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研究报告

Cloning and tissue-specific expression analysis of hepcidin gene in koi (*Cyprinus carpio*)

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Abstract: [Objective] Our aim is to clone cDNA sequence of hepcidin gene (k-hepc) and find its expression pattern in koi (*Cyprinus carpio*). **[Methods]** In this study, the full-length cDNA sequence of hepcidin gene in koi was cloned by RT-PCR and RACE PCR and sequenced. The liver, spleen, kidney, intestine, brain, heart, muscle and gill were obtained 0, 4, 8, 12, 24 and 48 h after the koi were challenged with *Aeromonas veroii* and evaluated by real time PCR to find gene expression of k-hepc. **[Results]** The sequence of k-hepc cDNA (GenBank No. KC795559) is 755 bp in length, and ORF is 276 bp long. The deduced amino acid sequence of k-hepc gene consists of 91 amino acids including signal peptide, prodomain and mature peptide. The mature peptide contains 8 cysteines, and is able to form 4 disulfide bonds. The deduced amino acid sequence of k-hepc has 93% similarity to hepcidins of known common carp and 29%−93% similarity to hepcidins of other fish species. Expression of k-hepc is found in all the tissues tested by our lab. The relative expression levels in normal fish showed high basal values in liver and low values in gill. The expression of k-hepc mRNA was significantly increased in the liver and heart but not significantly induced in other tissues after bacterial-challenge. **[Conclusion]** The protein encoded by k-hepc is a member of hepcidin family. Expression of k-hepc is mainly affected by intrinsic regulation factors.

Keywords: Hepcidin, *Cyprinus carpio*, Cloning, Sequencing, Gene expression

锦鲤 Hepcidin 基因的克隆及其组织特异性表达分析

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摘 要:【目的】克隆锦鲤 Hepcidin 全长 cDNA 序列(k-hepc),并获得此基因在鱼体内的表达模

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式。【方法】利用 RT-PCR 和 RACE PCR 的方法，从锦鲤肝脏中克隆锦鲤 Hepcidin 的全长 cDNA，进行序列测定和分析；锦鲤经肌肉注射维氏气单胞菌 0、4、8、12、24 和 48 h 后，分别取其肝、脾、肾、肠、脑、心、肌肉和鳃组织，采用实时荧光定量 PCR 的方法，以 β-actin 为内参基因，检测 k-hepc 基因的表达量。【结果】锦鲤抗菌肽(GenBank 登录号 KC795559)全长 755 bp，编码序列 276 bp，编码 91 个氨基酸，包括信号肽、原肽和成熟肽，成熟肽 C 端含有 8 个半胱氨酸，可形成 4 个分子内二硫键。与已报道的普通鲤鱼 Hepcidin 氨基酸序列的一致性为 93%，与其他鱼类 Hepcidin 氨基酸序列的一致性为 29%−93%。在本研究所检测的正常锦鲤的组织中，k-hepc 均有表达，其中在肝组织中表达量最高，鳃组织中表达量最低。经维氏气单胞菌感染后，k-hepc 在肝和心组织中的表达量明显增加，在其余组织中变化不显著。【结论】k-hepc 编码的蛋白是 Hepcidin 家族的成员之一。锦鲤 Hepcidin 的表达主要受内在调节因素影响。

关键词：Hepcidin，锦鲤，克隆，序列分析，基因表达

1 Introduction

Hepcidin is an antimicrobial peptide (AMP) and iron regulatory molecule, and is of importance in host defense against microbial infection. To date, large numbers of hepcidin have been isolated from human blood ultrafiltrate and urine, other mammals and fish. Mature peptide of hepcidin was isolated firstly in fish from the hybrid striped bass in 2002[1]. In addition, peptide sequences of hepcidins or expressed sequence tags have been predicted in Perciformes fishes, including *Lateolabrax japonicus*[2], gilthead sea bream[3], medaka, rainbow trout[4], winter flounder[5], long-jawed mudsucker[6] and Altlantic salmon[7] and so on. Fish hepcidin cDNA and genomic DNA organization have been determined in many fish, including hybrid striped bass[1], winter flounder[5], Atlantic salmon[7], zebrafish[8], rainbow trout[9], olive flounder[10], Japanese flounder[11], red sea bream[12], Japan sea bass[2], sea bass[13], black porgy[14], gilthead sea bream[3]. The hepcidin peptides contain unique structure among antimicrobial peptides, sharing rich cysteines at conserved positions with a distinctive disulfide bridge structure[1,15]. Cysteine-rich antimicrobial peptides of the defensin family have been detected in the fat body of insects and the haemolymph of mollusks[16-19]. Besides, hepcidin takes part in iron metabolism and relates to disorders in iron homeostasis resulting in iron deficiency or overload[20-24].

Arguments against hepcidin being predominantly expressed in the liver have recently occurred in a few publications[7,11,14], either in mammalian or in fish hepcidin studies. In mammals, Kulaksiz et al. suggested that hepcidin was not liver-specific but might be expressed also in the kidney[25-26]. While in the red sea bream and catfish, hepcidin mRNA was widely expressed in multiple tissues[27,21], from which the conclusion was derived that in fish hepcidin might have a non liver-specific expression.

Koi (*Cyprinus carpio*) is a very important economic species of cultured fish in China. Little is known about the hepcidin and its immune regulating mechanism in koi. This study aimed to present and analyze of cDNA sequences of hepcidin (including the deduced amino acid sequence) in koi and evaluate its expression profiles in several tissues before and after pathogenic bacteria *Aeromonas veronii* challenge.

2 Materials and Methods

2.1 Fish maintenance

Healthy koi (60±2 g) were obtained from a koi farm in Beijing. Fish were acclimatized in laboratory for 7 days at 25.0±0.5 °C, dissolved oxygen of 6.5% and fed with fish feed once per day.

2.2 Medium

Luria-Bertani (LB) broth and LB Agar were prepared as the document[28-29].

2.3 Reagents and instuments

PureLink™ RNA Mini Kit, Life technologies USA; SMARTer™ RACE cDNA Amplication Kit, Clontech USA; Wizard® SV Gel and PCR Clean-Up System, Promega USA; pEASY-T5 cloning vector, TransGen China; PrimeScript RT reagent kit, SYBR Premix Ex*Taq*™ Ⅱ, TaKaRa. 7500 Real Time PCR System, AB Applied Biosystem; Agarose gel electrophoresis, Bio-Rad.

2.4 Cloning and sequencing of koi hepcidin cDNA

Livers were collected from koi, frozen immediately in liquid nitrogen individually, and stored

at −80 °C for use. Total RNA from the liver of koi was extracted using PureLink™ RNA Mini Kit, according to the manufacturers' instructions. The quality of total RNA was assessed by electrophoresis on 1% agarose gel. In order to amplify the hepcidin cDNA from koi, RT-PCR and rapid amplication of cDNA ends (RACE) were performed following the SMARTer™ RACE cDNA Amplication Kit manual. The RACE reactions were performed with primers (Table 1). The pair of primers was designed based on the EST fragments from the common carp cDNA library established in the centre for applied aquatic genomics, and was in the open reading frame (ORF) of carp hepcidin (c-hepc). RACE PCR reactions were performed as following: 5 cycles of denaturation at 94 °C for 30 s, annealing at 72 °C for 2 min; 5 cycles of denaturation at 94 °C for 30 s, annealing at 70 °C for 30 s, and extension at 72 °C for 2 min; 25 cycles of denaturation at 94 °C for 30 s, annealing at 68 °C for 30 s and extension at 72 °C for 2 min. Amplified products were analyzed on agarose gel electrophoresis and purified from gel with a Wizard® SV Gel and PCR Clean-Up System. The purified PCR product was cloned in the pEASY-T5 cloning vector. After sequenced, 5′- end and -3′ end sequences were assembled to a k-hepc cDNA contig.

2.5 Bioinformatic analysis

Translation of the cDNA was performed using DNAStar software. The amino acid sequence of koi hepcidin (k-hepc) was analyzed using the BLAST at the NCBI (http://www.ncbi.nlm.nih.gov/blast). The cleavage site for the signal peptide was predicted by the SignalP (http://www.cbs.dtu.dk/services/SignalP/)[30]. Charges of the deduced mature peptides of k-hepc were calculated by the ProtParam tool (http://cn.expasy.org/tools/protparam.html)[31]. Multiple-sequence alignment of the k-hepc with hepcidin from other animals was performed with the ClustalX[32]. Homology searches were performed using BLASTn and BLASTp by the National Center for Biotechnology Information (http://www.ncbi.nlm.nih. gov/). Deduced aminoacid sequences from 23 hepcidin gene sequences were used to construct a prepro hepcidin multiple alignment by ClustalX software. Besides, a Neighbor-Joining phylogenetic tree of 23 prepro hepcidin sequences with Poisson Correction model, pairwise deletion option and 10 000 replicates of bootstrap was built with MEGA 4.0.2 software.

2.6 *Aeromonas veronii* challenge of koi and RNA sampling

The challenge experiment for assessing induction of gene expression was designed to intramuscular infection with *Aeromonas veronii*, a pathogenic bacterium (CGMCC 7231) isolate for this fish species. Twenty fish were injected with approximately 2×10^5 CFU/mL, and the equal quantities of fish were injected with 0.7% sterile physiological saline solution (PSS) as the control. The two treatment groups were kept in seperate water cages after injection. The different tissues of three fish in each group were sampled at 0, 4, 8, 12, 24 and 48 h post-injection from the *A. veronii*-challenged and PSS mock-challenged fish. The tissues including the liver, spleen, kidney, intestine, brain, heart, muscle, and gill were separately collected from each individual fish, and frozen immediately in liquid nitrogen individually, and stored at −80 °C. Tissue samples were homogenized in PureLink™ RNA Mini Kit, and total RNA was extracted.

2.7 Analysis of hepcidin expression by RT-PCR and real time PCR

The RT-PCR reactions for hepcidin expression were carried out (37 °C for 15 min, 85 °C for 5 s, followed by 4 °C) using PrimeScript RT reagent kit. The relative quantity of k-hepc mRNA was evaluated using the comparative C_t (Cycle threshold) method with a 7500 Real Time PCR System and SYBR Premix Ex*Taq*™ Ⅱ. The primers specific for k-hepc gene and the endogenous gene control are listed in Table 1. The cycling profile was as follows: stage 1: 1 cycle of denaturation at 95 °C for 30 s, stage 2: 40 cycles of PCR reaction at 95 °C for 5 s and 60 °C for 34 s, stage 3: dissociation stage at 95 °C for 15 s, 60 °C for 1 min and 95 °C for 15 s. The validation experiment was performed using three diluted cDNA series from the control liver to verify that efficiencies of the k-hepc mRNA and β-actin gene were approximately equal in real time PCR. Expression of k-hepc gene was normalized to an endogenous reference β-actin and presented as ΔC_t values. Tissue-specific expression of k-hepc gene was investigated in three normal fish, including the liver, spleen, kidney, intestine, brain, heart, muscle and gill. The expression patterns of k-hepc gene at the time course of *A. veronii*-challenge were investigated in the liver, spleen, kidney, heart, intestine, brain and muscle, using 0 h normal fish liver RNA pool as calibrator samples. All data were obtained in comparison with the same calibrator.

Table 1 Primers used in this study
表 1 引物

Primer	Sequence (5′→3′)	Size (bp)
R-cg3	ACGTCAAAGCCATCTGTCCCTGTGC	25
F-cg3	CGTCATCACATGCGTCTGCTTCCTC	25
F-qc1	TCATCACATGCGTCTGCTTCC	21
R-qc1	AGGGGATTTGGATTTGTTTCTGTC	24
β-actinF	GCTGTCCCTGTATGCCTCTGGT	22
β-actinR	GGCGTAACCCTCGTAGATGGG	21

2.8 Statistical analysis

7500 software V2.0.6 automatically calculates the relative quantification (RQ) value. $RQ=2^{-\Delta\Delta C_t}$. All data were analyzed by one-way analysis of variance (ANOVA). In addition, two-way ANOVA was used to determine the interactions of injection treatment and time. Duncan's multiple range tests and critical range was used to test differences among individual means. Graphs were made by the box-whisker plot. Difference were regarded as significant when $P<0.05$.

3 Results

3.1 Determination of k-hepc complete coding sequence (CDS)

Koi hepcidin CDS was obtained from the two EST sequences assembly and the primers were in the ORF of the k-hepc. Out of expectation, there was only R-cg3 without F-cg3 in 5′-RACE product of mRNA, which showed that cDNA sequence of k-hepc was not consistent with that of carp hepcidin even in the ORF sequence (Figure 1). The sequence of k-hepc cDNA (GenBank accession No. KC795559) is 755 bp in length, including 5′-untranslated region (5′-UTR) of 112 bp, -3′ untranslated region (-3′UTR) of 367 bp, and ORF of the 276 bp. Compared with other reported cyprinid fish hepcidin, cDNA sequences of k-hepc is similar with that of c-hepc as high as 94%. The deduced amino acid sequence of k-hepc (GenBank No. AGO64769.1) is 91 amino acids in length and consists of three domains: signal peptide (24 residues), prodomain (42 residues) and mature peptide (25 residues) (Figure 2). According to the analysis by the SignalP, the signal peptide cleavage site of the deduced k-hepc was predicted between Ala 24 and Val 25 (Figure 2). The mature peptide region of k-hepc was predicted, with "RX(F/R)R" as characteristic sequence for propeptide convertases, consisting of 25 amino acid residues at the C terminus of ORF. The processed mature peptide of k-hepc is predicted by ProtParam to be positively charged at neutral pH, having a theoretical pI of 8.34. It is thus a cationic protein. The peptide k-hepc molecular weight is 2 892.5 Da.

3.2 Amino acid sequence alignment

The deduced amino acid sequence of k-hepc has 29%−93% similarity to hepcidins of other fish species and mammals, sharing eight cysteines at the identical conserved position (Figure 3). The alignment showed that all listed hepcidins (23 hepcidin or hepcidin-like sequences searched on GenBank), including fish (18 hepcidin sequences), mammalian (4 hepcidin sequences) and reptile (1 hepcidin sequence) hepcidins were most characterized by eight cysteine residues conserved at identical positions in the mature peptide region. The predicted signal peptide was highly conserved between k-hepc and three other fish hepcidins, such as common carp, *Puntius sarana* and *Danio rerio* hepcidins (Figure 3), while the other 14 species fish hepcidins were conserved with each other.There was lower similarity in the signal peptide

Figure 1 Comparison of ORF sequences of k-hepc and c-hepc
图 1 k-hepc 与 c-hepc 的 ORF 序列的比较
Note: ORF sequences of k-hepc and c-hepc was listed in upper line and lower line, separately.
注：k-hepc 与 c-hepc 的 ORF 序列分别在上行和下行列出.

sequence of hepcidin between fish and mammals (Figure 3). The signal peptide cleavage site of all deduced fish hepcidins was between Ala 24 and Val 25. However, the 25th amino acid in some hepcidins was substituted by other amino acids (Ala 24-Ile 25, or Ala 24-Ser 25, or Ala 24-Phe 25) as shown in Figure 3. The deduced amino acid sequence of k-hepc showed 93% homology with c-hepc when analyzed by GenBank BLASTp, the highest in comparison with other fish hepcidins (Figure 3). Both hepcidin sequences are fully identical in the signal peptide. The RX (K/R) R motif typical of propeptide convertases is identified among all the tested animals (Figure 3).

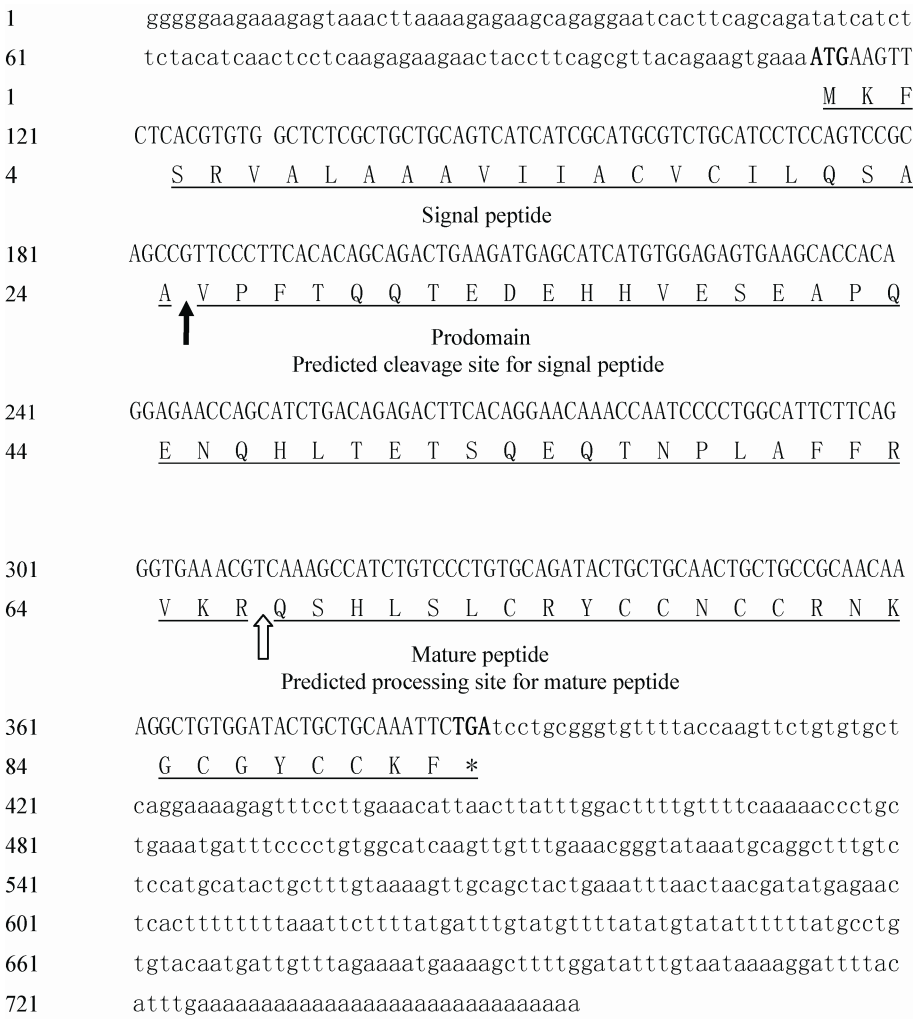

Figure 2 Full-length nucleotide sequence of k-hepc cDNA and deduced amino acid sequence of k-hepc

图 2 k-hepc 全长 cDNA 的核酸序列及其编码的氨基酸序列

Note: 5′-UTR and -3′UTR are in small letters, while ORF are in capital letters. Nucleotides and amino acids are numbered on the left of the sequences. Start codon (ATG) and stop codon (TGA) are both highlighted. Predicted cleavage site for signal peptide is marked by solid arrow, and predicted processing site for mature peptide is marked by hollow arrow.

注：5′-和-3′非翻译区用小写字母标出，而 ORF 用大写字母标出. 核苷酸和氨基酸在序列左侧计数. 起始密码子(ATG)和终止密码子(TGA)都加粗标出. 预测的信号肽位点用实心箭头标出，预测的加工位点用空心箭头标出.

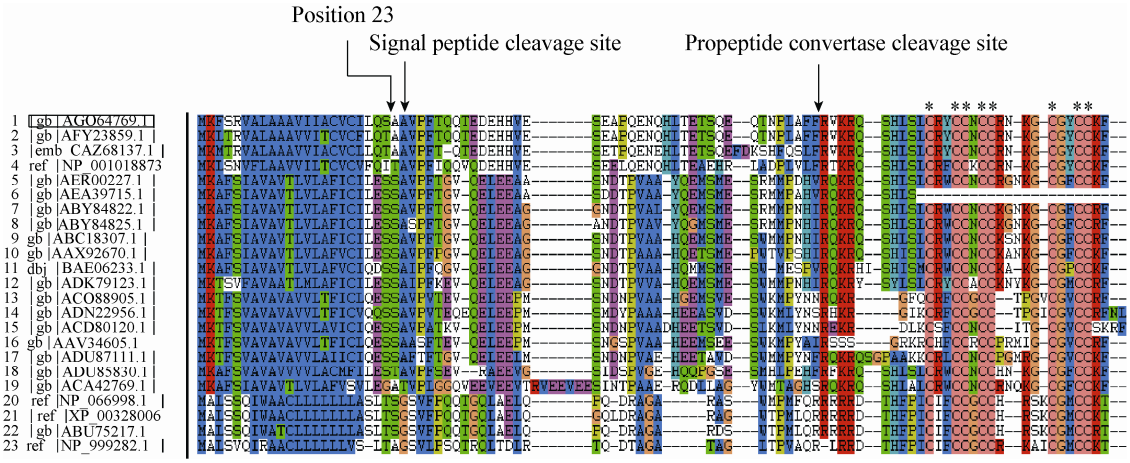

Figure 3 Complete amino acid sequence of koi hepcidin and alignment (ClustalX) with fish, mammalian and reptile hepcidin amino acid sequences

图 3 锦鲤抗菌肽的全长氨基酸序列及其与鱼、哺乳动物和爬行动物的抗菌肽氨基酸序列 ClustalX 比对

Note: Conserved cysteine residues of the mature peptide are marked with asterisks.

注：成熟肽中保守的半胱氨酸残基用星号标出.

3.3 Phylogenetic analysis of k-hepc

Phylogenetic analysis of the hepcidin-like family indicated that two clusters were present: mammalian and fish hepcidins (bootstrap value>95%). The deduced amino acid sequence from koi was in a branch position with that from common carp, zebra fish and *Puntius sarana* (Figure 4). The other branch of fish hepcidins were almost percomorpha and parapercomorpha peptides, which seems closer to each other than to cyprinid in hepcidin evolution.

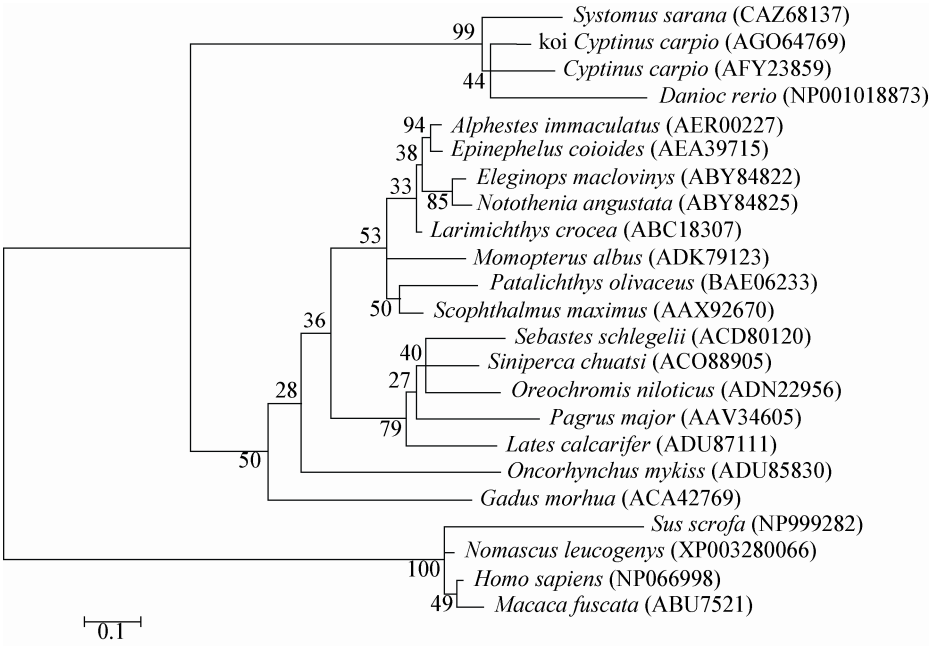

Figure 4 Phylogenetic tree of k-hepc and other vertebrates' hepcidin-like antimicrobial peptides

图 4 k-hepc 与其他脊椎动物 Hepcidin 样抗菌肽的发育树

Note: The evolutionary history is inferred by Neighbor-Joining with Poisson Correction model, built with MEGA 4.0.2 software. Numbers on the branch refer to the percentage of 10 000 bootstrap samples and the bar indicates the percentage of sequence divergence.

注：用 MEGA 4.0.2 中的 N-J 法泊松修正模型建树. 括号中的序号表示该基因在 GenBank 中的登录号，分支上的数字表示自举 10 000 次中的百分数，标尺表示序列差异的百分数.

3.4 Tissue expression profiles of k-hepc gene in normal koi

Expression of hepcidin was detected by means of RT-PCR and real-time PCR in all the assayed tissues, including the liver, spleen, kidney, intestine, brain, heart, muscle and gill (Figure 5). The highest amount of k-hepc mRNA transcripts was demonstrated in the liver and the lowest relative expression level was tested in the gill in normal fish (Figure 5).

3.5 Koi hepcidin gene expression in bacterial infected koi

The expression pattern of k-hepc was investigated in the liver, spleen, kidney, intestine, brain, heart and muscle at the time course of 0, 4, 8, 12, 24 and 48 h post injection with *A. veronii* and PSS, using real-time PCR. All the results are presented with β-actin as an endogenous control. A significant up-regulation of k-hepc expression was observed in liver at 4 h and in heart at 12 h after *A. veronii*-challenged (P<0.05) (Figure 6). The liver displayed the higher expression level over 20 fold compared with the control, and the heart displayed over 13 fold compared with the control. No significant up-regulation of k-hepc expression was observed in brain, intestine, kidney, spleen and muscle after *A. veronii*-challenged (Figure 6).

Two-way ANOVA (Table 2) showed that the expression of k-hepc mRNA in liver and heart were significantly affected by bacterial injection (P<0.05), and the expression of k-hepc in brain, intestine, kidney, spleen, and muscle were not obviously affected (P>0.05). Moreover, challenge time significantly affected the heart, brain, intestine, kidney (P<0.01) and muscle (P<0.05), but no obviously affected the liver and spleen (P>0.05). Interaction effects between injection time and bacteria in heart were significant (P<0.01), and not significant (P>0.05) in other tissues.

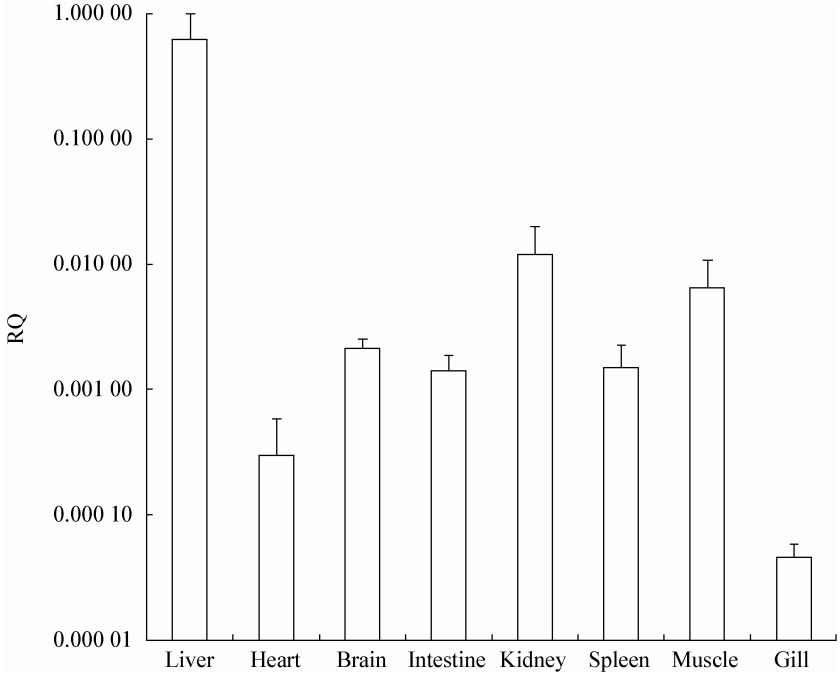

Figure 5 Distribution of k-hepc gene transcripts in various tissues in normal koi analyzed using real time PCR

图 5 实时定量 PCR 分析普通锦鲤的多种组织中 k-hepc 基因转录谱的分布

Note: β-actin gene was used as endogenous control. Among the tissues sample of fish (n=3) assayed, the relative quantification (RQ) value of liver located on the left side of the abscissa is the maximum and the RQ value of gill located on the right side of the abscissa is the minimum.

注：以 β-actin 为内参，在 3 条鱼的组织样本的实验中，位于横坐标左端的肝的 RQ 值最大，而位于横坐标右端的鳃的 RQ 值最小.

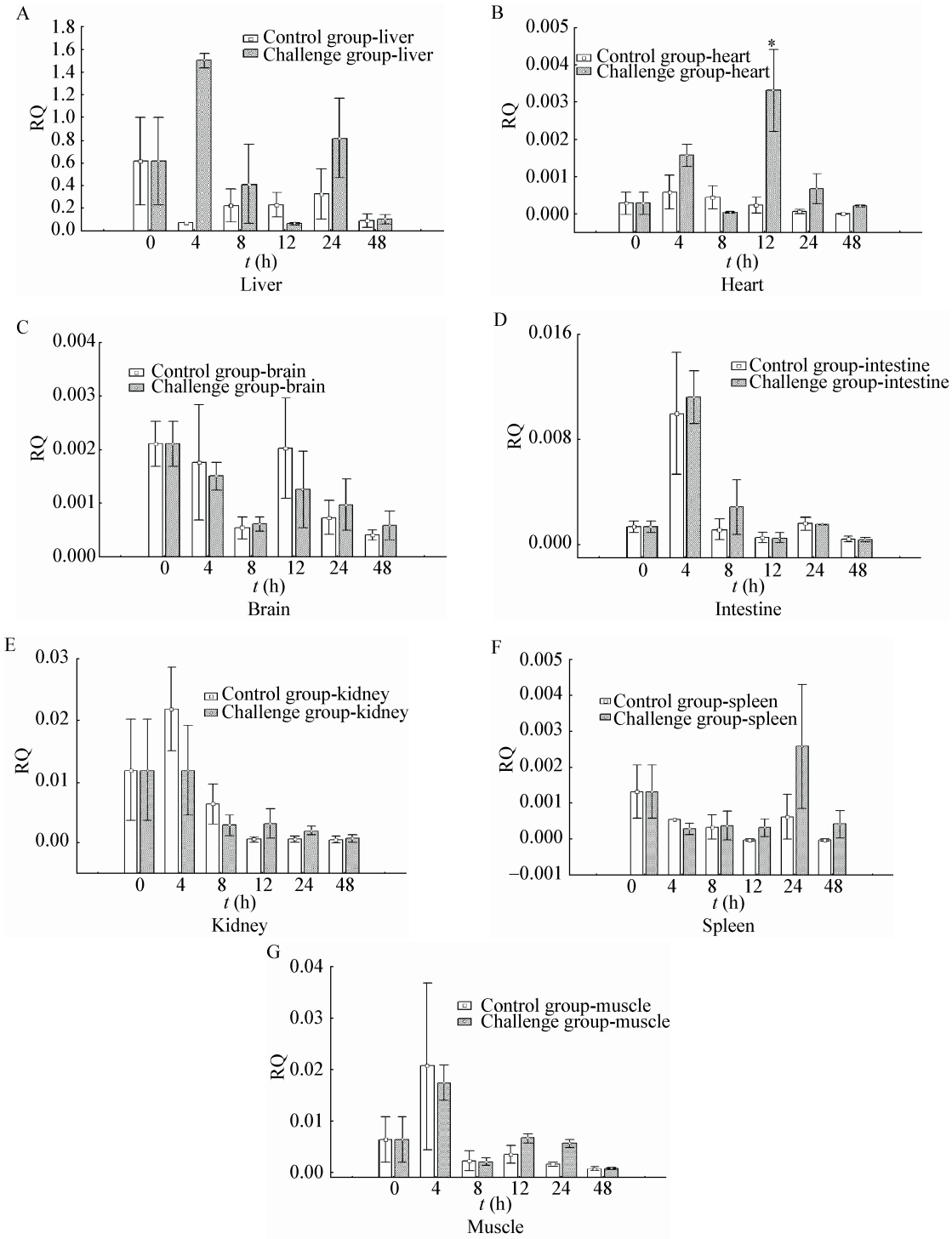

Figure 6 Quantitative analysis of the k-hepc gene expression in tissues of *A. veronii*-challenged koi was using real-time PCR

图 6 实时定量 PCR 对维氏气单胞菌感染锦鲤的组织中 k-hepc 基因表达进行定量分析

Note: All data were normalized relative to β-actin and represented by the means ± S.E. Results shown are the mean of three individual RNA sample of fish (n=3) with *A. veronii*-challenge. The gene expression of k-hepc in fish (n=3) inoculated with 0.7% sterile physiological saline solution (PSS) was shown in parallel.

注：所有经过 β-actin 均一化的数据用平均值±标准误标出. 结果显示的是 3 条经维氏气单胞菌感染鱼(n=3)的 RNA 样本平均值，注射生理盐水鱼的 k-hepc 基因表达作为对照组.

Table 2 The relative quantification (RQ) value analysis of different tissue of juvenile koi at the time course of 0, 4, 8, 12, 24 and 48 h post injected separately with *A. veronii* and physiological saline solution (PSS) with Two-way ANOVA analysis

表 2 不同时间采样和不同处理方式的锦鲤在不同组织中相对定量 RQ 值的双因子 ANOVA 分析

Item 项目	Time 时间	Injection Material 大小	Interaction 交互作用
RQ of the liver	NS	*	NS
RQ of the heart	**	**	**
RQ of the brain	**	NS	NS
RQ of the intestine	**	NS	NS
RQ of the kidney	**	NS	NS
RQ of the spleen	NS	NS	NS
RQ of the muscle	*	NS	NS
RQ of the liver	NS	*	NS

Note: *: Statistical significance (P<0.05, factorial ANOVA); **: Statistical significance (P<0.01, factorial ANOVA); NS: No statistical significance (P>0.05, factorial ANOVA).

注：*：有显著性差异(P<0.05)；**：有极其显著差异(P<0.01)；NS：无显著性差异(P>0.05).

4 Discussion

In this study, the deduced amino acid sequence of k-hepc from koi was comprised of 91 amino acids. Although several hepcidins from fish have been predicted or determined, there was little information about hepcidins of cypriniformes fish except common carp[33], *Puntius sarana* and zebrafish. So the nucleotide sequence of k-hepc might be different from those of other known cypriniformes hepcidins. The hepcidin-like peptide identified in this paper has the same subregions such as signal peptide, prodomain peptide and mature peptide with other hepcidins identified in fish and mammals, including human. The signal peptides were almost invariably 24 aa in length. Although Barnes et al[34] reported that the signal peptide regions were highly conserved among most of other fish, the cyprinid fish, such as koi, common carp, *Puntius sarana* and zebrafish, shared another type of signal peptide regions of hepcidin. They have not polar Ser but nonpolar Ala at amino acid position 23 (Figure 3). K-hepc contains a typical endoplasmic reticulum targeting signal sequence, a consensus cleavage site for prohormone convertases[35], a propeptide convertase site at amino acid position 66, and 8 cysteine residues as a characteristic of many hepcidins in fish and human[8,36]. These structures are highly conserved among all animals in Figure 3.

The expression of hepcidin genes was significantly induced in the liver and heart of koi after *Aeromonas veronii*-challenged, but not obviously changed in other tested tissues. Our observation on the hepcidin expression pattern in the liver completely matched reported for bacterially challenged white bass where up-regulation was most dramatic in liver[1]. Hilton et al[37] also summarized recently that hepcidin transcript levels in fish challenged with bacteria were increased primarily in the liver. Furthermore, the expression of hepcidin genes was significantly induced in the heart of koi after bacterial-challenged in this study. The Atlantic salmon hepcidin Sal1 and Sal2 transcripts were both up-regulated in multiple tissues with bacterial challenge[7]. These results indicate that the regulation of hepcidin-like transcripts from fish might be highly diverged in different species. K-hepc mRNA expression in the brain, intestine, kidney, spleen and muscle was not significantly changed during the period of 48 h after bacterial challenge with unchallenged normal fish, suggesting k-hepc was constitutively expressed in these tissues tested. In addition, according to the analysis of two-way ANOVA, we thought that the impact of time upon k-hepc mRNA expression in the brain, intestine, kidney and muscle was greater than the influence of bacteria. Apparently, different tissues of koi produce hepcidin-like peptides in a constitutive or inducible manner.

In conclusion, we have presented the sequences of hepcidin from koi. The k-hepc is close to the other three cyprinid fish hepcidins, with cysteine conformation and propeptide convertase cleavage sites. Hepcidin transcripts are widely distributed in various tissues of koi. Furthermore, the study describes the

expression pattern of hepcidin-like gene of koi and their patterns of expression level at different conditions and in different tissues, showing k-hepc might be not induced by bacteria-challenge but innate regulation with time.

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征 稿 简 则

1 刊物简介与栏目设置

《微生物学通报》是由中国科学院微生物研究所和中国微生物学会主办的，以微生物学应用基础研究及技术创新与应用为主的综合性学术期刊。刊登内容包括：工业微生物学、海洋微生物学、环境微生物学、基础微生物学、农业微生物学、食品微生物学、兽医微生物学、药物微生物学、医学微生物学、微生物蛋白质组学、微生物功能基因组、微生物工程与药物等领域的最新研究成果，产业化新技术和新进展，以及微生物学教学研究改革等。设置的栏目有：研究报告、专论与综述、生物实验室、高校教改纵横、专栏等。

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3 写作要求

来稿要求论点明确，数据可靠，简明通顺，重点突出。

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