012). In all the three tissues examined in S. paramamosain, the expression of SpAMPK mRNA at 15°C treatments was significantly higher than the other three temperature treatments. Besides AMPK, there were some other regulatory elements involved in cell energy supplying such as adenosine triphosphatase (ATPase) (Kong et al. 2008) and adenine nucleotide translocase (ANT) (Santamaria et al. 2004). ATPase could supply energy for facilitating ion movement across the membrane, and it was reported that activities of four kinds of ATPase at 15°C were higher than those at 27°C in S. paramamosain (Kong et al. 2012). In addition, SpANT2 in subadult crab S. paramamosain was involved in transporting ATP from mitochondria to the cytoplasm and simultaneously transferring ADP to mitochondria, and its profile was significantly increased under 15°C exposure, much higher than those at the 25 and 20°C treatments (Yu et al. 2014b). In the estuarine crab, Neohelice granulata, a slight drop in temperature led to an increase in blood sugar levels followed by the descending of glycogen since glycogen was broken down into glucose for the energy supply of metabolism (Valle et al. 2009). At 15°C, in mud crab, the soluble sugars were higher than those at 27°C, which could supply energy and protect cells (Kong et al. 2008). These data unveiled that the mud crab would strengthen metabolism and generate energy to cope with the slight cold stress of 15°C. Previous researches showed that AMPK protein expression and activity increased based on the upregulation of mRNA levels when exposed to temperature stress (Frederich et al. 2009; Zhang et al. 2014). Therefore, the sharp increase of SpAMPK mRNA at 15°C would contribute to regulate the whole-body energy metabolism by stimulating the ATP-generating pathways which occurred as a defense against cold stress.

At 10°C treatment, however, the SpAMPK mRNA in the three tissues did not continue to increase, and instead, turned into significantly lower levels than those in other temperature treatments. 10°C is already lower than the biological zero (12.19°C) of S. paramamosain (Hamasaki 2002), under which cells divided abnormally during the growth of embryo (Zeng 2007) as well as no moult occurred (Wu 1982). An inhibition of physical activities and growth, including slow physiological processes, could happen when temperature was too low and outside the normal range for selfregulation of crustaceans (Wang and Wang 2014). It was reported that with low metabolic rate at 10°C, the SpANT2 mRNA decreased sharply in S. paramamosain (Yu et al. 2014b). In this study, a significant reduction of SpAMPK mRNA levels was also observed. As both AMPK and ANT are participants in regulating energy metabolism, the downregulation of SpAMPK mRNA levels coincides with declined levels of metabolism at 10°C treatment. It was also suggested that cold stress at this temperature has beyond the ability of cellular protective mechanisms.

In conclusion, *SpAMPK* played a key role in cold stress for the mud crabs. Under a moderately low temperature (i.e. 15° C), the mud crabs could initiate the ATP-produced pathways through the high expression of *SpAMPK* mRNA. However, when the cold stress was far below the adaptive limits (i.e. 10 and 5°C), the mud crabs reduced the metabolism through the low expression of *SpAMPK* mRNA. Therefore, *SpAMPK* might serve as a bioindicator for monitoring the cold stress.

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