



Full length article

Functional characterization of purinergic receptor P2Y₁₄ in the Japanese flounder (*Paralichthys olivaceus*) head kidney macrophages

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ABSTRACT

Extracellular nucleotides and nucleotide sugars are important danger-associated signaling molecules that play critical roles in regulation of immune responses in mammals through activation of purinergic receptors located on the cell surface. However, the immunological role of extracellular UDP-glucose-activated P2Y₁₄ receptor (P2Y₁₄R) in fish still remains unknown. In this study, we identified and characterized a P2Y₁₄R paralog in the Japanese flounder (*Paralichthys olivaceus*). The mRNA transcripts of P2Y₁₄R are detected in all examined Japanese flounder tissues. Compared with the UDP-activated P2Y₆ receptor, however, P2Y₁₄R gene is highly expressed in Japanese flounder head kidney macrophages (HKMs). In addition, P2Y₁₄R is significantly up-regulated following inflammatory stimulation with LPS and poly (I:C) in the HKMs, suggesting a role of P2Y₁₄R in response to inflammation in fish. Furthermore, activation of P2Y₁₄ receptor with its potent and selective agonist MRS 2905 resulted in a decreased expression of LPS-induced pro-inflammatory cytokine *IL-1beta* gene in the HKMs. In contrast, inhibition of P2Y₁₄ receptor activity or down-regulation of the endogenous expression of P2Y₁₄R by small interfering RNA significantly upregulates the LPS-induced pro-inflammatory cytokine *IL-1beta* gene expression in the HKMs, demonstrating that P2Y₁₄R is involved in inflammation regulation in fish. Moreover, stimulation of the Japanese flounder HKMs with UDP-glucose evoked a rapid increase of extracellular signal-regulated kinase 1/2 (ERK1/2) phosphorylation in a dose- and time-dependent manner, indicating the involvement of P2Y₁₄R in activation of ERK1/2 signaling in fish immune cells. Taken together, we demonstrated that the inducible P2Y₁₄R plays an important role in regulation of fish innate immunity.

1. Introduction

Extracellular nucleotides such as ATP, ADP, UTP, and UDP and nucleotide sugars such as uridine 5'-diphosphoglucose (UDP-glucose) are important danger signaling molecules that play an important role in the regulation of immune responses through binding to and activating of different members of plasma membrane P2 receptors, which are widely expressed on immune cells [1–3]. P2Y receptors belonging to the G-protein-coupled receptors (GPCRs) superfamily, are a family of the metabotropic purinergic receptors for adenine and uridine nucleotides and nucleotide sugars. Eight P2Y receptor subtypes (P2Y₁, P2Y₂, P2Y₄, P2Y₆, P2Y₁₁, P2Y₁₂, P2Y₁₃ and P2Y₁₄) with differences in both pharmacology and downstream signaling pathways have been identified in mammals [4–6].

In particular, P2Y₁₄R that is potently and selectively activated by

UDP and UDP-sugars [7], is highly expressed in immune and inflammatory cells [7,8]. Activation of P2Y₁₄R regulates a range of immune responses including maturation of dendritic cells [9], inhibition of T lymphocyte proliferation [10], chemotaxis of bone-marrow hematopoietic stem cells [11] and neutrophils [12], and secretion of the potent neutrophil chemoattractant CXCL8/IL-8 in airway epithelial cells [13]. In addition, it has been demonstrated that UDP-glucose and its receptor P2Y₁₄R are key front line players able to trigger innate mucosal immune responses in mouse female reproductive tract [14].

We showed previously that extracellular UDP-activated P2Y₆ receptors functions importantly in the Japanese flounder *Paralichthys olivaceus* peripheral blood leukocytes [15]. Because extracellular UDP can also activate P2Y₁₄ receptors [8], we presumed the hypothesis that P2Y₁₄ receptors could play a role in Japanese flounder innate immunity. For this purpose, we cloned P2Y₁₄ receptor gene and

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characterized its expression under normal and inflammatory conditions in Japanese flounder head kidney macrophages (HKMs). By pharmacological activation or inhibition of P2Y₁₄R activities, and down-regulation of the P2Y₁₄R endogenous expression in the HKMs, we explored the potential role of the P2Y₁₄ receptor in Japanese flounder innate immunity. In addition, we investigated the consequence of P2Y₁₄R activation on ERK signaling in the HKMs. Taken our findings together, we for the first time demonstrated that the inducible P2Y₁₄R plays an important role in regulation of fish innate immune response and in activation of ERK signaling pathway in fish immune cells.

2. Material and methods

2.1. Experimental animals

Japanese flounder *P. olivaceus* were obtained from a local fish farm in Tianjin, China. Fish were cultured in an aerated recirculating seawater system at 21 °C in the laboratory for two weeks before use in experiments. Fish were handled and clinically examined as described in our previous study [16]. Only animals with healthy appearance and normal activity were used in experiments.

2.2. Chemicals and antibodies

UDP-glucose, LPS and poly (I:C) were obtained from Sigma-Aldrich. The potent and selective P2Y₁₄ receptor agonist 2-Thiouridine-5'-O-(α , β -methylene)diphosphate trisodium salt (MRS 2905) and high affinity and selective P2Y₁₄ receptor antagonist 4-[4-(4-Piperidinyl)-phenyl]-7-[4-(trifluoromethyl)-phenyl]-2-naphthalenecarboxylic acid (PPTN) were purchased from Tocris Bioscience. Rabbit monoclonal antibodies against phospho-p44/p42 MAPK (p-Erk1/2) and against total p44/p42 MAPK (Erk1/2) were purchased from Cell Signaling Technology. Lipofectamine[®] RNAiMAX transfection reagent, HRP-labeled goat anti-mouse and goat anti-rabbit secondary antibodies and mouse monoclonal antibody against beta-actin were obtained from ThermoFisher Scientific.

2.3. Preparation and cell culture of Japanese flounder head kidney macrophages

To collect head kidney tissues, Japanese flounder were anesthetized using 0.25 g/L tricaine methanesulfonate (Sigma-Aldrich) and the head kidney was rapidly dissected under sterilized conditions. The dissected head kidney tissues were used to prepare head kidney primary cells with the procedure described previously [17]. The head kidney macrophages (HKMs) were further purified from the obtained primary head kidney cell suspensions by discontinuous Percoll (GE Biosciences) gradient centrifugation with a previously described protocol [18]. The viability of the HKMs was greater than 95% which was examined by trypan blue exclusion assay. The HKMs were grown in RPMI-1640 medium (Invitrogen) supplemented with 10% fetal bovine serum and 1% penicillin-streptomycin liquid (Invitrogen) at 21 °C.

2.4. Identification of P2Y₁₄R cDNAs from Japanese flounder head kidney macrophages

To explore the immune functions of P2Y₁₄R in Japanese flounder *P. olivaceus* head kidney macrophages, we initially cloned its cDNA sequences. Based on the available sequence data, a pair of primer (F/R, Table 1) was designed and the ORF region of P2Y₁₄R (XM_020107896.1) was amplified from the Japanese flounder HKMs by RT-PCR. The amplification products were separated by electrophoresis on a 1.2% agarose gel containing ethidium bromide. The PCR products with the expected sizes were purified with a DiaSpin DNA Gel Extraction Kit (Sangon Biotech Co., Ltd., China) and cloned into a pMD18-T vector (TaKaRa) for DNA sequencing.

Table 1

Sequence of primers used in this study.

Primers	Sequence (5'→3')
F	ATGGATCCCTTCAACGTCAG
R	TCCTGTGTTCGGTTTCTCA
qP2Y ₁₄ R-f	GGGTCCGCTGTC TGGGTGA
qP2Y ₁₄ R-r	ATCCAACCGCAGCATCTTC
qP2Y ₆ R-f	AGTGCGGAGATGCGGGAC
qP2Y ₆ R-r	GGTATCGTGGCTGTGTGAAGTA
qP2Y ₂ R-f	TTCTCCACGCGAAGACG
qP2Y ₂ R-r	CAGACGGACGTAGCAACCAG
qP2Y ₁₂ R-f	ACTGGCCTGCGTGTGTTT
qP2Y ₁₂ R-r	AGATGGAGCCCGAGAGAAGC
q β -actin-f	AGGTTCCGTTGTCCCG
q β -actin-r	TGGTTCCTCCAGATAGCAC
qIL-1 β -f	CCTGTCTGTCTGGGCATCAA
qIL-1 β -r	CACCCCGCTGTCTGCTT

q: quantitative real-time PCR; f: forward; r: reverse.

2.5. Expression analysis of P2Y₁₄R mRNA transcripts in Japanese flounder tissues and head kidney macrophages

qRT-PCR analysis (see section 2.8) was performed to determine the relative basal gene expression level of P2Y₁₄R in various Japanese flounder tissues including blood, gill, head kidney, trunk kidney, heart, liver, skin, muscle, intestine and spleen with a protocol described in the previous study [21]. In addition, qRT-PCR analysis was also applied to compare the relative gene expression level of P2Y₂, P2Y₆, P2Y₁₂ and P2Y₁₄ receptors in the Japanese flounder HKMs. To this aim, total RNA from the HKM cells and tissues was purified with a PureLink[®] RNA Mini Kit and TRIzol reagent (Invitrogen), respectively, according to the manufacturer's recommendations. RNA was quantified by a NanoDrop spectrophotometer and treated with RNase Free DNase I (Invitrogen) to digest possible contaminating genomic DNA following the manufacturer's protocol. The treated RNA was then transcribed into cDNAs using a SuperScript III reverse transcriptase kit (Invitrogen) according to the manufacturer's directions. The relative gene expression levels for the individual P2Y receptor genes were determined by qRT-PCR (see section 2.8) with *beta-actin* serving as an internal reference gene.

2.6. In vitro immune challenge experiments in the Japanese flounder HKMs

To study the involvement of P2Y₁₄R in Japanese innate immune responses, Japanese flounder HKMs were challenged with pathogen-associated molecular patterns (PAMPs) LPS and poly (I:C) as described in a previous study [22]. Briefly, overnight-cultured Japanese flounder HKMs (5×10^6 cells/well) were stimulated with 20 μ g/ml LPS or poly (I:C) (final concentration, dissolved in cell culture medium) for 4, 8, 12, 24, 36 or 48 h. Cells without PAMP treatment served as controls. After treatment, total RNA was purified and transcribed into cDNAs, and the LPS- and poly (I:C)-induced P2Y₁₄R gene expression changes were measured by qRT-PCR.

2.7. Pharmacological treatments and knockdown of P2Y₁₄R endogenous expression in the Japanese flounder HKMs

To evaluate the potential role of P2Y₁₄R in inflammatory stimulation-induced innate immune response, P2Y₁₄R activity in the Japanese flounder HKMs were pharmacologically activated or inhibited by pre-incubation with the potent and selective P2Y₁₄ receptor agonist MRS 2905 at a final concentration of 20 μ M or antagonist PPTN at a final concentration of 10 μ M for 30 min, prior to treatment with 20 μ g/mL LPS for 2 h in the presence or absence of MRS 2905 or PPTN. The PAMP-induced *IL-1beta* gene expression changes following pharmacological treatment was assessed by qRT-PCR (see below).

In addition, the endogenous expression of P2Y₁₄R in the Japanese

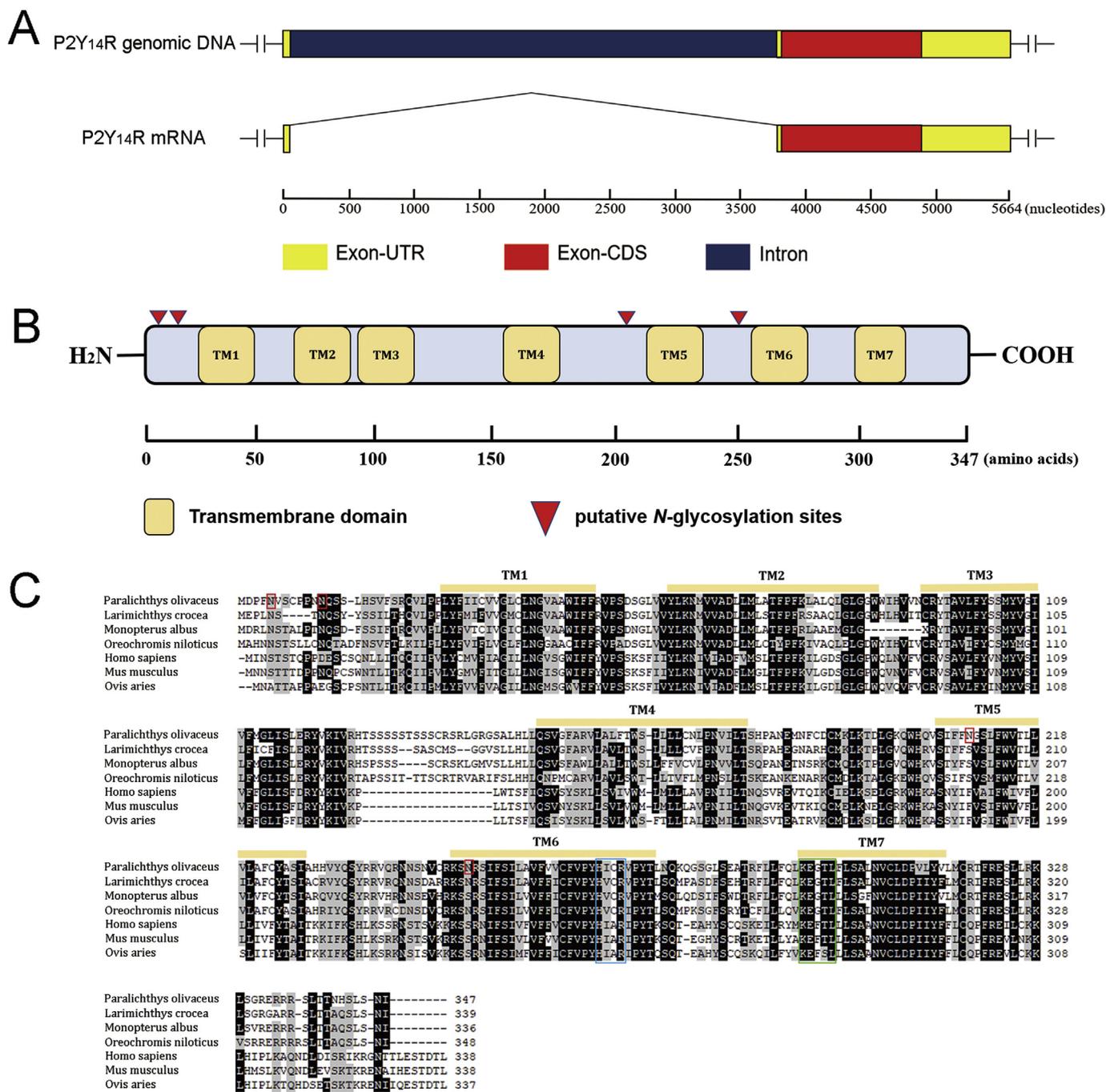


Fig. 1. Scheme showing the genomic and domain structures of Japanese flounder P2Y₁₄R and sequence alignment of selected mammalian and teleost P2Y₁₄R paralogs. (A) Genomic DNA structure of Japanese flounder P2Y₁₄R gene. Top panel shows the exon and intron structure of Japanese flounder P2Y₁₄R gene. Bottom panel shows the P2Y₁₄R mRNA structure derived from the genomic DNA sequence of Japanese flounder P2Y₁₄R. (B) Schematic domain structures of Japanese flounder P2Y₁₄R protein. The predicted N-glycosylation sites are indicated by red invert arrows on top of the rectangle. The transmembrane domains are shown as yellow boxes. (C) Multiple alignment of the amino acid sequences of Japanese flounder P2Y₁₄R and its counterpart proteins from representative vertebrate species using the ClustalW program. The GenBank accession numbers of P2Y₁₄ receptor proteins from selected vertebrate species are Japanese flounder *Paralichthys olivaceus* P2Y₁₄R (XP_019963455.1), yellow croaker *Larimichthys crocea* P2Y₁₄R (XP_019133030.1), rice swampee *Monopterus albus* P2Y₁₄R (XP_020478366.1), tilapia *Oreochromis niloticus* P2Y₁₄R (XP_005474964.1), human *Homo sapiens* P2Y₁₄R (NP_001074924.1), mouse *Mus musculus* P2Y₁₄R (AAH58558.1) and sheep *Ovis aries* P2Y₁₄R (XP_011956798.1). Identity is denoted by shaded white letters and similarity is shown by shaded black letters. The seven transmembrane domains are indicated on the top of the sequences. The predicted N-glycosylation sites in Japanese flounder P2Y₁₄R protein were boxed in red. The H-X-X-R/K motif that is crucial for agonist activity in the TM6 and the featured K-E-X-X-L motif for extracellular nucleotides binding in TM7 of all the P2Y₁₄ receptors are boxed in blue and green, respectively. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

flounder HKMs was down-regulated by small interfering RNA. For this purpose, negative control siRNA (sequence was not disclosed by the provider) and a set of synthetic small interfering RNAs (siRNAs) for P2Y₁₄R were ordered from RiboBio Inc. (Guangzhou, China). Because of

the lack of reliable anti-P2Y₁₄ Abs, knockdown efficiency of the three P2Y₁₄R siRNA candidates was evaluated 48 h post-transfection by qRT-PCR as described in section 2.8. The knockdown efficiency of the optimized siRNA with the target sequence of 5'-GGTGGATCCATGTGGT

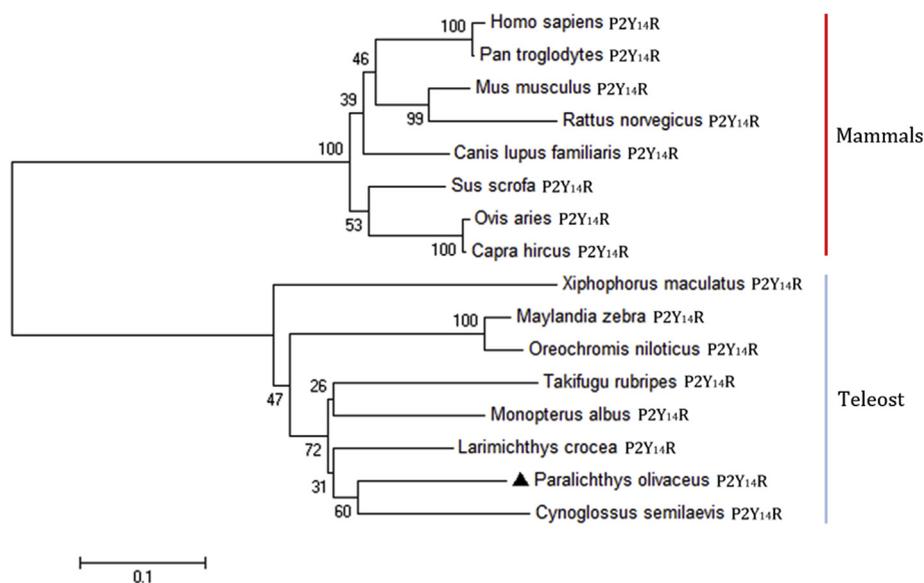


Fig. 2. Phylogenetic relationship of P2Y₁₄ receptor paralogs from Japanese flounder and other vertebrate species. The maximum-likelihood phylogenetic tree was constructed using MEGA 5.0 program. The GenBank accession numbers for the P2Y receptor paralogs from different species are *Cynoglossus semilaevis* P2Y₁₄R (XP_016887698.1), *Xiphophorus maculatus* P2Y₁₄R (XP_005808340.1), *Maylandia zebra* P2Y₁₄R (XP_004565057.2), *Takifugu rubripes* P2Y₁₄R (XP_003979142.1), *Capra hircus* P2Y₁₄R (XP_005675495.2), *Rattus norvegicus* P2Y₁₄R (NP_598261.1), *Canis lupus familiaris* P2Y₁₄R (XP_005634627.1), *Pan troglodytes* P2Y₁₄R (XP_001145005.1), *Sus scrofa* P2Y₁₄R (XP_020925281.1) and the list in the legend of Fig. 1.

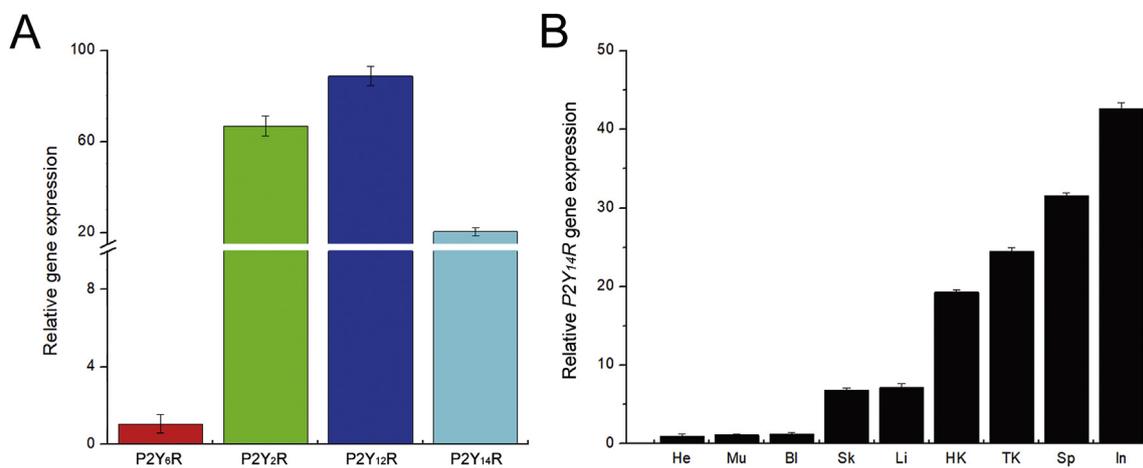


Fig. 3. qRT-PCR analysis of the relative gene expression of P2Y₂R, P2Y₆R, P2Y₁₂R and P2Y₁₄R receptors in Japanese flounder head kidney macrophages. (A) Comparative analysis of the relative gene expression levels of P2Y₂, P2Y₆, P2Y₁₂ and P2Y₁₄ receptors in Japanese flounder head kidney macrophages. (B) qRT-PCR analysis of the gene expression pattern of P2Y₁₄R in healthy *P. olivaceus* tissues. Bl: blood; Mu: muscle; HK: head kidney; TK: trunk kidney; He: heart; Li: liver; Sk: skin; Sp: spleen; In: intestine. Error bars indicate standard deviation (n = 3).

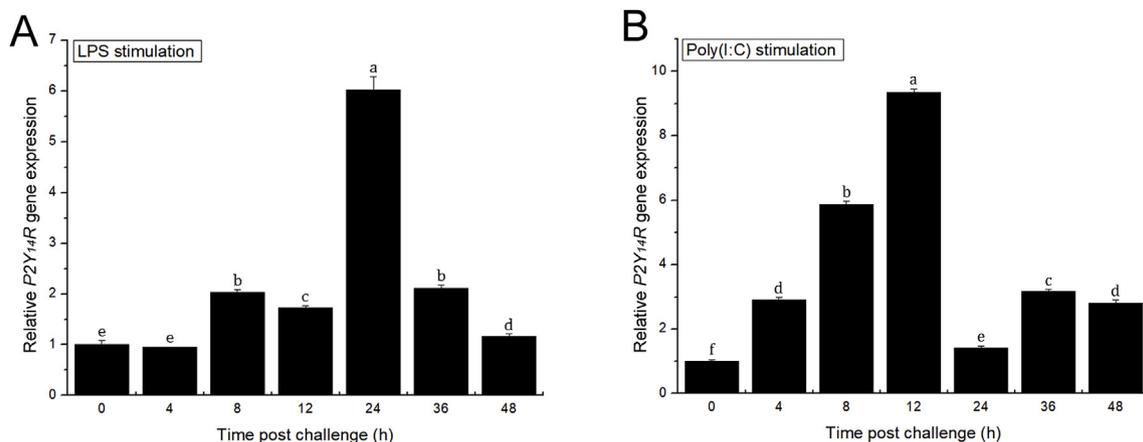


Fig. 4. Inflammatory stimulation-induced P2Y₁₄R gene expression in *P. olivaceus* head kidney macrophages. Japanese flounder HKMs were stimulated with 20 μg/ml (final concentration) LPS (A) or poly(I:C) (B) for the indicated time points. After 0, 4, 8, 12, 24, 36 and 48 h post stimulation, total RNA was extracted and the P2Y₁₄R gene expression changes relative to the untreated controls were determined by qRT-PCR. *Beta-actin* was served as an internal reference gene. Values labeled with different lowercase letters indicated significant difference at p < 0.05 among treatments. Data are the mean ± standard deviation of triplicate treatments from one representative experiment; similar results were obtained on two other separate occasions.

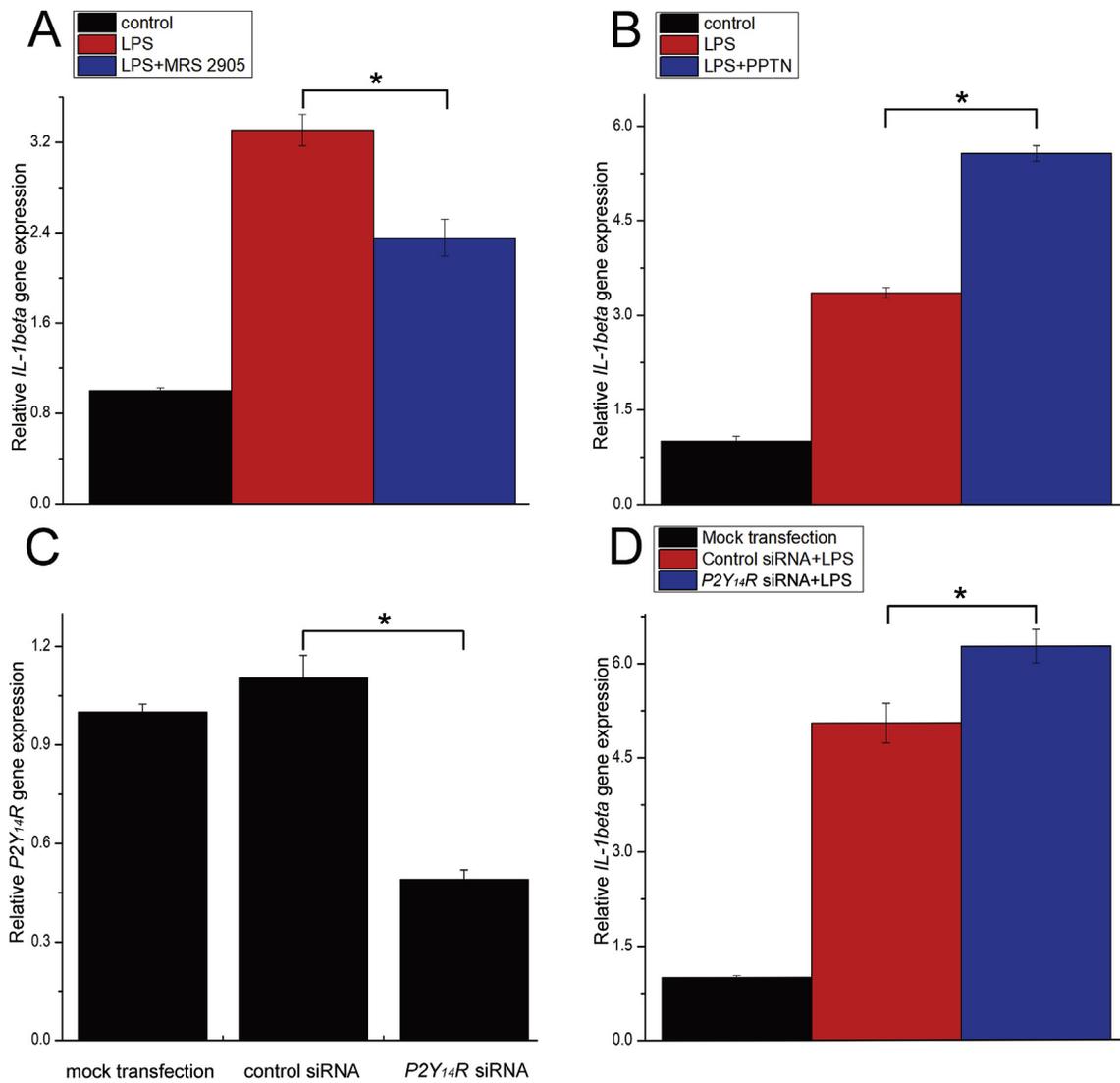


Fig. 5. The role of P2Y₁₄R in inflammatory stimulation-induced pro-inflammatory cytokine *IL-1beta* gene expression in the Japanese flounder HKMs. (A and B) Pharmacological activation or inhibition of P2Y₁₄ receptors activity affects LPS-induced *IL-1beta* gene expression in the Japanese flounder HKMs. Japanese flounder HKMs were pre-incubated with or without 20 μM potent and selective P2Y₁₄R agonist MRS 2905 (A) or 10 μM antagonist PPTN (B) for 30 min followed by stimulation with 20 μg/mL LPS for 2 h in the presence or absence of MRS 2905 or PPTN. The relative pro-inflammatory cytokine *IL-1beta* gene expression levels were examined by qRT-PCR and were normalized to untreated control cells (set to 1). Significant difference between PAMP treated groups and PAMP plus MRS2905 or between PAMP treated groups and PAMP plus PPTN treated groups was determined by the Student's t-test and is indicated by brackets and asterisks at $p < 0.05$. Data are presented as means \pm standard deviations of triplicate determinants from one representative experiment. Similar results were obtained in other two separate experiments. (C) Evaluation of the silencing efficiency of optimized P2Y₁₄R siRNA. Japanese flounder HKMs were mock transfected or transfected with negative control siRNA or P2Y₁₄R siRNA for 48 h at a final concentration of 150 nM. The relative P2Y₁₄R gene expression levels were determined by qRT-PCR and normalized to the expression level in mock transfected cells (set to 1). Asterisks (*) mark the significant decrease of P2Y₁₄R gene expression in P2Y₁₄R siRNA transfected cells compared with the negative control siRNA transfected control cells ($p < 0.05$). (D) Down-regulation of P2Y₁₄R expression upregulates the LPS-induced pro-inflammatory cytokine *IL-1beta* gene expression in the Japanese flounder HKMs. Japanese flounder HKMs were mock transfected or transfected with negative control siRNA or optimized P2Y₁₄R siRNA for 48 h at a final concentration of 150 nM. After transfection, the HKMs were stimulated with 20 μg/mL LPS for 2 h. The LPS-induced gene expression of *IL-1beta* in the P2Y₁₄R down-regulated HKMs were evaluated by qRT-PCR with *beta-actin* as an internal reference gene. Asterisks (*) indicate the significant increase of *IL-1beta* gene expression in P2Y₁₄R siRNA transfected cells compared with the negative control siRNA transfected control cells ($p < 0.05$). Values are presented as means \pm standard deviation ($n = 3$).

CAA-3' on the Japanese flounder P2Y₁₄R was about 50% as determined by qRT-PCR (Fig. 5C). After evaluation, overnight-cultured Japanese flounder HKM cells at a cell density of 5×10^6 cells/well in a 24-well plate were transfected with 150 nM optimized P2Y₁₄R siRNA or equal amount of negative control siRNA using Lipofectamine® RNAiMAX reagent (Invitrogen) followed by the manufacturer's protocol. After 48 h of silencing, the cells were stimulated with 20 μg/ml LPS for 2 h and the gene expression changes of *IL-1beta* were determined by quantitative real-time PCR (qRT-PCR) (see below).

2.8. Quantitative real-time PCR

Quantitative real-time PCR (qRT-PCR) was performed on an Applied Biosystems® 7500 Fast Real-Time PCR System (ThermoFisher Scientific) using a FastStart Universal SYBR Green Master (Rox) kit (Roche) according to the manufacturer's instructions. The primers for the detection of Japanese flounder P2Y₂, P2Y₆, P2Y₁₂, P2Y₁₄, *IL-1beta* and *beta-actin* genes are listed in Table 1. Gene expression levels were evaluated using the comparative $2^{-\Delta\Delta C_t}$ quantification method with *beta-actin* as an internal reference gene. Melting curve analysis and gel

electrophoresis were performed at the end of amplification. The PCR products were further sequenced to ensure the specificity of amplification.

2.9. Western blots analysis of UDP-glucose-induced ERK1/2 phosphorylation in the HKMs

Overnight-cultured Japanese flounder HKMs were incubated with UDP-glucose at different concentrations for the indicated time points. The effect of UDP-glucose treatment on ERK signaling in the HKMs was evaluated by Western blot analysis. The procedure for Western blot analysis was described previously [16]. Briefly, after treatment, cells were washed twice with cold TBS and lysed at 4 °C in a lysis buffer containing 50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 1% NP-40, 0.1% SDS, and 1 mM EDTA supplemented with a protease inhibitor cocktail (Roche). The cell lysates were then centrifuged at 13000 rpm for 15 min. The extracted supernatants were separated by electrophoresis through an SDS-polyacrylamide gel and subsequently transferred onto polyvinylidene fluoride membranes (Millipore). The membranes were incubated with rabbit monoclonal antibodies specific for phospho-p44/p42 MAPK (1:600) and total p44/p42 MAPK (1:1000) followed by incubation with goat anti-rabbit secondary antibody conjugated to horseradish peroxidase (1:3000, Pierce). Beta-actin (1:5000) was served as a loading control to show that equal amount of protein was applied. Target proteins were visualized using a SuperSignal West Pico detection kit (Pierce) on a Molecular Imager ChemiDoc™ XRS + Imaging System (Bio-Rad) according to the manufacturer's directions.

2.10. Statistical analysis

Data are presented as the mean ± standard deviation from triplicate experiments. Statistical analysis was performed with Student's t-test for the comparison between two groups. Multiple group comparison was conducted by one-way ANOVA followed by Duncan's analysis using SPSS software version 11.0. Statically differences were considered significant at $p < 0.05$.

3. Results and discussion

3.1. Sequence analysis of Japanese flounder *P2Y₁₄R* proteins

The GenBank database was researched and two putative Japanese flounder *P2Y₁₄R* cDNA sequences with accession numbers XM_020107896.1 and XM_020107895.1, respectively, were retrieved. Blast against the Japanese flounder genomic DNA sequence available in the NCBI database revealed that these two genes are located in different regions of the assembled Japanese flounder genomic scaffold, indicating that they are duplicated genes in *P. olivaceus* [19,20]. However, no significant sequence similarity was found between the two putative Japanese flounder *P2Y₁₄R* genes, and the latter expresses much lower than the former in the Japanese flounder HKMs (data not shown). Further sequence analysis revealed that the putative Japanese flounder *P2Y₁₄R* with accession number XM_020107895.1 does not harbor the conserved signature motif K-E-X-X-L for extracellular nucleotides binding in TM7 of all identified *P2Y₁₄* receptors. In addition, phylogenetic analysis revealed that it can not be clustered into either the clade of mammalian *P2Y₁₄Rs* or the clade of fish *P2Y₁₄Rs*. These data indicate that XM_020107895.1 is a non-functional receptor. Thus, XM_020107896.1 was served as a target in the current study and was amplified from the Japanese flounder HKMs.

Compared with the *P2Y₁₄R* reference sequence (accession No. XM_020107896.1) retrieved from the GenBank database, the cloned Japanese flounder *P2Y₁₄R* cDNA has 4 nucleotide changes. These differences resulted in 4 amino acid substitutions. Genomic structure analysis showed that the Japanese flounder *P2Y₁₄R* gene has two exons and one intron, and the 5'-UTR is comprised of the entire first

exon and the partial second exon (Fig. 1A). Sequence analysis of the Japanese flounder *P2Y₁₄R* revealed that it encoded a full-length open reading frame of 347 amino acids with a predicted molecular mass of 39 kDa and an isoelectric point of 9.71. Domain analysis revealed that the Japanese flounder *P2Y₁₄R* protein processes seven transmembrane domains (TMs) and an extracellular amino-termini and a cytoplasmic carboxyl-termini. In addition, the Japanese flounder *P2Y₁₄R* possess four potential *N*-linked glycosylation sites including ⁵Asn, ¹²Asn, ²⁰⁹Asn and ²⁵⁰Asn, respectively (Fig. 1B). The Japanese flounder *P2Y₁₄R* shares about 42% sequence identity and 65% sequence similarity with human being *P2Y₁₄* receptor. In addition, Japanese flounder *P2Y₁₄R* exhibits 24%, 22%, and 38% sequence identity with the known Japanese flounder *P2Y₂*, *P2Y₆* and *P2Y₁₂* receptors [15,23], respectively, indicating their different structures for ligand binding. Multiple sequence alignment of Japanese flounder *P2Y₁₄R* with its counterparts from the selected vertebrate species revealed that the TM6 and TM7 are highly conserved among the *P2Y₁₄R* members from different species (Fig. 1C). Specially, the H-X-X-R/K motif that is crucial for agonist activity in the TM6 shared by all cloned *P2Y* receptors, and the featured K-E-X-X-L motif for extracellular nucleotides binding in TM7 of mammalian *P2Y₁₄* receptors [24] are found in the fish *P2Y₁₄* receptors, suggesting that a conserved mode of agonist binding remains in *P2Y₁₄* receptors during evolution. Phylogenetic analysis further showed that the *P2Y₁₄* receptors are well separated into the mammalian and fish clusters and the Japanese flounder *P2Y₁₄R* shows a closer relationship with *Cynoglossus semilaevis* *P2Y₁₄R* (Fig. 2).

3.2. Differential expression of *P2Y* receptors in the Japanese flounder HKMs

In human beings, the prominent expression of *P2Y₁₄R* was found in immune cells including neutrophils, lymphocytes, and megakaryocytic cells [25]. Using *P2Y₁₄R* knockout mice, it was demonstrated that *P2Y₁₄R* plays a key role in recruitment of macrophages [26]. GPCRs are usually co-expressed in mammalian macrophages [27]. Our previous studies showed that multiple *P2Y* receptor subtypes are expressed in the Japanese flounder HKMs [15,23]. We therefore compared the gene expression level of *P2Y₁₄R* with three known *P2Y* receptor subtypes including *P2Y₂*, *P2Y₆* and *P2Y₁₂* in the Japanese flounder HKMs. As shown in Fig. 3A, *P2Y₁₄* together with *P2Y₂*, *P2Y₆* and *P2Y₁₂* receptors are co-expressed in the HKMs. Considering that several *P2X* receptors also express in the Japanese flounder HKMs [28], the presence of multiple *P2* receptors indicates that diverse and complicated purinergic immune signaling pathways may exist in the Japanese flounder HKMs. However, the expression level of ATP/UTP-activated *P2Y₂R* and ADP-activated *P2Y₁₂R* is much higher than that of other *P2Y* receptors in the HKMs. Interestingly, compared with *P2Y₁₄Rs*, the UDP-activated *P2Y₆R* expresses much lower in the HKMs. As *P2Y₁₄R* also could be activated by UDP, the relative high expression level of *P2Y₁₄R* suggests that *P2Y₁₄R* may play a primary role in UDP-activated immune signaling in the Japanese flounder HKMs.

3.3. Constitutive expression of *P2Y₁₄R* in Japanese flounder tissues

The relative gene expression level of *P2Y₁₄R* in Japanese flounder tissues was examined by qRT-PCR. As shown in Fig. 3B, *P2Y₁₄R* is present in all examined Japanese flounder tissues including blood, heart, head kidney, intestine, liver, muscle, spleen, skin and trunk kidney. This is in general agreement with the constitutive tissue expression properties of other *P2* receptors in the Japanese flounder [15,23,28–30]. Similarly, *P2Y₁₄R* is also broadly expressed in several human tissues, including the placenta, adipose tissue, stomach, intestine, spleen, lung and brain [5,31], and mouse tissues such as brain, heart, kidney, spleen and thymus [32]. Compared with the UDP-activated Japanese flounder *P2Y₆* receptor that is dominantly expressed in liver [15], however, the most abundant expression of *P2Y₁₄R* was

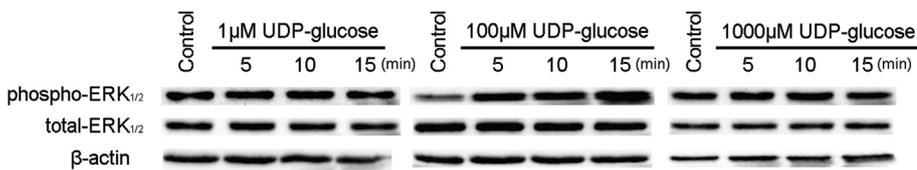


Fig. 6. UDP-glucose promotes ERK1/2 activation in the Japanese flounder HKMs. The Japanese flounder HKMs were incubated with 1, 100 or 1000 μ M UDP-glucose for the indicated durations. The untreated cells served as controls. Western blot analysis using anti-phospho-ERK1/2 revealed that ERK1/2 protein phosphorylation increased only after 100 μ M UDP-glucose treatment while total ERK1/2 phosphorylation did not change. Beta-actin served as a loading control to show equal amount of proteins was loaded. Results shown are representative of three individual experiments.

observed in Japanese flounder intestine. In addition, the lowest expression of Japanese flounder *P2Y₆R* is in spleen while the least expression of *P2Y₁₄R* is in Japanese flounder heart. These observations revealed that the Japanese flounder *P2Y₆R* and *P2Y₁₄R* receptors have different tissue distribution preference even though both of them can be activated by UDP. The preferred tissue expression of *P2Y₆R* and *P2Y₁₄R* receptors also indicate that they may contribute differently in the UDP-mediated purinergic signaling in a given Japanese flounder tissue.

3.4. Inflammatory stimulation-regulated *P2Y₁₄R* expression in the Japanese flounder HKMs

To examine the response of *P2Y₁₄R* to inflammatory stimulation, the Japanese flounder HKMs were stimulated with canonic inflammatory stimuli LPS and poly (I:C) to mimic different pathogen infections. As shown in Fig. 4, *P2Y₁₄R* expression was significantly induced (greater than 6-fold than untreated controls) upon both LPS and poly (I:C) challenges in the HKMs. The highly inducible expression of *P2Y₁₄R* in the HKMs suggests that *P2Y₁₄R* may play an important role in responses to inflammatory challenges in the Japanese flounder. Similar to our observation, *P2Y₁₄R* was also markedly upregulated after immunological challenge with LPS in rat [25]. In addition, it has been demonstrated that *P2Y₁₄R* plays an important role in protecting mice from vesicular stomatitis virus infection [1]. Notably, the Japanese flounder *P2Y₁₄R* was upregulated as early as 4 h after poly (I:C) stimulation and was maximally induced (approximate 10-fold than control) 12 h after treatment, indicating that *P2Y₁₄R* may perform an essential role in response to viral infection in fish.

3.5. *P2Y₁₄R* modulates PAMP-induced inflammatory response in the HKMs

It has been demonstrated that *P2Y₁₄R* is a key cell surface signaling protein in mammalian innate immune responses [33]. To explore the potential role of *P2Y₁₄R* in Japanese flounder innate immunity, we treated the HKMs with canonical inflammatory molecule LPS to induce inflammatory responses and examined the consequence of inflammatory stimulation-induced multifunctional pro-inflammatory cytokine *IL-1beta* gene expression when *P2Y₁₄R* receptor activity was activated by the potent and selective agonist MRS 2905 [34] or inhibited by its selective and potent antagonist PPTN [33]. As expected, LPS stimulation significantly promotes *IL-1beta* expression in the HKMs. However, the LPS-induced *IL-1beta* expression was attenuated when *P2Y₁₄R* receptor was activated by its potent agonist MRS 2905 (Fig. 5 A). In contrast, the LPS-induced *IL-1beta* expression was significantly augmented when *P2Y₁₄R* was inhibited with the high affinity and selective *P2Y₁₄R* receptor antagonist PPTN (Fig. 5 B). These observations suggest that *P2Y₁₄R* may negatively regulate the PAMP-induced immune responses in fish.

To support this hypothesis, we down-regulated the endogenous expression of *P2Y₁₄R* by small interfere RNA in the HKMs. For this purpose, a set of siRNA that targets on the different regions of *P2Y₁₄R* was designed and one optimized siRNA that could significantly down-regulate the endogenous expression level of *P2Y₁₄R* in the HKMs was obtained (Fig. 5C). In consistent with the results obtained by pharmacologic experiments, the enhanced gene expression of inflammatory stimuli-induced *IL-1beta* was also observed in the *P2Y₁₄R* down-

regulated HKMs that were silenced by the optimized *P2Y₁₄R* siRNA (Fig. 5D). The above complementary experiments demonstrated that in addition to the UDP-activated *P2Y₆R* receptor, the UDP/UDP-glucose-activated *P2Y₁₄R* receptor could represent an additional molecule for “fine-tuning” PAMP-induced inflammatory responses in fish.

3.6. Activation of ERK signaling by UDP-glucose in the Japanese flounder HKMs

Mitogen-activated protein (MAP) kinase signaling pathways are often stimulated by activation of Gi-coupled receptors [7]. *P2Y₁₄R* is known to couple to heterotrimeric G proteins of the $G_{\text{ai/o}}$ family [7]. Although *P2Y₁₄R* could be activated by UDP, it is the only subtype known to be uniquely and potently activated by UDP-glucose [35], an endogenous damage-associated molecular pattern molecule (DAMP) released by injured cells [36,37]. We therefore examined the phosphorylation status of ERK1/2 protein following *P2Y₁₄R* activation in the HKMs. As shown in Fig. 6, ERK1/2 protein was quickly phosphorylated as early as 5 min following 100 μ M UDP-glucose treatment in the HKMs; associated with the extended stimulation process, ERK1/2 protein phosphorylation was increased. In addition, the UDP-glucose-activated ERK1/2 phosphorylation shows a concentration-dependent manner as ERK1/2 phosphorylation did not changed at lower (1 μ M) or higher (1 mM) concentration of UDP-glucose stimulation. These findings indicate that the Japanese flounder *P2Y₁₄R* is functional and that activation of this receptor by UDP-glucose results in the activation of ERK signaling in the fish macrophages.

In conclusion, we characterized an inducible UDP-glucose-activated *P2Y₁₄R* that is involved in regulation of fish innate immunity.

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