

## Molecular cloning and characterization of taurine transporter from turbot (*Psetta maxima*) and its expression analysis regulated by taurine *in vitro*

Xuan Wang, Gen He, Kangsen Mai, Wei Xu & Huihui Zhou

Key laboratory of Aquaculture Nutrition (Ministry of Agriculture), Ocean University of China, Qingdao, China

**Correspondence:** Dr G He, Key Laboratory of Aquaculture Nutrition (Ministry of Agriculture), Ocean University of China, 5th Yushan Road, Qingdao 266003, China. E-mail: hegen@ouc.edu.cn

### Abstract

Taurine is one of the conditionally essential amino acids for fish. Its metabolism has attracted much attention in fish nutrition due to the substitution fishmeal with plant ingredients, which barely contain taurine. However, little is known about the mechanisms of taurine homeostasis in turbot (*Psetta maxima*), an economically valuable carnivorous fish with limited taurine biosynthesis ability. In this study, we obtained the full-length cDNA of turbot taurine transporter (*PmTauT*) and classified its tissue distribution in juvenile turbot and substrate regulation in isolated turbot muscle cells. Full-length *PmTauT* cDNA was 2566 bp containing a 58 bp 5' untranslated region (UTR), a 633 bp 3'UTR and a 1875 bp open reading frame (ORF) encoding 624 amino acid residues. The deduced protein contained 12 putative transmembrane domains and showed highest similarity with taurine transporter from Senegalese sole (*Solea senegalensis*), another flatfish species. By quantitative real-time PCR analysis, *PmTauT* transcript was predominantly detected in liver and intestine, while was lesser expressed in gill and stomach. In addition, *PmTauT* in isolated turbot muscles was down-regulated by taurine in a dose-dependent manner. These results suggested that *PmTauT* was involved in taurine homeostasis in turbot.

**Keywords:** *Psetta maxima*, taurine transporter, tissue expression, substrate regulation

### Introduction

Taurine (2-aminoethane sulphonic acid) is one of the most abundant nonpeptidic amino acid in

animal tissues (Schuller-Levis & Park 2003; Bouckennooghe, Remacle & Reusens 2006). It has been considered as an essential nutrient for many fish species due to their limited taurine biosynthesis abilities (Takagi, Murata, Goto, Endo, Yamashita & Ukawa 2008; Li, Mai, Trushenski & Wu 2009; Espe & Holen 2013; Lim, Oh, Khosravi, Cha, Park, Kim & Lee 2013; Salze & Davis 2015). Taurine has multiple physiological functions in fish, such as growth stimulation (Lunger, McLean, Gaylord, Kuhn & Craig 2007), osmoregulation (Takagi, Murata, Goto, Hayashi, Hatate, Endo, Yamashita & Ukawa 2006a; Kato, Yamamoto, Peerapon, Fukada, Biswas, Yamamoto, Takii & Miyashita 2014), bile salt conjugation (Kim, Matsunari, Takeuchi, Yokoyama, Murata & Ishihara 2007), antioxidant defence (Espe & Holen 2013) and larvae development (Pinto, Figueira, Ribeiro, Yúfera, Dinis & Aragão 2010).

During the past decades, taurine metabolism has attracted much attention in fish nutrition studies due to the fact that plant ingredients replacement of fishmeal in aquafeeds (Li *et al.* 2009; Kuzmina, Gavrovskaya & Ryzhova 2010; El-Sayed 2014; Salze & Davis 2015). The sources of taurine in fish are *de novo* synthesis and dietary. However, many fish species have extremely low taurine biosynthesis abilities and they are much more dependent on dietary intake (Yokoyama, Takeuchi, Park & Nakazoe 2001; Goto, Matsumoto, Murakami, Takagi & Hasumi 2003; Kim, Matsunari, Takeuchi, Yokoyama, Furuita, Murata & Goto 2008). Fishmeal is known to be the major source of taurine in aquafeeds. Due to the high price and limited supply, numerous studies on replacing fish meal with plant ingredients have been carried out, which usually resulted in a

deficiency of taurine in diets (Tacon & Metian 2008). Many defects associated with taurine deficiency have been observed in fish, such as growth depression (Lunger *et al.* 2007; Chatzifotis, Polemitou, Divanach & Antonopoulou 2008; Al-Feky, El-Sayed & Ezzat 2015), poor disease resistance (Maita, Maekawa, Satoh, Futami & Satoh 2006), oxidative stress (Espe, Ruohonen & El-Mowafi 2012) and high mortality (Salze, Craig, Smith, Smith & McLean 2011). Supplementation of taurine to plant protein diets has been proved indispensable to sustain comparable levels of feed intake and fish growth (Lunger *et al.* 2007; Al-Feky *et al.* 2015). It is important to further clarify the mechanism of taurine absorption and its homeostasis in fish.

The absorption of dietary taurine and its homeostasis in organisms were mainly regulated by taurine transporter (SLC6A6; TauT), a high-affinity, low-capacity sodium and chloride dependent transporter (O'Flaherty, Stapleton, Redmond & Bouchier-Hayes 1997). It transports taurine against a concentration gradient, driven by transmembrane sodium and chloride gradients and membrane potentials. TauT has been cloned and characterized in several fish species, including zebrafish (Kozłowski, Chen, Zhuang, Fei, Navarre & Ganapathy 2008), carp (Takeuchi, Toyohara & Sakaguchi 2000b), Atlantic salmon (Zarate & Bradley 2007), tilapia (Takeuchi, Toyohara, Kinoshita & Sakaguchi 2000a), Japanese eel (Chow, Ching, Wong & Wong 2009) and Senegalese sole (Pinto, Rønnestad, Jordal, Gomes, Dinis & Aragão 2012). These studies have demonstrated that TauT was important for maintenance the taurine body pool and its significant role of TauT in osmoregulation. However, the regulation of fish TauT by diet, which is critical for understanding taurine homeostasis in fish and defining taurine supplementation in aquafeeds, was rarely addressed. Previously studies has shown that taurine transport capacity of the renal tubular cell was down-regulated by the dietary intake of taurine in mammals (Rozen & Scriver 1982; Chesney, Gusowski & Dabbagh 1985) and the feedback regulation of TauT by taurine was through modifying the transport maximal velocity (Han, Patters, Jones, Zelikovic & Chesney 2006). It is important to explore the substrate regulation of fish TauT.

Turbot *Psetta maxima* is an economically valuable carnivorous fish widely cultured in Europe and Asia. Previous studies have suggested that

turbot has limited taurine biosynthesis ability (Conceição, van der Meer, Verreth, Evjen, Houlihan & Fyhn 1997; Qi, Ai, Mai, Xu, Liufu, Yun & Zhou 2012; Yun, Ai, Mai, Xu, Qi & Luo 2012; Wang, He, Wang, Mai, Xu & Zhou 2014), while the homeostasis of taurine in turbot remains unexplored. In this study, we obtained the full-length cDNA of turbot *P. maxima* taurine transporter (denoted as *PmTauT*). The tissue distribution of *PmTauT* in juvenile turbot and its feedback regulation by taurine in primary cultured turbot muscle cells were also investigated. These results will provide new insights into taurine homeostasis in teleost.

## Materials and methods

### Sample collection

The juvenile turbot *P. maxima* (30–57 g in mass) was collected from a commercial farm in Qingdao (Shandong, China). Seawater was pumped from the coast adjacent to the farm and filtered with sand filters. During rearing at the farm, water temperature was ranged from 18.0 to 22.0°C; pH from 7.4 to 8.2; salinity from 26‰ to 30‰; ammonia nitrogen was lower than 0.1 mg L<sup>-1</sup>; nitrite was lower than 0.1 mg L<sup>-1</sup>; dissolved oxygen was higher than 5.0 mg L<sup>-1</sup>. Fish was fed with commercial diet (Great Seven Bio-Tech, 49.5% protein, 10.2% lipid, 1.08% taurine) twice everyday. Before sampling, fish was fasted overnight to clear dietary influences (Kaushik & Luquet 1977). Fish was euthanized with 3-aminobenzoic acid ethyl ester (MS222) at 100 µg mL<sup>-1</sup>. Samples of liver, muscle, stomach, intestine, heart, gill, brain and eye were rapidly removed and immediately frozen in liquid nitrogen. The samples were stored at -80°C until use. All procedures performed in study were in strict accordance with the ethical standards of the Helsinki declaration as revised in 1975.

### RNA extraction and cDNA cloning

The full-length cDNA cloning of *PmTauT* was carried out as described previously (Sambrook & Russell David 1989). Total RNA was extracted from tissues using Trizol RNA isolation reagent (Invitrogen, Carlsbad, CA, USA) following the manufacturer's instructions. The quality and concentration of RNA were measured by NanoDrop 2000 (Thermo Fisher Scientific, Waltham, MA, USA).

First strand cDNA was produced by SMART RACE cDNA Amplification Kit (Clontech, Palo Alto, CA, USA) and used as template for 3' or 5' rapid amplification of cDNA ends (RACE) PCR. To obtain the full-length cDNA of *PmTauT*, degenerative primers were designed on the conserved regions from different species using CODEHOP online software firstly. Subsequently, specific primers were further designed for RACE PCR. The RACE PCR amplification was conducted with a thermal cycling according to the manufacturer's instructions. All PCR products were separated by agarose gel electrophoresis and the expected-size DNA fragments were obtained, gel purified and then ligated into pEASY-T1 vector (TransGen, Beijing, China). After transformed into the competent cells of *E. coli* DH5 $\alpha$ , the positive recombinants were identified through ampicillin selection and PCR screening with M13-F and M13-R. The positive clones were sequenced by Sangon Biotech (Shanghai, China). The full-length cDNA sequence of *PmTauT* was deposited to the GenBank database (GenBank accession no. KT369001). All primers used in this study were listed in Table 1.

### Sequence and phylogenetic analysis

The *PmTauT* sequence was analysed using the National Center for Biotechnology Information BLAST algorithm (<http://www.ncbi.nlm.nih.gov/blast>). The deduced amino acid sequence was analysed with the Expert Protein Analysis System (<http://www.expasy.org>). The putative transmembrane domains were predicted using TMHMM 2.0 (<http://www.cbs.dtu.dk/services/TMHMM>). Potential glycosylation sites were predicted by NetNGlyc 1.0 Server (<http://www.cbs.dtu.dk/services/NetNGlyc>).

Multiple sequence alignments of the deduced amino acid sequence of *PmTauT* was conducted using the ClustalW software (<http://www.ebi.ac.uk/tools/msa/clustalW2>). Phylogenetic analysis was performed with MEGA 4.0. The phylogenetic tree was constructed on the basis of amino acid sequences using the neighbour-joining (NJ) method (Saitou & Nei 1987). Confidence in the resulting phylogenetic tree branch topology was measured by bootstrap analysis with 1000 replicates (Felsenstein 1985; Hedges 1992).

### Tissue-specific expression of *PmTauT* mRNA

The mRNA expression of *PmTauT* in different tissues of juvenile turbot was measured by quantitative real-time PCR (qRT-PCR). Total RNA was extracted from liver, muscle, stomach, intestine, heart, gill, brain and eye. First strand cDNA was synthesized using the PrimeScript<sup>®</sup> RT Reagent Kit (Takara, Dalian, China). The qRT-PCR was carried out using the SYBR Green real-time PCR kit (Takara) with a quantitative thermal cycler CF96 (Bio-Rad, Foster City, CA, USA). GAPDH was used as the reference gene for internal standardization. The PCR program was as follows: (1) 15 s at 95°C for 1 cycle and (2) 10 s at 95°C, 10 s at 60°C and 20 s at 72°C for 40 cycles. The melting curve analysis of the amplification products was performed to demonstrate the specificity of the PCR products. Six samples of each tissue were analysed and each sample was run in triplicate ( $n = 6$ ). Target gene expression levels were quantitated by the  $2^{-\Delta\Delta Ct}$  method (Livak & Schmittgen 2001). The *PmTauT* expression levels of Gill were normalized to 1.0 and the rest tissues were expressed as relative expression values to the Gill group.

**Table 1** Sequences of the primers used in this study

Name	Primer sequence (5' – 3')	Description
TauT-F	CTKCTGCTDYTGCCCTCGACAG	Degenerate PCR
TauT-R	GGCTTNHTCAAGCCHYYGTTCC	Degenerate PCR
TauT-race F1	ACGAAAGCGGCATGTATGT	3' RACE PCR
TauT-race F2	TACAATGTGAAGGGCGAGTT	3' RACE PCR
TauT-race R1	ATGGCGAGTCCCAGGAGATA	5' RACE PCR
TauT-race R2	GTCCCTGTAGCAGTTGTATTTG	5' RACE PCR
TauT-rt F	GGGATCGAGGACATAGGG	Real-time PCR
TauT-rt R	GTAGGCGGTCAGGTTAG	Real-time PCR
GAPDH-rt F	AGCAGCAGCCATGTGACACC	Real-time PCR
GAPDH-rt R	TTGGGAGACCTCACCGTTGTAAC	Real-time PCR
M13-F	TGTAAACGACGGCCAGT	Universal primer
M13-R	CAGGAAACAGCTATGACC	Universal primer

### Isolation and culture of turbot muscle cells

Fish (about 15 g) was obtained from a commercial farm in Qingdao (Shandong, China) and maintained in a tank (60 cm × 60 cm × 60 cm, about 20 fish per tank) connected with a closed-water flow circuit for a week. During the maintaining period, fish was fed with a commercial diet (Great-Seven Bio-Tech, 2# feed for turbot, 49.5% protein, 10.2% lipid, 1.08% taurine) and water temperature was ranged from 19.5 to 20.5°C; pH from 7.3 to 8.0; salinity from 30‰ to 31‰; ammonia nitrogen was lower than 0.1 mg L<sup>-1</sup>; nitrite was lower than 0.1 mg L<sup>-1</sup>; dissolved oxygen was higher than 5.0 mg L<sup>-1</sup>. Before the sampling, fish was fasted for 24 h and sacrificed by a blow to the head and the skin was sterilized by immersion in 70% ethanol for 30 s. Turbot muscle cells were isolated according to the published protocols with slight modification (Castillo, Le Bail, Paboeuf, Navarro, Weil, Fauconneau & Gutierrez 2002). White dorsal muscle was excised under sterile conditions and collected in cold L-15 medium (Sigma, St. Louis, MO, USA) with antibiotics (penicillin 400 U mL<sup>-1</sup>, streptomycin 400 µg mL<sup>-1</sup>; Gibco, Gaithersburg, MD, USA). The tissue was minced and the fragments were centrifuged (300 g, 10 min at 4°C) and collected. Enzymatic digestion was performed with 0.05% Trypsin at room temperature on a shaker for 30 min. The reaction was neutralized with L-15 medium containing 10% foetal bovine serum (FBS, #10099141, taurine 237.4 ± 31.2 µM; Gibco). The cell suspension was purified through a cell strainer of 70-µm mesh size (BD Falcon, San Jose, CA, USA). The isolated muscle cells were collected in 15-mL sterilized centrifuge tubes and centrifuged (300 g, 10 min at 4°C). The cell pellets were resuspended with cold L-15 medium supplemented with 10% FBS, 20 mM HEPES, 1% antibiotics (penicillin 100 U mL<sup>-1</sup>, streptomycin 100 µg mL<sup>-1</sup>), 2 mM GlutaMAX™ and basic fibroblast growth factor (2.5 ng mL<sup>-1</sup>; Gibco). Cells were cultured in 6-well plastic plates (Corning, New York, NY, USA) at 24°C in a normal atmosphere incubator. Observations and morphology were regularly made to control the state of the cells.

### Substrate regulation of *PmTauT* *in vitro*

In order to explore the effect of taurine on the expression of *PmTauT* transcript, this study was carried out in turbot muscle cells adapted to a

taurine-free chemically defined medium (Jayanthi, Ramamoorthy, Mahesh, Leibach & Ganapathy 1995; Bitoun & Tappaz 2000). Briefly, the cells were seeded in 6-well plastic plates at a density of 2 × 10<sup>5</sup> cells/well and allowed to grow for 24 h in the complete growth medium (10% FBS). Following this, the cells were adapted to a medium containing 5% FBS for 24 h and finally incubated for an additional 24 h in a chemically defined medium in the absence of serum (L-15 medium containing 20 mM HEPES, 1% antibiotics, 2 mM GlutaMAX™ and 2.5 ng mL<sup>-1</sup> bFGF). And then, the cells were treated with experimental medium which contained various concentrations of taurine (0, 10, 25, 50, 100, 500 µM, respectively), which cover the physiological content in turbot muscle (Qi *et al.* 2012; Wang *et al.* 2014). The treated cells were harvested after 24 h to analyse the expression of *PmTauT* transcript. All cell culture experiments were repeated for four times (*n* = 4). The *PmTauT* expression levels of taurine-free group were normalized to 1.0 and the rest tissues were expressed as relative expression values to it.

### Statistical analysis

The tissue distribution of *PmTauT* was analysed using one-way ANOVA by SPSS 19.0 (SPSS, Chicago, IL, USA). Prior to the statistical tests, data were examined for homogeneity of variances (*F*-test). As the data were heterogeneous, we analysed them after log-transformed. Differences between the means were tested by Tukey's multiple range tests. The level of significance was chosen at *P* < 0.05 and the results were presented as means ± SEM (standard error of the mean). The result of substrate regulation of *PmTauT* was estimated by broken-quadratic regression analysis.

## Results

### cDNA cloning and sequencing characterization of *PmTauT*

The complete nucleotide and deduced amino acid sequence of *PmTauT* were shown in Fig. 1. The full-length cDNA of *PmTauT* was 2566 bp, containing a 5' untranslated region (UTR) of 58 bp, a 3' UTR of 633 bp and an open reading frame (ORF) of 1875 bp encoding 624 amino acids. The predicted molecular mass of *PmTauT* was 69.7 kDa. The deduced protein

**Figure 1** The full-length cDNA sequence and deduced amino acid sequence of *PmTaut*. The deduced amino acid sequence was shown upon the nucleotide sequence. The asterisk indicated the stop codon. Nucleotides were numbered from the first base at the 5' end. Four potential N-glycosylation sites were boxed. Twelve transmembrane domains were shadowed.

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1      ACATGGGACAGCTGAGCGAGAGCAGCAGCACACATCGTCGAGCCATGAAGAAATCATGGCACAAAAGAGAACTCCAATGCCTGAA
12     D F H K D T L K F S P G K S P G T R P E D A E G K A F Q R
91     GGACTTCCACAGAGACCCCTGAAACCTTCACGGGGAGAGCCCGGACCCGCGAGCGAGCGGGAGAGCCCTCCAGAG
42     E K W A T K L L D F V L S V G L E S L G N Y W R E V L C
181    GGAGAATGGCCAGTAGCTCGACTTTGCTGCTGTGGCCGAGGCTTCGTTGGATTAGGAAGCTCTGGCGGTCCTCGACTTTG
72     Y K N G G G A F L I P Y T I F L F G G G L P V F F L E V A L H
271    CTATAAAATGGTGGAGGTGCATTCCTTATCCTTACACCATCTTCCTGTTGGGGGTGGCCCTGCCGTTCTCTCGAGAGTGCAC
102    G Q Y T S E G G I T C W A K L C P I F T S I G Y A S V V I V
361    GGGCCAGTACACTCTGAGAGGAGGATCACCTGCTGGCCAAAGCTTCGCCCATCTTCACTGGTATTAGCCCTCTGTGTGATCGT
132    S L L N I Y Y I V I L A W G L Y Y L F Q C F Q P E L P W A K
451    ATCGCTACTAAACATCTACTACTCGTGATCTGGCCCTGGGGCTTACTACCTGTTCCAGTGLTTLACAGCCGAGCTCCCTGGCGAA
162    C K Q P W N T E H C V E D T V R K K I T L W L A A I T D N F
541    GTGCAAGCAGCCGTGAACACAGAGACTGTGGAGGACAGGGTCCGCAAGAACAGCCCTTTGGTTGGCAGCAATATTACCAACT
192    T S P V T E F W E H N V L S I S S G I E D I G F L K W E D A
631    CACCTCCCTGTCACTGATCTCGGAACACAACTCTGAGCATCTCTCTGGATCGAGGACATAGGCCCTGGAATGGCCAGCTGGC
222    L C L L A V V V I C F P F C I W K G V K S T G K V V Y I T A T
721    CCTGTCTCTAGCAGTGTGGTATCTGCTTCTTGCATCTGGAAGGAGTCAAGTCCACTGGAAAGTGTGTTACATAACACGGAC
252    F P F V M L I V L L I R V V T I P G A S E G I K F Y L Y P I
811    TTTCCATTGGTATGCTCATTGTGCTGTGATTGTGTAGTGACCTGCCGGGGCATCCGAAGGGATAAATTTTACCTTTACCTAA
282    L T R L Q D P E V W I D A G T Q I F P S Y A I C L G A M T S
901    CCTGACCCGCTACAGGATCCAGAGGTGGATTGACGAGAACCCAGATTTTCTTCTCCTATGCCATTTGCTGGAGCCATGCGC
312    L G S Y N K Y K Y N C Y R D C L L L G G L N S G T S F V S G
991    ACTGGGAGCTACAACAAGTACAACAACACTGCTACAGGACTGTTTCTGCTGGAGGCTCAACAGCGGTACAGTITCTGGTGG
342    F A L F S V L G F E M A Q E Q G V D I A D V A E S E P G L A F
1081   CTTCGCAATTTTCGTCGGCTTCATGGCACAGAACCAAGGGGTGGACATGCCGATGGCGATGAGCTAGCTGCTGGCTTGCCT
372   I A Y P K A S M F M P L E W A F E L L L D
1171   CATTGCTACCCCAAGCTGTGTCATGATGCGGATGCCAACCTCTGGCCATCTCTCTTATCATGCTGCTGTCTGGGCCCTGA
402   S O F V E V E G Q I T S I A V D L Y P A L L R K Y G R R E I F
1261   CAGCCAGTTTGTGAAGTGAAGGACAGATCACATCTATTGGATCTGATCCAGCTCTCAGAGGGGTACCGGGGAGAGATCTT
432   I A V M C F S Y L L G L A M V T K G M Y V F Q L F D Y Y
1351   TATAGCTGTGATGTTCATGACATCTCTGGGACTCCGCAATGGTACGAAAGGGCCATGTGATGTTTCAACTCTTGTGATTA
462   A A S G V E C L L W V A F F E C I A V A W V Y V D N F Y D A
1441   TGCAGCCAGCGGTGTGCTCTTTTGGGGTGGCATTCTTGAATGCATTGCTGAGCCCTGGGTATGGAGTGGATAACTCTTACAGCC
492   V E D M I G Y R P N P W H E W S W F I F E Y L G G F F W
1531   ACTCGAGATGATGGTACAGCCAAATCCAGATGAACTGGAGTGAACCTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
522   S L L Y K P L T Y N K Y Y E Y P D W A I G V G R G C I A H
1621   CTTTTCTGGTGAAGTACAGCCCTTGACTATAACAAGGTGTATGATATCTGACTGAGCCATCTGCTGGCCCTGTGTTGGCCCT
552   S S M I C I P M V M V I K I L Q S E G S L I E R I K A V A A
1711   GTCCTCCATGATGTCATCCCAATGGTGTGTCATCAAGATCTTCGAGTCCGAGGATCACTGATCGAGCGGATAAAGAGTCCAGCCG
582   P A K S G V S S R P K E Y N V K G E L T L P L D P N G N G
1801   CCCGGCCAGTCAAGTGTGAGCTCCCGCCGAGGAGTACAATGTGAAGGGCGAGTTGACACTCCCGCTCCCGCCGACCCAAACGG
612   L I K P T H T I V E T T M *
1891   CTTGATCAAGCCACCCACCATTTGTAGAAACAACGATGTGAGCGCTCTCTGTGAGAGAAATGATGTTGTGCTATCTGTGTATCA
1981   TATTTGCTACCTGATATGTTGATGTCACATTTGTCCTCAATATTCACGTTAGAAAATACCCGGTTGATTTTATATGTTATTTGT
2071   CTATTTCTCTCTGAAATTTTTTTTTCTACTATACGATATGTTGATGTTACACTCTGCTGATGTTGGCCAGTCCATCTATTAG
2161   CGAGTATTTGAGATAGAACTGTTCACTGTTTACTACTTCTCTGTTGATCTCGGAAATAGATGATGCTTTTGGGGGGGGGG
2251   GGTATATAGAGAAATATGAAATTTTCACTTAACATGAATGAGTACAACTAACCAATGAAAGGTAGAAAGACTCTAATAC
2341   CTTGCTGACTGTGACAGTCCCTGCCAAGTTTACTCTGATCTATATTTGCTGTATGATCCCAAGTGAATGATGATCTAT
2431   TGCAATAGCAGATTTTCTGAGGTTCAATAAGCCCTTGGCCAAATCTGTAGAAATGCACTCATCCAGAGAAACATCTCTGAAACA
2521   ACCAAGCAAAAATAATAATAAGAAAAAAAAAAAAAAAAAAAAAAAAA
    
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contained 12 putative transmembrane domains. In addition, four potential N-glycosylation sites were identified in deduced amino acid sequence of *PmTaut*.

**Homology and phylogenetic analyses of *PmTaut***

The multiple amino acid sequence alignment revealed that taurine transporter showed high homology across species, while the C-terminus of the protein contained a more variable region (Fig. 2). Taurine transporter from turbot shared 93% identity with *Solea senegalensis*, no less than 89% with other teleost and at least 77% identity with mammals. Moreover, a Cysteine was found in amino acid residue 322 of *PmTaut* while it was serine in mammals, which was a phosphorylation site of protein kinase C that controlled TauT activity.

A phylogenetic tree was constructed to evaluate the molecular evolutionary relationships of *PmTaut* against other TauT proteins (Fig. 3). Based on the phylogenetic analysis, the TauTs from invertebrates and vertebrates were classified into two distinct clades. *PmTaut* was most closely related to sequences from *Solea senegalensis* and *Salmo salar* with high bootstrap support. TauTs

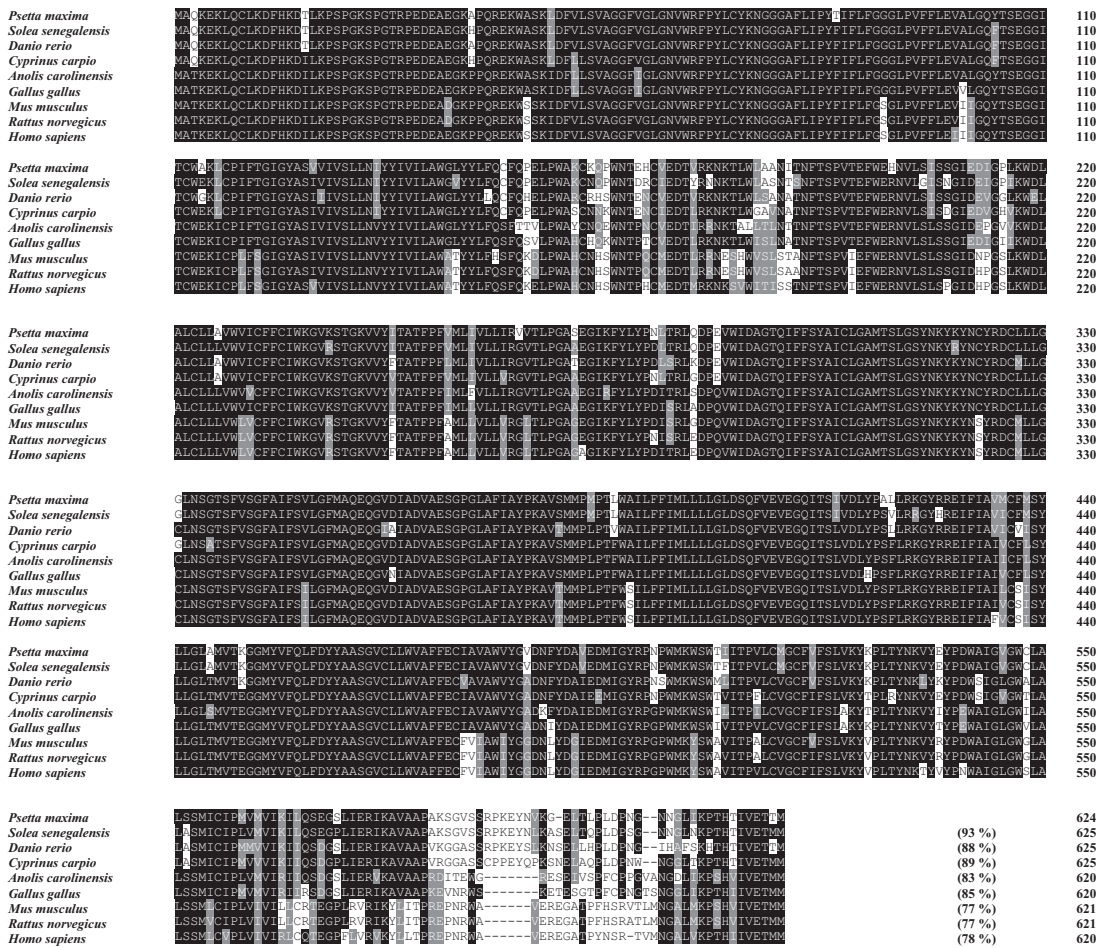
from mammals fell into two subclusters with other vertebrates that were in accordance with the results of homology analysis. The phylogenetic tree indicated that the evolution of TauT was almost in accord with the evolution of species.

**Tissue-specific expression of *PmTaut***

The real-time PCR assay showed that *PmTaut* was ubiquitously observed in all examined tissues, including brain, eye, gill, heart, intestine, liver, muscle, and stomach (Fig. 4). The highest expression levels of *PmTaut* were found in liver and intestine. The expression levels of *PmTaut* transcript in gill and stomach were lower than that in other tissues.

**Substrate regulation of *PmTaut* expression in turbot muscle cells**

Broken-quadratic regression analysis of the mRNA levels of *PmTaut* was shown in Fig. 5. The expression levels of *PmTaut* showed a dose-dependent decrease when taurine concentration was below 88.75 μM. The mRNA levels of *PmTaut* were almost constant when taurine concentration was over 88.75 μM.



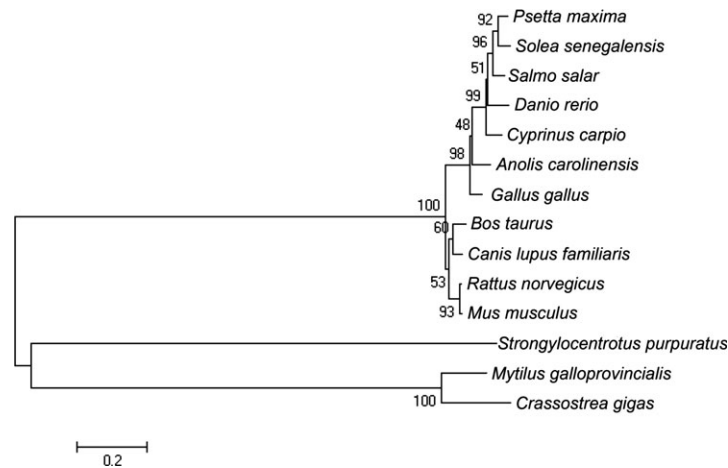
**Figure 2** Multiple sequence alignment of TauTs. Highly conserved residues were indicated with black backgrounds and similar residues were shaded. Dashes indicated gaps. The putative phosphorylation site of mammal TauT was boxed. Per cent identities of amino acids sequences with *PmTauT* were shown in parentheses at the end. From top to bottom, the sequences were from *Psetta maxima* (KT369001), *Solea senegalensis* (ADM88612), *Danio rerio* (NP\_001119858), *Cyprinus carpio* (BAA89537), *Anolis carolinensis* (XP\_003217787), *Gallus gallus* (NP\_001025771), *Mus musculus* (NP\_033346), *Rattus norvegicus* (AAA42304) and *Homo sapiens* (NP\_003034).

**Discussion**

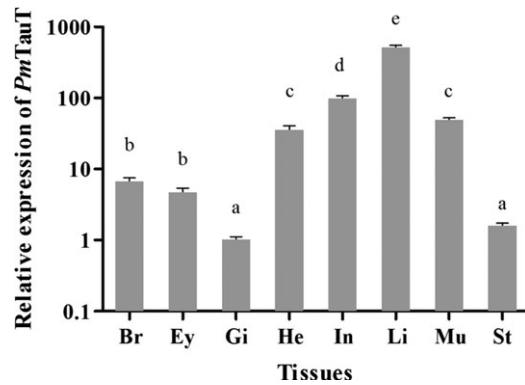
In this study, we obtained the full coding cDNA sequence of turbot (*P. maxima*) taurine transporter (*PmTauT*) for the first time. Twelve transmembrane domains were identified in the deduced amino acid sequence of *PmTauT*, which was in accord with TauTs from other species (Zarate & Bradley 2007; Pinto *et al.* 2012). *PmTauT* exhibits highly homology to TauTs from other species, which suggests the highly evolutionary conservation of TauT.

Previous studies showed that TauT activity was regulated by phosphorylation through

protein kinase C (PKC) (Jones, Miller, Dowling & Chesney 1991; Brandsch, Miyamoto, Ganapathy & Leibach 1993; Loo, Hirsch, Sarkar & Wright 1996; Tappaz 2004). The activation of PKC inhibited the activity of TauT through decreasing the maximal velocity or reducing the number of active transporter in the plasma membrane. Among the putative phosphorylation sites, serine-322 has been proved to be critical for activity regulation through PKC (Han, Budreau & Chesney 1999). Replacement of ser-322 with alanine could increase threefold transport activity of Madin–Darby canine kidney cell taurine transporter, which was through improving the

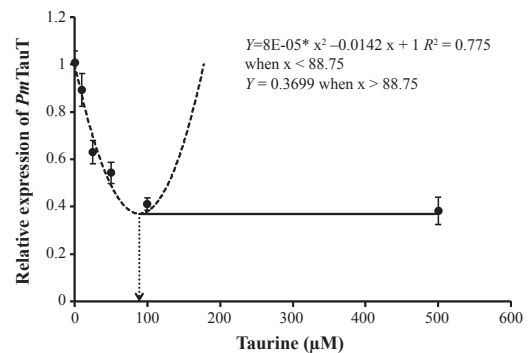


**Figure 3** Phylogenetic tree of deduced amino acid sequences of TauT. The tree was constructed using MEGA 4.0 software with the neighbour-joining method. The bootstrap sampling was performed with 1000 replicates. The numbers at the forks indicated the bootstrap. From top to bottom, the sequences were from *Psetta maxima* (KT369001), *Solea senegalensis* (ADM88612), *Salmo salar* (AAM90737), *Danio rerio* (NP\_001119858), *Cyprinus carpio* (BAA89537), *Anolis carolinensis* (XP\_003217787), *Gallus gallus* (NP\_001025771), *Bos taurus* (NP\_777035), *Canis lupus familiaris* (NP\_001003311), *Rattus norvegicus* (AAA42304), *Mus musculus* (NP\_033346), *Strongylocentrotus purpuratus* (XP\_011676091), *Mytilus galloprovincialis* (BAD91313) and *Crassostrea gigas* (NP\_001292278).



**Figure 4** Tissue distribution of TauT in juvenile turbot. Relative *PmTauT* mRNA levels were measured by quantitative real-time PCR (qRT-PCR) and normalized by GAPDH. The detected tissues were *Br* brain, *Ey* eye, *Gi* gill, *He* heart, *In* intestine, *Li* liver, *Mu* muscle and *St* stomach. The TauT expression levels of *Gi* was normalized to 1.0 and the rest tissues were expressed as relative expression values to the *Gi* group. The data were expressed as means  $\pm$  SEM ( $n = 6$ ). Different letters above the bars denote significant differences between groups at the  $P < 0.05$  level.

transport capacity  $V_{max}$  rather than the affinity  $K_m$  (Han *et al.* 2006). Sequence analysis showed that Ser-322 was only conserved in mammal TauTs and this position was occupied by cysteine in fish, reptiles and birds (Fig. 2). Since cysteine



**Figure 5** Relative mRNA expression levels of *PmTauT* in response to taurine concentrations in isolated turbot muscle cells. Turbot muscle cells were isolated and treated with various levels of taurine (0, 10, 25, 50, 100, 500  $\mu$ M). The *PmTauT* mRNA levels were measured by quantitative real-time PCR (qRT-PCR) and normalized by GAPDH. The *PmTauT* expression levels of taurine-free group was normalized to 1.0 and the rest tissues were expressed as relative expression values to it. The data were expressed as means  $\pm$  SEM ( $n = 4$ ).

could not be phosphorylated by PKC, it indicates that TauTs from non-mammals vertebrates might have a higher transport capacity and the regulation of TauT activity was different between mammals and non-mammalian vertebrates. These

results were also in accord with the phylogenetic tree analysis that TauTs from mammals and other vertebrates fell into two subclusters. However, the regulation of TauT activity in non-mammalian vertebrates needs to be further studied.

TauT was ubiquitously expressed in all examined tissues in juvenile turbot, which was similar with that in other fish species (Takeuchi *et al.* 2000a; Zarate & Bradley 2007; Pinto *et al.* 2012). The expression levels of TauT might be in connected with the physiological roles of taurine in different tissues (Sturman, Rassin & Gaull 1977). In this study, *PmTauT* was predominantly detected in the tissues of liver and intestine. Liver is the major site for sulphur amino acids metabolism and taurine biosynthesis (Garcia & Stipanuk 1992). Taurine plays a significant role in conjugation with bile acids in liver (Huxtable 1992). However, due to the limited biosynthesis ability of turbot, taurine homeostasis in liver was also partly dependent on transportation (Wang *et al.* 2014). In the digestive tract of turbot, *PmTauT* was expressed at a higher level in intestine than stomach. It indicates that intestine was the major site of taurine absorption in juvenile turbot. However, Pinto *et al.* (2012) reported that TauT was actively expressed in stomach of juvenile Senegalese sole and the absorption of dietary taurine might start in the stomach region. These differential results might be due to the different developmental stages or species. In addition, the high expression of TauT in intestine was critical for enterohepatic circulation of taurine in turbot, which was important for maintaining taurine body pool (Hofmann 2008). Moreover, *PmTauT* was also well detected in muscle, heart, brain and eye. Previous studies have found that taurine was high in these organs and it played many important physiological roles (Huxtable 1992). Interestingly, *PmTauT* was less expressed in turbot gill, an important organ regulating the internal osmotic pressure (Hoar 1988). As the transporter of taurine, a well-established osmolyte, TauT showed a hypertonicity-induced expression pattern (Takeuchi *et al.* 2000a). The low expression level of *PmTauT* in turbot gill might indicate that the environment of seawater in this study was suitable for the growth of turbot.

Dietary taurine levels has a significant contribution of the taurine body pool in several fish species, such as Senegalese sole (Pinto *et al.* 2010),

red seabream (Takagi, Murata, Goto, Ichiki, Endo, Hatate, Yoshida, Sakai, Yamashita & Ukawa 2006b), Japanese flounder (Kim *et al.* 2008) and turbot (Qi *et al.* 2012; Wang *et al.* 2014). As the conditional essential amino acid for fish, supplementation of taurine to plant protein based aquafeeds has been proved necessary. In this study, the expression level of *PmTauT* was high when the turbot muscle cells were exposed in taurine-free medium and it was down-regulated by taurine in a dose-dependent manner. Analogous results were also found in early studies (Friedman, Albright, Gusowski, Padilla & Chesney 1983; Bitoun & Tappaz 2000). The regulation of TauT expression by substrate suggests that the capacity of taurine absorption is high when dietary taurine level is low. Our previous study has suggested that hepatic taurine content in different stages of rainbow trout was controlled in a fairly tight range (Wang, He, Mai, Xu & Zhou 2015). Meanwhile, the taurine level in plasma and liver yellowtail did not further increase when the supplemental taurine increased from 30 to 60 g kg<sup>-1</sup> (Takagi *et al.* 2006a). The sensitive regulation TauT by taurine might be critical for the physiologically effects of taurine (Tappaz 2004). Furthermore, it has been established that the down-regulation of TauT by taurine resulted from a decreased transcription rate of the TauT gene (Han, Budreau & Chesney 1997).

In conclusion, we isolated taurine transporter from turbot and found that *PmTauT* was down-regulated by taurine in a dose-dependent manner. These results provide an expanded perspective on the homeostasis of taurine in turbot. Furthermore, this finding may be of vital importance for defining the supplementation of taurine in aquafeeds.

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