



Full length article

The physiological performance and immune responses of juvenile Amur sturgeon (*Acipenser schrenckii*) to stocking density and hypoxia stress



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ABSTRACT

Stocking density and hypoxia are considered priority issues in aquaculture research. In this study, two experiments were carried out in order to investigate the effects of chronic stress (stocking density) and acute stress (hypoxia) on the immune physiology responses (hematology, serum cortisol, glucose, total protein and the mRNA expression of *CYP 1A*) of juvenile Amur sturgeon (*Acipenser schrenckii*). In the chronic stress study, three triplicate groups of Amur sturgeon (42.0 ± 2.3 g) were reared in nine square concrete ponds ($4.4 \times 4.4 \times 0.45$ m³) at three stocking densities (3.7, 6.9 and 9.0 kg/m³) for 50 days. In the acute stress study, three triplicate groups: normal group (7 mg/l), hypoxia group 1 (5 mg/l) and hypoxia group 2 (3 mg/l) were used in nine 100 L indoor tanks. Sampling was performed at the end of the stocking density experiment (50 days) and at 0, 0.5, 1.5, 3 and 6 h after hypoxia stress. The results showed that increased stocking density reduced the morphological indexes (hepatosomatic index, spleen-somatic index and kidney-somatic index), while total protein and hemoglobin increased significantly in the stressed group. In response to hypoxia, the levels of cortisol, glucose and hematological parameters elevated significantly after this stress. As for spleen-somatic index, there was a decline after hypoxia though H1 group returned to the normal level at 3 h and 6 h after hypoxia stress. Additionally, in order to better understand the immune response of Amur sturgeon to chronic and acute stressors, we cloned the complete coding sequence of Amur sturgeon *CYP 1A* for the first time and investigated its tissue-specific expression and stress-induced expression. *CYP 1A* mRNA in liver showed over expressions both in crowding condition and in hypoxia stress. The same trend was also found in spleen and kidney which may provide evidence that *CYP 1A* could serve as a good indicator of immune response in Amur sturgeon. In addition, the result suggested a typical immune response both in high stocking density and hypoxia stress. But the chronically stressed fish might have an adaptation capability to survive under a stable crowding condition without a change in some immune parameters (cortisol, glucose, WBCs and RBCs).

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1. Introduction

Sturgeons are notable because they are chondr-ganoid scale fish, with some characters between chondrichthyes and osteichthyes [1] and all living representatives of sturgeons are listed in CITES (Convention on International Trade in Endangered Species of Wild Fauna and Flora) [2,3]. At present, sturgeons have been raised in many countries for its considerable value in economy and ecology [4,5]. Amur sturgeon, *Acipenser schrenckii*, distributed throughout the Amur River (Heilongjiang River in Chinese) basin

and in the Ussuri and Sungari River, has becoming one of the popular cultured species in China and accounting for 50% of the total sturgeon production in China [6]. Li reported the effect of stocking density on serum concentrations of thyroid hormones on this species [7]. Yang studied the growth performances of juvenile Amur sturgeon in different stocking density [8]. But little is known about the effect of acute and chronic stressors on the immune response of this species.

Stocking density and low dissolved oxygen are two major stressors in aquaculture. Stocking density is considered one of the most important variables in intensive aquaculture because it directly influences physiology, welfare and behavior of farmed fish [9–13]. Many former studies revealed that high density may impair the welfare of some fish species [11,14,15]. In contrast, null effects of

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high densities upon production were reported in wedge sole (*Dicologlossa cuneata*) and winter flounder (*Pseudopleuronectes americanus*) [16,17]. The pattern of these responses appears to be species specific. Respiration, whether by terrestrial or aquatic animals requires oxygen. For terrestrial animals oxygen in the environment is rarely limiting. But in the aquatic environment, oxygen is one relevant factor to consider. The ecological and physiological effects of hypoxia have been studied extensively in fishes [18,19]. In addition, low oxygen (in the present paper defined as hypoxia) has been shown to induce stress responses in fish [20–22]. These two adverse environmental factors might disturb the balance and harmony between fish and the environment, causing stress response in fish [23].

Spleen and kidney are major lymphoid organs of fishes [24,25]. The spleen functions as major secondary immune organ, as found in mammalian species, with abundant IgM⁺ mature B cells [26–28]. It also plays a major role in the clearance of blood-borne antigens and immune complexes [29,30]. The spleno-somatic index (SSI) of fish is widely used as a simple measurable immune parameter with a potential role in immune response [31]. The entire kidney (including anterior kidney, mesonephric kidney and posterior kidney) is also a vital immune organ in fish. The head kidney/anterior kidney has the highest concentration of developing B lymphoid cells [26,28,32] and assumes hemopoietic functions [33,34]. In contrast, posterior kidney possesses both renal and immune function [27,28,35].

When subjected to a stressor, fishes employ a host of physiological adjustments to overcome the challenge [36]. One of the primary responses is mediated by the hypothalamus–pituitary–interrenal (HPI) axis, and is characterized by increased circulating levels of cortisol [37]. In fish, an increase in plasma cortisol has been widely employed as a quantitative measure of stress [38–40]. The changes of serum total protein and glucose are the secondary response to stress environment. Serum total protein content reflects the nutritional and metabolic status of fish, and indirectly reflects the level of non-specific immunity [41]. Serum glucose is also considered reliable markers of stress in animals such as brown trout, *Salmo trutta* and rainbow trout, *Oncorhynchus mykiss* [38,39].

The changes in levels of fish blood parameters will give an insight of fish's health status [42]. White blood cells in fish are considered to have immune functional role to play. Ellis found that, white blood cell count can be used to detect certain diseases and injury in fish body, as rearing environment can affect a number of circulating leukocytes in fish [43]. Rafatnezhad found that hemoglobin and red blood cell count may be influenced by stocking density [44].

The cytochromes P450 constitute a multigene family of enzymes involved in the oxidation of many endogenous and xenobiotics substrates [45]. Member of the cytochrome P450 gene family 1 (*CYP 1A*) is a useful biomarker in assessing contamination of the aquatic environment [46,47]. *CYP 1A* catalyze the activation of numerous hydrocarbon carcinogens and are induced by polynuclear and planar halogenated aromatic hydrocarbons and various natural compounds [48]. *CYP 1A* genes in non-mammalian taxa may be particularly important in evaluating the ecological or physiological pressures [49]. Gornati observed an increasing mRNA expression of *CYP 1A* in liver confirming that *CYP 1A* is an unspecific biomarker of stress response [50].

Due to the importance of stocking densities and hypoxia in commercial fish production, it is crucial to establish the physiological responses and the molecular mechanisms under these stressors in order to warrant an optimal welfare of Amur sturgeon. In the present study we cloned and characterized the complete coding sequence of Amur sturgeon *CYP 1A* gene for the first time. In addition, in order to establish the potential biological action of

Amur sturgeon *CYP 1A*, the tissue-specific *CYP 1A* expression and the expression of *CYP 1A* in different tissues including spleen, kidney and liver in fish with different stress were detected. To better understand the immune response to acute and chronic stress we also determined the hematological indexes, serum cortisol and some serum biochemical parameters (glucose and total protein) of Amur sturgeon.

2. Methods and materials

2.1. Fish maintenance

The experiment was taken place in a commercial farm in Shandong province of China. Prior to the start of the experiment, fish were initially acclimated to experimental conditions in a square cement pool (10 × 10 × 1 m³) for two weeks. During both the adaptation and experimental period, pelleted feed (Ningbo Tech-Bank, containing 42% of crude protein) was provided three times (8:00, 16:00, 23:00) daily at a feeding rate of 2% fish body weight per day.

2.2. Treatments and protocols

2.2.1. Chronic stress

After the adaptation period, fish (42.0 ± 2.3 g) were randomly distributed into three stocking densities (LSD = 3.7 kg/m³, MSD = 6.9 kg/m³ and HSD = 9.0 kg/m³, respectively). The experiment was conducted in 9 square concrete ponds (4.4 × 4.4 × 0.45 m³) for a period of 50 days. At the end of the experimental period, 36 fish (4 from each tank) were captured, quickly anesthetized with tricaine methane sulfonate (MS-222) at a concentration of 200 mg/l, weighed and sampled within 20 min.

2.2.2. Acute stress

Nine 100 L indoor tanks were used in this experiment. There were three experimental groups (three replicate tanks in each group): normal group (N, 6 mg/l), hypoxia 1 group (H1, 3 mg/l) and hypoxia 2 group (H2, 1 mg/l). Nitrogen gas bubbling was used to quickly reduce the DO concentrations. Fish were euthanized, weighed (wet weight, liver weight, kidney weight and spleen weight) and tissue sampled prior to hypoxia stress (baseline levels in both groups) and at 0.5, 1, 3 and 6 h post-stress.

2.3. Blood and tissue sampling

Blood samples were taken gently from the caudal vein by 1–ml plastic syringe. Two different aliquots of blood were used for different analyses. The first aliquot was transferred to a plastic tube coated with EDTA-K₂ as anticoagulant and was used for hematological indexes determination. A second aliquot was transferred to a plastic tube without EDTA-K₂, clot at 4 °C, centrifuged at 3000 g for 10 min, and then stored at –20 °C for subsequent analysis. Tissues were immediately frozen with liquid nitrogen and stored at –80 °C until mRNA analysis could be completed.

Biometric measurements including hepatosomatic index (HSI) = liver weight (g)/body weight (g) × 100, spleen-somatic index (SSI) = fresh spleen weight (g)/body weight (g) × 100 and kidney-somatic index (KSI) = kidney weight (g)/body weight (g) × 100 were also recorded from each fish.

2.4. Radioimmunoassay

Serum levels of cortisol in the serum of Amur sturgeon were measured using Iodine [¹²⁵I] Radioimmunoassay Kits (Tianjin Nine Tripods Medical & Bioengineering Co., Ltd., Sino-US joint-venture

enterprise). The binding rate is highly specific with an extremely low cross reactivity to other naturally occurring steroids, which was less than 0.014% to most circulating steroids. The coefficients of intra-assay and inter-assay variation were 7.3% and 11.6%, respectively. Any samples with coefficient of variation higher than 10% were not included in the analyses. The assay sensitivity reached to 0.21 µg/dl by the kit protocol.

2.5. Biochemical and hematological assays

Serum biochemical parameters including glucose and total protein were determined with an automated biochemistry analyzer (Mindray BS180, China) according to Rehulka's method [51]. Hematological indexes including the numbers of white blood cells (WBCs), red blood cells (RBCs), neutrophilic granulocytes (NEUT) and hemoglobin values were measured using an automatic blood analyzer (Mindray, B1800, China).

2.6. Isolation and PCR amplification of CYP 1A cDNA

Total RNA was extracted from Amur sturgeon liver using RNAiso reagent (Takara, Japan) following the manufacturer's protocols. Then first-strand cDNA was synthesized respectively with 1 µg total RNA from each sample using random primers and Reverse Transcriptase M-MLV (Takara, Japan) in a 20 µl reaction. In order to isolate the CYP 1A cDNA from the Amur sturgeon, a 498 bp cDNA fragment of CYP 1A was first obtained from PCR amplification using specific primers (CYP 1AF1 and P450R1, Table 1). PCR reaction was carried out using PCR program as follows: 5 min denaturing step at 94 °C, 40 cycles of 30 s at 94 °C, 30 s at 64 °C and 40 s at 72 °C, followed by additional 10 min at 72 °C for extension. PCR product was then electrophoresed on a 1.5% agarose gel. The target cDNA fragments were purified using TIANGEN midi Purification Kit (TIAGEN, China) then ligated into pGEM-T Vector (Promega, USA) and transformed into DH5α competent cells. Finally, recombinant plasmids were isolated and sequenced using the ABI3730XL sequencer to give at least 3-fold coverage.

3' and 5' ends RACE were performed using SMART™ RACE cDNA Amplification Kit (Clontech, USA). Gene specific primers (CYP 1A 5' and CYP 1A 3' listed in Table 1) were designed based on Amur sturgeon CYP 1A cDNA fragment. RACE was carried out according to the manufacturer's protocol. All DNAs subsequent to PCRs were gel purified and cloned, then sequenced as described above. BLASTN searches were used to verify gene identity.

2.7. Phylogenetic analysis and sequence analysis

To examine the similarity of Amur sturgeon CYP 1A to those of other species, eighteen CYP 1A amino acid sequences (Table 2) from various animals were retrieved from National Center for Biotechnology Information. Multi-sequences with deduced amino acid

Table 1
Primer sequences for cloning and mRNA expression analysis.

Primer	Nucleotide sequence(5' to 3')	Application
CYP 1AF1	CTGAGGGACGAGTTTGGGCG	CYP 1A amplification
CYP 1AR1	GGTGAAGGGGAGGAAGGAGG	CYP 1A amplification
CYP 1A 5'	GAAGGAGCGGTAGTGGTCGG	5' RACE
CYP 1A 3'	ATTGTGACCGACCACCTACCGCT	3' RACE
CYP 1A ex1	CAAGCAAGGGGAGGACTATG	RT-PCR and Q-PCR
CYP 1A ex2	CGGTGGAGAAAAGCGAAG	RT-PCR and Q-PCR
18SF	GCCACACGAGATGGAGCA	Q-PCR
18SR	CCTGTCCGGCAGAGGTTAG	Q-PCR

Table 2

Amino acid identities between CYP 1A in Amur sturgeon and CYP 1A in fish and other vertebrates.

Number	Species	Abbreviations	Accession number	Identities (%)
1	<i>Acipenser ruthenus</i>	CYP 1A 1	AEN19340.2	95
2	<i>Anguilla japonica</i>	CYP 1A	BAA88241.1	70
3	<i>Salmo salar</i>	CYP 1A	AAM00254.1	69
4	<i>Danio rerio</i>	CYP 1A 1	AAL54873.2	67
5	<i>Oncorhynchus mykiss</i>	CYP 1A 1	AAB40626.1	67
6	<i>Gobiocypris rarus</i>	CYP 1A	ABV01348.1	67
7	<i>Dicentrarchus labrax</i>	CYP 1A	CAB63650.1	67
8	<i>Paralichthys olivaceus</i>	CYP 1A	ABO38813.1	66
9	<i>Pseudopleuronectes americanus</i>	CYP 1A	ADV36120.1	66
10	<i>Takifugu obscurus</i>	CYP 1A	ABV24057.1	66
11	<i>Pelteobagrus fulvidraco</i>	CYP 1A	ABU62828.1	65
12	<i>Oreochromis niloticus</i>	CYP 1A	ACJ60906.2	64
13	<i>Balaenoptera acutorostrata</i>	CYP 1A	BAE46562.1	60
14	<i>Xenopus laevis</i>	CYP 1A	BAA37079.1	59
15	<i>Mus musculus</i>	CYP 1A 1	CAA68277.1	58
16	<i>Gallus gallus</i>	CYP 1A 5	NP_990477.1	58
17	<i>Corvus macrorhynchos</i>	CYP 1A 5	BAE75841.1	57
18	<i>Homo sapiens</i>	CYP 1A 1	NP_000490.1	55

sequences for CYP 1A of Amur sturgeon were aligned using Clustal X (version 1.83) [52]. MEGA 4.0 software package [53] was used to construct and analyze phylogenetic tree using the Neighbor-Joining method with 1000 bootstrap trials [54]. Protein sequence analysis was performed with the ExpASY Molecular Biology Server (<http://www.expasy.org/>) scanning all known PROSITE motifs. Percent identities of proteins motifs between Amur sturgeon and other species were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/clustalw2/index.html>).

2.8. PCR analysis

The expression profiles of CYP 1A mRNA in different tissues were studied through semi quantitative RT-PCR with specific-primers (CYP 1A ex1 and CYP 1A ex2, Table 1), including heart, liver, spleen, kidney, brain, pituitary, gill, stomach, intestine, fin and muscle from four fish. The expression levels of spleen, kidney and liver CYP 1A in fish exposed to acute and chronic stress were carried out on a LightCycler® 480 System (Roche, Switzerland) through quantitative PCR using SYBR Green (Takara, Japan) with specific-primers (CYP 1A ex1 and CYP 1A ex2, Table 1). PCR amplification of 18S ribosomal RNA was applied as internal control to normalize the concentration of templates for Q-PCR. PCR reaction was optimized as follows: 30 s denaturing step at 94 °C, 35 cycles (for CYP 1A) or 25 cycles (for 18S ribosomal RNA) of 30 s at 94 °C, 30 s at 58 °C (for CYP 1A) or 60 °C (for 18S ribosomal RNA) and 30 s at 72 °C. In order to confirm the amplification of a single product per primer set, a melt curve analysis was performed at the end of the PCR run. After the program finished, the Ct values of the CYP 1A and 18S genes were obtained from each sample. The relative expression level of gene could be calculated by 2^{-ΔΔCT} method [55].

2.9. Statistical analyses

A one-way ANOVA with Duncan's test was used to test the effects of the treatments (SPSS 13.0). All data are presented as means ± standard error of mean (SEM), and a probability level of less than 0.05 was considered significant.

1 GGCACTCCGTTGATCGGAAGATTTGAGCAAGTATCAGAATGCGGAAGATAGACTTGCAAAGTCGATTACAGTATACACTGTGTGACT
 91 CGACTGATCGCCCCCAAGGCTGGGATCAAACCCAGCGGCCAAGCAAATGACAAGTTCTTTAAACAGATATTTGAGCTCTGAGATCT
 181 GTGTGGGGCATTAAAAACCTTTGAAAAGGAAAAACA**ATGG**CGCTCATATCTCTACCCATCCTTGGGCCATCTTGGTGCTGAGAGCC
 1 M A L I S L P I L G P I L V S E S
 271 TGGTGCCTGGCAACGTTGTGCGCAGTGTACCTGTGTCTGCGGCTTGTGCGCACAGAGATCCAGCGGGTCTGCGCAGACCCCCGGC
 18 L V A V A T L C A V Y L L L R V L R T E I P A G L R R P P G
 361 CCACACCCTACCCCTGATCGGAAACGTGCCGAGTTAGGAGGCAACCCACCTCAGCTGACCAAGATGATCCAACGTTACGGAGACG
 48 P T P L P L I G N V P E L G G N P H L S L T K M I Q R Y G D
 451 TCACGCAGATCCAGATTGGCACCCGCCGTGGTGGTGTGAGCGGGAGGAGCGGTGCGCCAGGCCCTCATCAAGCAAGGGGAGGACT
 78 V T Q I Q I G T R P V V V L S G R E T V R Q A L I K Q G E D
 541 ATGCTGGACGGCTGACCTCAACAGTATACAGTTCATATCTAACGGCAAGCGCATGACCTCCATAATGTCCATGCCGATGTGCAGCGAG
 108 Y A G R P D L N S I Q F I S N G K R M T F H N V H A D V Q R
 631 CCCGGCAGACCTAGCCAAATGCCCTTCGCTCTTCTCCACCGTTGAAAGCCCAACCAGCAGCTACTCCTCGTGCTTGAGGAGACA
 138 A R R R P S P N A L R S F S T V E S P T S S Y S C V L E E H
 721 TCTCCCTGGAGCGGAATACTTGGTGAAGCGCTCTCTGGGATCATGGAAGCTGATGGGAGTTTGGACCCCTTCCGCCACATTTGGTCT
 168 I S L E A E Y L V K R L S G I M E A D G S F D P F R H I V V
 811 CGGTGGCAATGCATCTGTCCATGTGCTTCGGCCGGCTACAGCCATGACGACCAGGAGCTGGTAAATCTGGTGAACCTGAGGGACG
 198 S V A N V I C A M C F G R R Y S H D D Q E L V N L V N L R D
 901 AGTTTGGCGTGATCGCCAGCGCAATCCTGCCACTTCATCCCTGCTCTCCGCATCCTGCCAACCCCAACATGCGCGCTTCATCG
 228 E F G R V I A S G N P A D F I P A L R I L P N R N M R A F I
 991 GCATCAGCAACAGATTCAACACCTTCATCCAGAATTTGACCGACCACTACCGCTCCTTCGACAAGAGCAACATTCGTGACATCACTG
 258 G I S N R F N T F I Q N I V T D H Y R S F D K S N I R D I T
 1081 ACTCACTGATTGAGCATTGCCAGGACAAGAAGTGGACGAGAACCCAACATTCAGATCTCTGACGAGAAAATGTGTCCATTGTTAATG
 288 D S L I E H C Q D K K V D E N A N I Q I **S D E K I V S I V N**
 1171 ACCTTTTGGAGCTGGCTTTGATACAATCAGCACTGCTCTCTCTGGTGTAAATGTACTTGGTGTCCACCCCTGATATCCAGAAGA
 318 **D L F G A G F D T** I S T A L S W C L M Y L V S H P D I Q K K
 1261 TCCACCAGGATTAGATGAGCATGTGGGCGAGGAGCGTAGCCAGGCTCTCTGATAGACCAGCCTGCCGATGTAGAAGCCTTCATCC
 348 I H Q V L D E H V G R E R S P R L S D R P S L P Y V E A F I
 1351 TGGAGACCTTCGCCACTCCTCCTCCTCCCTCACCATCCCTCACTGCACGACGAAGGACAGGGCTCTCAATGGCTTTACATCCCA
 378 L E T F R H S S F L P F T I P H C T T K D T A L N G F Y I P
 1441 AGGACACGTGTATCTTGTGAACAGTGGCAGGTCAACACGACCCGAGTCTGTGAAGGATCCCTCCACCTTCTCTCCAGAGCGCTTCC
 408 K D T C I F V N Q W Q V N H D P S L W K D P S T F S P E R F
 1531 TGAATGCAGAGGCACTGGTATCAACAAGGCTGAGTCGAGAAGGTATGCTGTTCGGGTGGGGAAGCGGCTGCATTGGCGAGTCTA
 438 L N A E G T G I N K A E S E K V M L **F G L G K R R C I G E** S
 1621 TCGGCCGAGTGAAGTCTTCTCTTCTCTGGTGTGCTCCTGCAGCGGCTGGGTTTCGACGCTACCTGGCCAGAAGCTGGACCTCACCC
 468 I G R S E V F L F L A V L L Q R L G F R S L P G Q K L D L T
 1711 CCGAGTACGACTCACAATGAAGCACAAGCGATGCCAATCAGCGCCTCCTGCTCGGCCGGGGAGCGGATGTTTCTCAGCTGA
 498 P E Y G L T M K H K R C Q L S A S L L G R G S G C F L S

Fig. 1. The cDNA and deduced amino acid sequence of the *CYP 1A* gene in Amur sturgeon. The initiation codon and termination codon were indicated in bold, the putative heme binding region was boxed, a highly conserved sequence among fish *CYP1As*, 308-SDEKIVSIVNDFGAGFDT-326 was also boxed, the nucleotides and amino acids were numbered along the left margin.

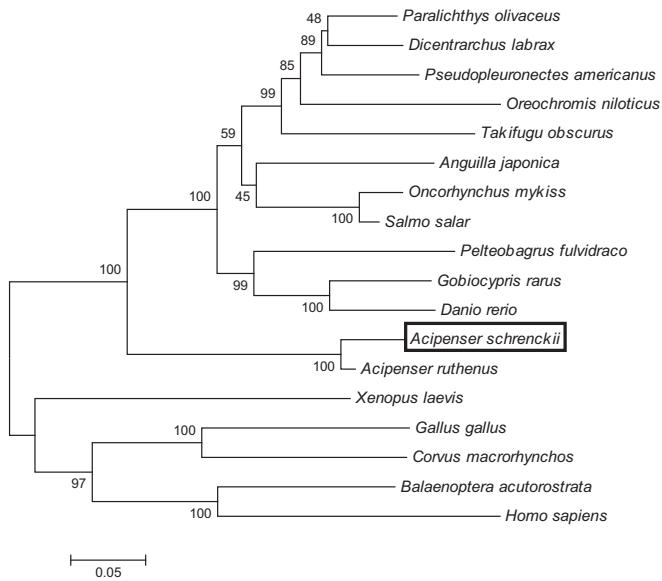


Fig. 3. Phylogenetic tree based on amino acid sequences for *CYP 1A* in vertebrates.

456, in a typical P450 signature sequence of FGLGKRRICG. The sturgeon gene also has a sequence 308-SDEKIVSIVNDLFGAGFD-326 that is very highly conserved among fish *CYP1As* (Fig. 2).

3.2. Homology analysis

Phylogenetic analysis, based on deduced amino acids, was applied to determine the evolutionary position of Amur sturgeon *CYP 1A* (Fig. 3). As expected, Amur sturgeon *CYP 1A* was placed in the fish clade, closest related to Sterlet (*Acipenser ruthenus*) *CYP 1A*. The relationships displayed in the phylogenetic tree were in agreement with the concept of traditional taxonomy, the sequence homology implicates that the *CYP 1A* are more similar to fish *CYP 1A* than the tetrapod *CYP 1A*. The results of ClustalW2, also showed that the deduced protein of *CYP 1A* in Amur sturgeon exhibited high identity with those of other fish. The comparison results of deduced amino acid sequences between Amur sturgeon *CYP 1A* and other similar *CYP 1A* was shown in Table 2. The amino acid sequences showed highest similarity (95%) to that in *A. ruthenus*. However, the homology was poorly conserved with terrestrial vertebrates: *Mus musculus* (58%), *Gallus gallus* (58%), *Corvus macrorhynchos* (55%) and *Homo sapiens* (55%).

3.3. Expression of *CYP 1A* in different tissues

The mRNA expression in different tissues was showed in Fig 4. *CYP 1A* mRNA was abundant in liver, and moderate in gill, kidney, heart and stomach. No *CYP 1A* mRNA was observed in adipose tissue, fin, muscle, pituitary, brain, intestines and spleen, but we could not exclude its presence. In addition, the levels of 18S rRNA were used as an internal control and were found in all tissues studied at a similar intensity.

3.4. Effects of stocking density on Amur sturgeon

Table 3 showed the morphological indexes data in different stocking densities. At the end of the experiment, SSI varied inversely with regard to stocking density ($P < 0.05$). Similarly, the maximum HSI and KBI (3.39 ± 0.12 and 0.54 ± 0.03 , respectively) were observed in LSD group ($P < 0.05$).

It is noticed that serum cortisol showed no significant difference among different stocking densities. Similarly, glucose was also not directly related to stocking density. However, TP in HSD group and MSD group were significantly higher than that in LSD group ($P < 0.05$) (Table 4).

Hematological indexes in different stocking densities including white blood cells, red blood cells and hemoglobin are showed in Table 5. The level of white blood cells as well as neutrophilic granulocytes appeared to be stable and there was no significant difference in different stocking densities. Red blood cells also showed no statistical difference among different stocking densities. However, hemoglobin revealed a significant increase in MSD group and HSD group.

At the end of the experiment, the liver *CYP 1A* mRNA expressions in HSD group and MSD group were significantly greater than that in LSD group ($P < 0.05$). Similar results were also found in spleen and kidney. But it's worth noting that crowding stress significantly induced *CYP 1A* mRNA expressions with spleen being more responsive (4.76–5.07 fold of control) than liver and kidney (Table 6).

3.5. Effects of hypoxia on Amur sturgeon

The morphological indexes data among different dissolved oxygen are compared in Fig. 5. Differences in spleno-somatic index were apparent. Spleno-somatic index in H1 and H2 group decreased significantly at 0.5 and 1.5 h after hypoxia stress. At 3 h and 6 h after hypoxia stress, the spleno-somatic index in H1 group returned to the normal group. However, spleno-somatic index in

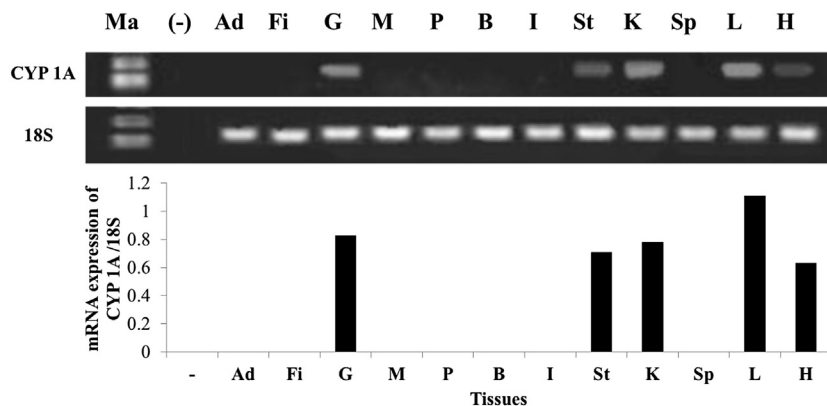


Fig. 4. RT-PCR expression analysis of *CYP 1A* in tissues of Amur sturgeon in normal condition. PCR amplification of 18S ribosomal RNA was used as an internal control for relative quantity of cDNA. Ad: adipose tissue; Fi: fin; G: gill; M: muscle; P: pituitary; B: brain; I: intestine; St: stomach; K: kidney; Sp: spleen; L: liver; H: heart; (-): mRNA not reversed transcribed; Ma: marker.

Table 3
Morphological indexes from Amur sturgeon reared in different stocking densities.

Parameter	LSD	MSD	HSD
SSI	0.27 ± 0.02b	0.21 ± 0.01a	0.20 ± 0.02a
KBI	0.54 ± 0.03b	0.43 ± 0.02a	0.45 ± 0.03a
HSI	3.39 ± 0.12b	2.54 ± 0.12a	2.46 ± 0.11a

Values are expressed as mean ± standard error of mean. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test). LSD: low stocking density, MSD: medium stocking density, HSD: high stocking density, SSI: spleen-somatic index, KBI: kidney-somatic index, HSI: hepatosomatic index.

H2 group was significantly decreased 3 h and 6 h after hypoxia stress. Kidney-somatic index showed no significant difference either in H1 group or H2 group. There were no significant changes in hepatosomatic index in relation to the hypoxia stress, except for the 3 h after hypoxia stress which resulted significantly higher in the H2 group, compared to normal group and H1 group.

The levels of serum cortisol were significant increased after hypoxia stress except those at 6 h after hypoxia in H2 group, which showed no significant difference with the normal group (Fig. 6a). A significant increase of serum glucose levels occurred at 0.5 h, 1.5 h and 3 h after hypoxia stress in the H1 group and at 0.5 h and 1.5 h in H2 group. However, there was an obviously decline at 6 h after hypoxia stress in H1 group and 3 h after hypoxia stress in H2 group. No glucose concentration was detected at 6 h after hypoxia stress (Fig. 6b). Serum total protein exhibited no significant alteration except the final sampling point (6 h after hypoxia stress) which resulted significant increase with the decline of the dissolved oxygen content (Fig. 6c).

It is imperative to state that as not enough blood was sampled at 6 h after the hypoxia stress (Group H1 and H2) due to the bad condition of the fish, we failed to detect the hematological indexes at 6 h after this stress. The responses of white blood cells in different dissolved oxygen are showed in Fig. 7a, with significant increases at 1.5 h and 3 h after hypoxia stress in H1 group ($P < 0.05$). Similarly, white blood cells in H2 group showed significant increase at 0.5 h and 1.5 h after hypoxia stress. However, there is no significant difference 3 h after hypoxia stress in H2 group. The alterations of red blood cells were similar to those in white blood cells (Fig. 7b). Hemoglobin was significantly elevated during the hypoxia stress both in H1 and H2 group compared to the hemoglobin in normal group (Fig. 7c). Hypoxia significantly increased the numbers of neutrophilic granulocytes both in H1 and H2 group (Fig. 7d).

Fig. 8 showed the *CYP 1A* mRNA expression in different dissolved oxygen groups. The levels of *CYP 1A* mRNA expression in liver indicated a remarkable increase after hypoxia stress. However, there was a significant decrease at 6 h after hypoxia stress ($P < 0.05$). To our surprise, *CYP 1A* mRNA levels in H1 group were higher than those in H2 group (significant at 0.5 h and 6 h after hypoxia stress) (Fig. 8c). The changes of *CYP 1A* mRNA expression in kidney were similar to those in liver (Fig. 8a and b) with an up-regulation at 0.5 h and a down-regulation at 6 h after hypoxia stress. Remarkably, the increasing of *CYP 1A* mRNA expression in

Table 4
Serum biochemical values (cortisol, glucose and total protein) in different stocking densities.

Parameter	LSD	MSD	HSD
Cortisol	0.29 ± 0.02	0.27 ± 0.04	0.26 ± 0.03
Glucose	1.32 ± 0.04	1.31 ± 0.19	1.31 ± 0.25
Total protein	15.48 ± 0.97a	25.85 ± 2.36b	23.03 ± 2.14b

Values are expressed as mean ± standard error of mean. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test) LSD: low stocking density, MSD: medium stocking density, HSD: high stocking density.

Table 5
Hematological indexes from Amur sturgeon reared in different stocking densities.

Parameter	LSD	MSD	HSD
WBCs	200.04 ± 10.63	198.73 ± 11.10	183.95 ± 14.50
NEUT	92.43 ± 5.32	90.04 ± 7.83	91.04 ± 7.66
RBCs	0.17 ± 0.02	0.20 ± 0.03	0.22 ± 0.04
HGB	59.36 ± 1.15a	67.70 ± 2.95b	68.06 ± 3.75b

Values are expressed as mean ± standard error of mean. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test). LSD: low stocking density, MSD: medium stocking density, HSD: high stocking density, WBCs: white blood cells, NEUT: neutrophilic granulocytes, RBCs: red blood cells, HGB: Hemoglobin.

spleen was more sensitive (~30 fold at 3 h) than in liver (~9 fold at 3 h) and kidney (~5 fold at 3 h).

4. Discussion

This study aimed to evaluate the effect of stocking density and hypoxia on the immuno-modulation in an endangered species, the Amur sturgeon. Barcellos found that acute and chronic stress lead to a decreased disease resistance in *Rhamdia quelen* Quoy and *Gaimard pimelodidae* [56]. Similar results were obtained by Salas-Leiton [57]. Fast reported the immune-related effects of Atlantic salmon (*Salmo salar*) subjected to short and long-term stress [22]. In addition, hypoxia has been shown to induce primary, secondary and tertiary stress responses in fish. Kvamme studied the effect of hypoxia on innate immune responses in Atlantic salmon [58]. But the appearance of immune parameters and defensive competence varies greatly between fish species, even between closely related species [59].

As found in mammalian species, the spleen as a secondary lymphatic and scavenging organ plays a vital role in hematopoiesis and antibody production processing [60]. In this study, spleno-somatic index decreased after hypoxia stress. The result showed a significant spleen contraction which might be related to hematopoiesis to improve oxygen carrying capacity in hypoxia condition. This hypothesis was further backed by rapid increases in red blood cells count observed in our study. Rapid increases in red blood cells count were also observed in hypoxia in juvenile Tambaqui (*Colosoma macropomum*) and silver trevally (*Pseudocaranx dentex*) [61,62]. Similarly, spleno-somatic index showed a decline with the increasing of the stocking density. Kidney is the main immuno-competent organ [63–65]. In addition, the kidney serves as an important immune–endocrine organ with key regulatory functions. Zwollo reported that head kidney has the highest concentration of developing B lymphoid cells [28]. In our research, stocking density negatively affected kidney somatic index. The result may suggest an immune response and/or physiological alteration exposed to this stressor. However, kidney somatic index showed no change in hypoxia condition.

Hepatosomatic index (HSI) has proved valuable as indicators of health status of fish cultured at different environment [66]. The

Table 6
CYP 1A mRNA expression in spleen, kidney and liver in different stocking densities.

Parameter	LSD	MSD	HSD
CYP 1A-S	1.03 ± 0.07a	4.76 ± 0.54a	5.07 ± 0.48a
CYP 1A-K	0.93 ± 0.11a	2.32 ± 0.35a	2.03 ± 0.31a
CYP 1A-L	1.07 ± 0.12a	1.78 ± 0.20b	1.93 ± 0.22b

Values are expressed as mean ± standard error of mean. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test) LSD: low stocking density, MSD: medium stocking density, HSD: high stocking density, CYP 1A-S: *CYP 1A* mRNA expression in spleen, CYP 1A-K: *CYP 1A* mRNA expression in kidney, CYP 1A-L: *CYP 1A* mRNA expression in liver.

result of our study revealed that HSI in LSD group was significant higher than those in MSD and HSD groups indicating a high welfare status. The reduction of HSI by high stocking density has also been reported by previous studies [67,68]. With regard to hypoxia, HSI showed no significant difference except that at 3 h after hypoxia in H2 group. But we could not give a reasonable explanation for this phenomenon. Future studies are needed to focus on this mechanism.

Cortisol is an important stress hormone secreted from the hypothalamus–pituitary–interrenal axis (HPI) when fish is subjected to stress situation. The increase of cortisol in serum can be seen as the sensitive signal of fish stress [69]. It has been reported that serum glucose level might be up-regulated with the increasing of the level of cortisol [38,39]. The reason may be that cortisol can promote gluconeogenesis and glycogenolysis to meet the increasing demand of energy from fish under stress [69,70]. In our

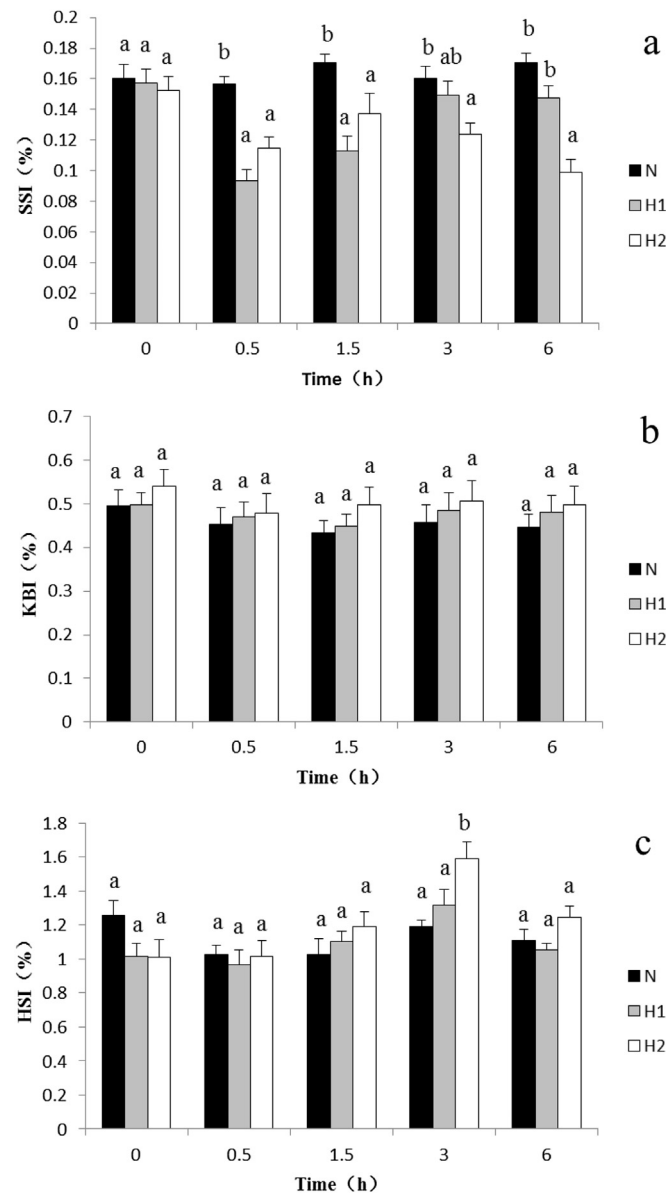


Fig. 5. Morphological indexes from Amur sturgeon exposed to different dissolved oxygen. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test). SSI: spleen-somatic index, KBI: kidney-somatic index, HSI: hepatosomatic index, N: normal group (6 mg/l), H1: hypoxia 1 group (3 mg/l), H2: hypoxia 2 group (1 mg/l).

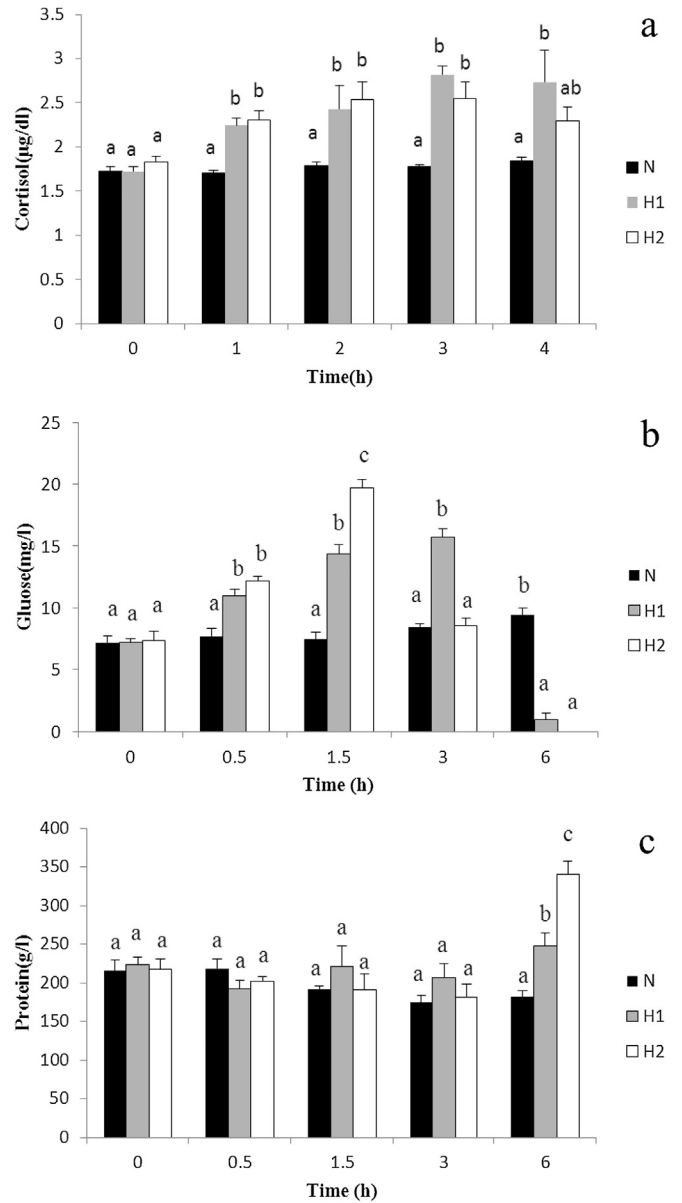


Fig. 6. Serum biochemical values (cortisol, glucose and total protein) from Amur sturgeon exposed to different dissolved oxygen. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test). N: normal group (6 mg/l), H1: hypoxia 1 group (3 mg/l), H2: hypoxia 2 group (1 mg/l).

research, there were significant increase of serum cortisol and glucose levels during the period of hypoxia stress similar to observations in Siberian sturgeon (*Acipenser baeri*) and spotted wolffish (*Anarhichas minor*) [71,72]. This may indicated a mobilization of these metabolites to overcome the hypoxia disturbance. However, our results showed no significant differences among different stocking densities. It is generally believed that serum total protein reflects the level of non-specific immunity [41]. In our study, fish under crowding and hypoxia stress (6 h after hypoxia stress) showed a significant increase in the levels of the serum total protein. It is speculated that fish may increase specific proteins such as lysozyme or complement to enhance the immunity level to cope with stress [41,73].

White blood cells involve in defending the body against both infectious disease and foreign materials, playing an important role in the immune system [74]. An increase trend was observed after

hypoxia stress in this study which might be associated with an enhanced immune response. Red blood cells in our study also significantly elevated after hypoxia stress. The increase in the number of red blood cells may raise blood oxygen capacity and improves oxygen delivery to the tissues. This response has also been described in many studies [75,76]. However, in our study,

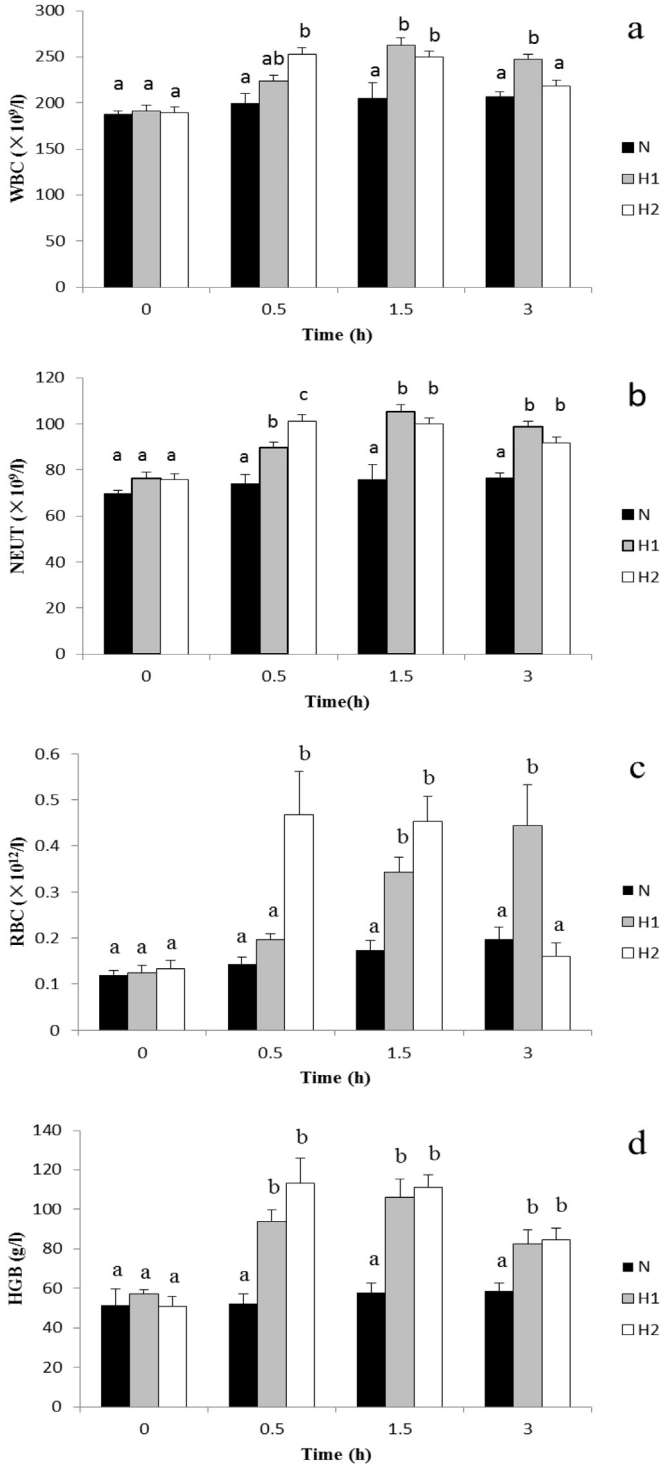


Fig. 7. Hematological indexes from Amur sturgeon in different dissolved oxygen. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test). WBCs: white blood cells, NEUT: neutrophilic granulocytes, RBCs: red blood cells, HGB: Hemoglobin, N: normal group (6 mg/l), H1: hypoxia 1 group (3 mg/l), H2: hypoxia 2 group (1 mg/l).

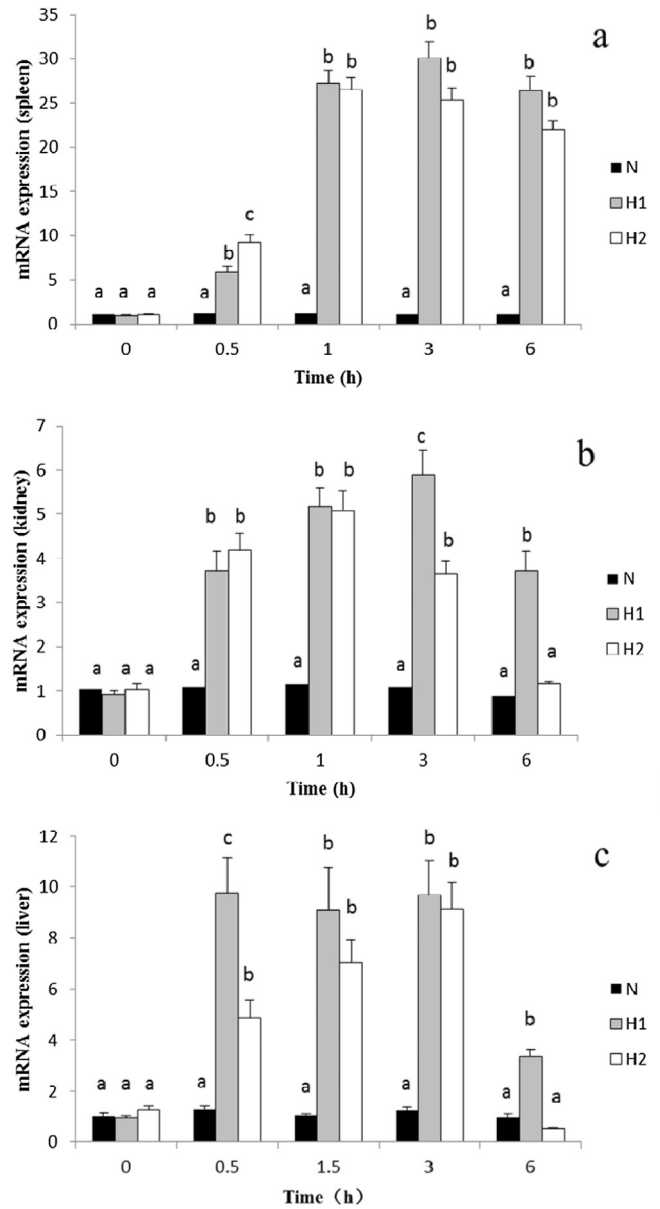


Fig. 8. *CYP 1A* mRNA expression of spleen (a), kidney (b) and liver (c) in different dissolved oxygen. Different letters indicate significant difference ($P < 0.05$, one-way ANOVA, followed by Duncan's test), N: normal group (6 mg/l), H1: hypoxia 1 group (3 mg/l), H2: hypoxia 2 group (1 mg/l).

neither white blood cells nor red blood cells showed significant alteration under different stocking densities. In our study, hemoglobin was significantly elevated during the hypoxia and crowding stress. Similarly, Qureshi reported that hemoglobin level in *Cyprinion watsoni* was significantly increased after hypoxia stress [77].

The cytochromes P450 gene superfamily consists of a large number of genes encoding P450 enzymes involved in the oxidation of many endogenous and xenobiotics substrates [44]. *CYP 1A* gene products catalyze the oxidation of environmental carcinogens and are therefore used as biomarker when assessing exposure to contaminants in environmental system [46,78]. In this study, we first cloned and characterized the complete CDS of *CYP 1A* in Amur sturgeon. Comparing the predicted amino acid sequence of *CYP 1A* with those of other species, we found all *CYP 1A* in fish shared higher identity, suggesting that *CYP 1A* was highly conservative during fish evolution.

Tissue distribution of *CYP 1A* mRNA was analyzed through semi quantitative RT-PCR. *CYP 1A* mRNA was strongly expressed in many tissues. The highest level of transcripts was found in liver. This result confirmed the expression pattern of *CYP 1A* reported in other fish species including zebrafish (*Danio rerio*), crucian carp (*Carrasius carassius*) and Fugu obscurus (*Takifugu obscurus*) [79–81]. The tissue-specific distribution of *CYP 1A* may indicate its physiological function for detoxification in fish.

In our study, we observed an increasing expression of *CYP 1A* in spleen, kidney and liver both in crowding environment and hypoxia stress suggesting that *CYP 1A* is an unspecific biomarker to the old species, Amur sturgeon. Gornati also observed an over expression of *CYP 1A* mRNA in crowding environment [50]. At the 100 µg/L BNF dose, hypoxia strongly increased *CYP 1A* expression in killifish embryos. However, hypoxia did not significantly influence *CYP 1A* expression in zebrafish embryos [82]. Rahman also reported a down-regulation of *CYP 1A* mRNA expression in Atlantic Croaker [83]. The differences seem to be related to fish species, fish size and the environment condition. It is worth noting that *CYP 1A* mRNA expression in hypoxia stress was significantly higher than that in crowding environment (in liver, 9 fold at 3 h after hypoxia stress and 1.78–1.93 fold in crowding stress, respectively). These results may suggest that the *CYP 1A* was more sensitive in acute stress (hypoxia).

In conclusion, the present study provides the first evidence that *CYP 1A* showed an up-regulation in some immune organs both in high stocking density and hypoxia stress which may provide an important implication that *CYP 1A* could serve as a good indicator of immune response in Amur Sturgeon. In addition, the integration of morphological indexes, hematological indexes, serum biochemical indexes and *CYP 1A* mRNA expression suggests a typical immune response both in high stocking density and hypoxia stress. However, the levels of some immune parameters (i.e. white blood cells, red blood cells and glucose) showed no significant changes in high stocking density. This may suggest that the chronically stressed fish might have an adaptation capability to survive under a stable crowding condition without a change in these immune parameters. To our knowledge, this is the first to study the immune response to acute and chronic stress in juvenile Amur sturgeon. It is imperative to conduct further studies on the influence of these stressors on other physiological aspect and provide a thorough understanding of the immune mechanisms of this species.

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