Coenzyme Q10 mitigates high-fat-diet-induced hepatic steatosis in spotted bass (*Lateolabrax maculatus*) through modulating mitochondrial function

Xiaojiang Mao[1], Xueshan Li[1], Ling Wang[1], Kai Song[1], Chunxiao Zhang[1], Bei Huang[1], Kangle Lu[1] *, Samad Rahimnejad[2]

[1]State Key Laboratory of Mariculture Breeding; Fisheries College, Jimei University, Xiamen, 361021, China

[2]Faculty of Fisheries and Protection of Waters, University of South Bohemia in České Budějovice, South Bohemian Research Centre of Aquaculture and Biodiversity of Hydrocenoses, Vodňany 389 25, Czech Republic

***Corresponding author:** Fisheries College, Jimei University, Xiamen, 361021, People's Republic of China; Tel: 86-0592-6182723; E-mail address: lukangle@jmu.edu.cn (Kangle Lu).

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List of abbreviations:

AST: aspartate aminotransferase

ALT: alanine aminotransferase

ATGL: Adipose triglyceride lipase

ATP: Adenosine triphosphate

CPT-I: Carnitine palmitoyltransferase I

COQ10 : Coenzyme Q10

CS: Citrate synthase

FAS: Fatty acid synthetase

FI: Feed intake

HFD: high-fat diet

HSL: Hormone sensitive lipase

NAFLD: nonalcoholic fatty liver disease

NFD: normal fat diet

PER: Protein efficiency ratio

SDH: Succinate dehydrogenase

T-CHO: total cholesterol

TAG: Triacylglycerol

WG: Weight gain

Abstract

This study elucidated the impacts of coenzyme Q10 (COQ10) supplementation in a high-fat diet on growth, lipid metabolism, and mitochondrial function in spotted seabass (*Lateolabrax maculatus*). Totally five diets were formulated: a diet with normal fat content (11% lipid, NFD), a high-fat diet (17% lipid, HFD), and three additional diets by supplementing 5, 20 or 80 mg/kg of COQ10 to the HFD. After an 8-week culture period, samples were collected and analyzed. The results demonstrated that COQ10 inclusion prevented the HFD-induced deterioration of growth performance and feed utilization. COQ10 alleviated the deposition of saturated fatty acids following HFD intake and promoted the assimilation of n-3 and n-6 polyunsaturated fatty acids. Moreover, COQ10 administration inhibited the surge in serum transaminase activity and reduced hepatic lipid content following HFD ingestion, which was consistent with the results of oil red O staining. In addition, HFD feeding led to reduced hepatic citrate synthase and succinate dehydrogenase activities, and decreased ATP content. Notably, COQ10 administration improved these indices, and up-regulated the expression of mitochondrial biogenesis-related genes (*pgc-1α, pgc-1β, nrf-1, tfam*) and autophagy-related genes (*pink1, mul1, atg5*). In summary, supplementing 20-80 mg/kg of COQ10 in the HFD promoted growth performance, alleviated hepatic fat accumulation, and enhanced liver mitochondrial function in spotted seabass.

Keywords: Spotted seabass; High-fat feed; Coenzyme Q10; Liver health; Mitochondrial function

Introduction

In the context of rising cost of feed raw materials, optimizing strategies to minimize feed expenses has become an urgent priority. Among the macronutrients in aquafeeds, protein is recognized as the most crucial and costly component. High protein levels not only increase production costs but also contribute to environmental pollution through nitrogenous waste [1]. Lipids, being energy-dense macronutrients, are efficiently metabolized by most fish species. As a result, high-fat diets (HFDs) have gained popularity in modern aquaculture due to their lower cost, reducing nitrogenous emissions, and protein-sparing effects [1–3]. However, long-term use of HFDs often leads to liver steatosis and triggers various physiological stresses, including oxidative stress, inflammatory responses, apoptosis, and metabolic dysfunction [4,5]. These conditions can compromise immune function [6], reduce resistance to pathogens, increase mortality rates, and impair growth performance [7]. Liver dysfunction, in particular, can disrupt lipid metabolism, posing serious risks to fish health [8]. Consequently, functional additives are often employed in practical aquaculture to mitigate the detrimental effects associated with prolonged consumption of HFDs.

Mitochondria play a pivotal role in cellular energy metabolism, and alterations in their structure and functionality are closely linked to the onset of metabolic disorders such as obesity and type 2 diabetes [9,10]. The liver, being one of the most mitochondria-rich organs, relies heavily on mitochondrial homeostasis to regulate lipid metabolism [11]. Under conditions of overnutrition, particularly excessive fat intake, mitochondria become highly susceptible to metabolic stress [12], which can lead to abnormal lipid accumulation [13]. Research in fish models has demonstrated that fatty liver disease is often associated with mitochondrial dysfunction [14–16]. Therefore, safeguarding mitochondrial integrity may represent a viable strategy for mitigating the development of nutrition-induced hepatic steatosis in fish.

Coenzyme Q10 (COQ10) is a lipid-soluble quinone compound found ubiquitously in most eukaryotic cells. It plays a critical role in scavenging free radicals and facilitating energy metabolism [17–20]. In mammals, COQ10 has been shown to alleviate nonalcoholic fatty liver disease (NAFLD) and atherosclerosis by enhancing mitochondrial function [21–24]. Similarly, research on European eels (*Anguilla anguilla*), Pacific white shrimp (*Litopenaeus*

vannamei), rainbow trout (*Oncorhynchus mykiss*), and European seabass (*Dicentrarchus labrax*) revealed that COQ10 can significantly promote growth, regulate lipid metabolism, and improve both antioxidant capacity and immune function [25–28]. These findings underscore the vast potential of COQ10 for applications in aquaculture.

Spotted seabass, the second most cultured marine fish in China [29], is often subjected to HFDs during breeding to promote rapid growth and yield. However, this long-term feeding approach can easily lead to lipid metabolism disorders, resulting in fatty liver, which severely compromises the health and quality of the fish and causes substantial economic losses for the aquaculture industry. Accordingly, developing strategies to mitigate nutritional fatty liver in spotted seabass is of significant economic importance. While COQ10 shows potential in modulating hepatic fat deposition in fish, its precise mechanisms of action remain unclear. Therefore, this study was designed to evaluate the effects of supplementing different doses of COQ10 in a HFD on growth, lipid metabolism, and mitochondrial function in spotted seabass.

2. Materials and methods

2.1. Feed preparation

Fish meal, poultry by-product meal, soybean meal, and wheat gluten meal were used as the main protein sources, and fish oil, soybean oil, and lecithin were used as the main lipid sources. A diet containing 45% protein, and 11% fat was prepared and used as the normal fat diet (NFD), and a HFD was prepared with 17% fat. Three additional diets were produced by supplementing the HFD with 5, 20 or 80 mg/kg of COQ10 (HFD+COQ10-5, HFD+COQ10-20 and HFD+COQ10-80 diets, respectively). The raw materials were thoroughly mixed using a sequential expansion mixing technique. COQ10 was precisely weighed in a dark environment and immediately mixed with fish oil, soybean oil, and lecithin through a gradient mixing process. The prepared mixture was subsequently incorporated into the pre-homogenized dry feed ingredients [30]. After 15 minutes of mixing, 30% water was added to the mixture. The dough was pelleted using a twin-screw extruder with a 2 mm diameter. To avoid degradation of COQ10, the pellets were dried in a dark, dry environment [31], and then stored at -20°C until used. The formulation and proximate composition of the experimental diets are presented in Table 1, and their fatty acid composition is shown in Table 2.

2.2. Fish and experimental design

During the feeding period, all the procedures were conducted in accordance with the Committee on the Ethics of Animal Experiments of Jimei University, China (protocol code 2011-58, approved on 20 December 2011). The feeding trial was carried out at the experimental facility of the School of Fisheries of Jimei University (Xiamen, China). Spotted seabass juveniles were purchased from a commercial hatchery in Zhangzhou (Fujian province, China). The feeding trial was conducted in a recirculating aquaculture system (RAS). Prior to the start of the trial, the fish were temporarily housed in a 1000-L tank and fed a commercial diet for two weeks. Then, 300 healthy and uniform fish (12.00 ± 0.1g) were randomly assigned to 15 tanks (200-L capacity each) connected to the RAS, with 20 fish per tank. According to the principle of experimental randomness, the 15 tanks were randomly divided into 5 groups, with 3 replicates per group [29]. During the experiment, water temperature was maintained at 27.0 ± 0.5°C, dissolved oxygen at 6.0 ± 1.0 mg/L, and pH at 7.4 ± 0.2. Following stocking and acclimatization, experimental diets were fed to spotted seabass twice daily (08: 00 and 16:00 h) for 8 weeks, each feeding lasting approximately 1 h until the fish reached apparent satiation.

2.3. Sampling

At the conclusion of the feeding trial, all fish were subjected to a 24-h fasting before being individually weighed. Subsequently, 10 fish per tank were randomly selected and anesthetized with 100 mg/L of MS-222. Blood samples were drawn from the caudal vein using non-heparinized syringes and centrifuged at 3500 rpm for 10 min to separate the serum, which was then aliquoted and stored at -80℃ for later analyses. Following blood collection, the same 10 fish were promptly dissected to obtain their visceral mass, which was weighed. The liver and abdominal fat were individually excised, weighed, and recorded. Liver tissues from these 10 fish were flash-frozen in liquid nitrogen and transferred to a -80°C freezer for molecular analyses. Additionally, liver samples from two additional fish per tank were sectioned into 5 mm^3 fragments and fixed in 4% paraformaldehyde for histological examination.

2.4. Proximate and fatty acid compositions analyses

The proximate composition of whole-body, muscle, and diet samples was analyzed following standardized protocols established by the American Association of Official Analytical Chemists (AOAC) [32]. Moisture content was determined by oven-drying at 105°C to a constant weight, crude fat content by Soxhlet extraction method using ether as extraction solvent, and ash content by the combustion method, where samples were incinerated in a muffle furnace at 550°C for 8 h. Crude protein content was determined using an 828 Series Hydrocarbon/Nitrogen analyzer (LECO, St. Joseph, Michigan, USA).

Fatty acids in the diets and whole-body samples were extracted using the hydrolysis method outlined in GB5009.168-2016, the "National Food Safety Standard for the Determination of Fatty Acids in Food". Briefly, the freeze-dried samples (1 g) were placed into a 10-mL volumetric flask, followed by the sequential addition of 2.5 mL each of petroleum ether and benzene. After thorough mixing and standing for 2 h, 0.5 mL of 2 mol/L potassium hydroxide methanol solution was added, and the sample was allowed to stand for an additional 30 minutes. A saturated sodium chloride solution was added until it reached 1 cm from the top of the flask, and the sample was left to stand until the supernatant became clear. The supernatant was then filtered through a 0.22-μm organic membrane and analyzed using a Shimadzu gas chromatograph (GC2010). Fatty acids were quantified, and the relative percentage content of each fatty acid was calculated using the area normalization method.

2.5. Serum and liver biochemical parameters

Serum aspartate aminotransferase (A010-2-1, AST) and alanine aminotransferase (C009-2-1, ALT) activities were quantified using commercial assay kits (Nanjing Jiancheng Bioengineering Institute, Nanjing, China). Additionally, the concentrations of triacylglycerol (A110-1-1, TAG) and total cholesterol (A111-1-1, T-CHO) in both serum and liver samples, as well as liver free fatty acids (A042-2-1, NEFA) were determined using corresponding commercial kits from the same manufacturer. For the evaluation of oxidative stress markers, liver superoxide dismutase (A001-3-2, SOD), catalase (A007-1-1, CAT), and glutathione peroxidase (A005-1-2, GPX) activities were measured, along with the malondialdehyde (A003-1-2, MDA) concentration, utilizing validated kits (Nanjing Jiancheng Bioengineering Institute, Nanjing, China).

Liver citrate synthase (A108-1-2, CS), malate dehydrogenase (A021-2-1, MDH) and coenzyme I (A114-1-1, NADH/NAD^+) levels were measured using commercially available kits from Nanjing Jiancheng Bioengineering Institute (Nanjing, China). Additionally, liver succinate dehydrogenase (BC0955, SDH) activity was assessed using a kit from Beijing Soleibao Technology Co., Ltd. (Beijing, China), while hepatic ATP content (S0027, ATP) was quantified with a Beyotime kit (Beyotime Biotechnology, Shanghai, China). These biomarkers were employed to comprehensively evaluate alterations in hepatic mitochondrial function.

2.6. Liver histology

Liver tissues fixed in 4% paraformaldehyde for over 24 h were removed and subsequently dehydrated in a 20% (w/v) sucrose solution. The samples were then embedded in an optimal cutting temperature (OTC) compound (G6059, Servicebio) for cryosectioning. Cryosections were prepared using a cryostat (CRYOSTAR NX50, Thermo Scientific) maintained at -20°C. Lipid droplets were visualized using Oil Red O staining solution (G1015, Servicebio), while nuclei were counterstained with hematoxylin solution (G1004, Servicebio). Stained sections were examined under a Leica DM5500 B optical microscope.

2.7. Gene expression

Total RNA was extracted using a commercial RNA isolation kit (RC101-01, Vazyme Biotech Co., Ltd., Nanjing, China) following the manufacturer's instructions. To eliminate any residual genomic DNA, RNA samples were treated with DNase. The purity and integrity of the RNA were assessed as described in our previous study [33]. Complementary DNA (cDNA) was synthesized from 0.5 μg of RNA using a cDNA synthesis kit (R211-01, Vazyme Biotech Co., Ltd., Nanjing, China), adhering to the manufacturer's guidelines. The resulting cDNA was utilized for quantification of mRNA expression levels via quantitative real-time PCR (qRT-PCR), following the protocols established in our earlier work [33]. Gene expression levels were normalized and analyzed using the $2^{-\Delta\Delta Ct}$ method. The specific primers used for qRT-PCR are listed in Table 3.

2.8. Statistical analysis

Data were subjected to statistical analysis using one-way analysis of variance (ANOVA) in the SPSS 20 software package. Prior to conducting statistical comparisons, the Kolmogorov–Smirnov test was employed to assess the normality of the data distribution, and Levene's test was used to verify the homogeneity of variance across groups. Post-hoc multiple comparisons between treatment groups were performed using Duncan's multiple range test. Statistical significance was determined at a threshold of $P < 0.05$. Results are expressed as mean values ± standard error (SE).

3. Results

3.1. Growth and whole-body composition

The group fed HFD exhibited significantly lower weight gain (WG), final body weight (FBW), and specific growth rate (SGR) than those fed the NFD (Table 4) (P =0.001). The addition of COQ10 to the HFD significantly improved WG, FBW and SGR, with the highest values obtained for the HFD+COQ10-80 group (P =0.001). Additionally, the HFD+COQ10-20 and HFD+COQ10-80 groups demonstrated higher protein efficiency ratios (PER) than the HFD group (P =0.03). In contrast to the NFD group, the feed conversion ratio (FCR) was markedly elevated in the HFD group; however, supplementation with COQ10 resulted in a significant reduction in FCR, with the HFD+COQ10-20 group exhibiting the lowest FCR of all treatments (P =0.01). Furthermore, the intraperitoneal fat ratio (IPF) in the HFD group was nearly double that of the NFD group, while COQ10 supplementation significantly decreased IPF values (P =0.001).

Fish whole-body fat content showed a marked increase in the HFD group relative to the NFD group (P =0.033); however, supplementation with COQ10 did not result in any significant alterations (Table 5) (P =0.372). Muscle lipid content, on the other hand, was significantly increased in the COQ10-supplemented groups compared to the NFD group (Table 5) (P =0.02). Despite these changes in lipid deposition, no significant variations were observed in the protein, moisture, or ash contents of either whole-body or muscle tissue across the experimental groups (P=0.38).

3.2. Whole-body fatty acid profile

As presented in Table 6, the HFD group exhibited a significant increase in the ratios of saturated fatty acids (SFA), palmitic acid (C:16), and stearic acid (C:18), compared to the NFD group, while the proportion of monounsaturated fatty acids (MUFA) significantly decreased (P =0.001). However, supplementation with COQ10 effectively reversed these trends. Moreover, the HFD group showed a marked increase in the ratios of n-6 polyunsaturated fatty acids (n-6 PUFA), specifically linoleic acid (C18:2n-6), as well as n-3 PUFA and alpha-linolenic acid (ALA) (C18:3n-3) (P = 0.001). Notably, supplementation with 20-80 mg/kg COQ10 resulted in a significant reduction in the levels of n-6 PUFA, n-3 PUFA, ALA, and the long-chain n-3 PUFAs such as eicosapentaenoic acid (EPA) (C20:5n-3) and docosahexaenoic acid (DHA) (C22:6n-3) (P = 0.012).

3.3. Serum and liver biochemical parameters

Serum AST and ALT activities significantly increased in HFD group compared to the NFD group (P =0.001). However, COQ10 supplementation in the HFD resulted in a substantial reduction in the activities of both enzymes (Fig. 1A & B) (P =0.001). Furthermore, the HFD group exhibited remarkably higher concentrations of serum TAG and T-CHO compared to the other dietary treatments (P =0.02), in addition, there were no significant differences in serum TAG and T-CHO levels between the NFD group and the COQ10 groups (P =0.166) (Fig. 1C & D).

Similarly, in comparison to the NFD group, HFD feeding resulted in a significant accumulation of TAG, T-CHO and NEFA in the liver (P =0.001). However, supplementation with COQ10 effectively attenuated these hepatic lipid elevations, significantly reducing the concentrations of TAG, T-CHO and NEFA (P =0.002). Notably, the levels of T-CHO and NEFA in the COQ10-supplemented groups were comparable to those observed in the NFD group (Table 7) (P =0.326), indicating a normalization of lipid metabolism.

3.4. Liver fat metabolism-related enzymes activity

As shown in Figure 2 (A, B), compared with the NFD group, the liver fatty acid synthase (FAS) activity in the HFD group was significantly increased, and its activity was decreased in a dose-dependent manner by COQ10 supplementation (P =0.001). On the

contrary, the activity of adipose triglyceride lipase (ATGL) was significantly decreased in HFD, but the activity of ATGL was significantly restored by the addition of COQ10 (P =0.006).

3.5. Liver histology

As illustrated in Fig. 3A, oil red O staining of liver revealed a marked accumulation of lipid droplets in the HFD group compared to the NFD group, indicating substantial hepatic lipid deposition. However, supplementation with COQ10 clearly alleviated fat accumulation in the liver. Quantification of lipid droplets was performed using ImageJ software, and the results are presented in Fig. 3B. The analysis demonstrated a significant increase in lipid droplets area in the HFD group relative to the NFD group (P =0.01), whereas COQ10 supplementation led to a pronounced, dose-dependent reduction in lipid droplets area across all treatment groups (P =0.01), underscoring its protective effect against hepatic steatosis.

3.6. Liver antioxidant capacity

The activities of key liver antioxidant enzymes, including CAT, SOD, and GPX, were significantly depressed in the HFD group compared to the NFD group (P =0.022). Conversely, a marked increase in MDA concentration was observed, indicating increased oxidative stress and lipid peroxidation in the liver (P =0.007). Notably, supplementation with COQ10 dose-dependently restored the activities of these antioxidant enzymes and attenuated the elevated MDA levels, thereby reversing the oxidative alterations associated with HFD feeding (P =0.01).

3.7. Expression of fat metabolism-related genes

Feeding HFD resulted in a significant up-regulation of fat synthesis-related genes including *fas*, *srebp-1c*, *acc*, along with a significant down-regulation of lipolysis-related genes, such as *atgl* and *hsl*, indicating increased fat synthesis in the liver and inhibition of lipolysis metabolism (Fig.5) (P=0.001). However, COQ10 supplementation reversed the expression levels of these fat metabolism-related genes (P =0.013). Additionally, the expression of fatty acid β-oxidation-related genes, including *ampkα1*, *pparα* and *cpt-1α* in the liver of HFD group (P=0.035) was inhibited. Importantly, the expression of these

β-oxidation-related genes was significantly restored after COQ10 treatment, indicating that COQ10 promoted the utilization of fatty acids in the liver of spotted seabass(P=0.004) (Fig.5).

3.8. Mitochondrial function

Feeding the HFD resulted in a significant decline in the activity of key mitochondrial function-related enzymes, including CS and SDH, in the liver of spotted seabass (P =0.012). However, COQ10 administration significantly enhanced these enzyme activities (Fig. 6A & B) (P =0.032). Additionally, HFD feeding led to an increased NADH/NAD+ ratio, along with a reduction in malate dehydrogenase activity (Fig. 6C & D) (P =0.001). The HFD group exhibited a substantial decrease in liver ATP content, which was effectively reversed by COQ10 treatment (Fig. 6 E), indicating that COQ10 plays a critical role in restoring mitochondrial energy balance in the liver of spotted seabass (P =0.003).

3.9. Mitochondrial biogenesis and autophagy

The expression profiles of genes associated with mitochondrial biogenesis and autophagy are presented in Fig 7. In the HFD group, there was a significant downregulation of mitochondrial biogenesis-related genes, including *pgc-1α*, *pgc-1β*, *nrf1*, and *tfam*, compared to the NFD group (P =0.001). Similarly, autophagy-related genes, such as *pink1*, *mul1*, and *atg5*, were also significantly downregulated (P =0.003). Notably, COQ10 supplementation significantly upregulated the expression of both mitochondrial biogenesis-related and autophagy-related genes, suggesting its potential role in enhancing mitochondrial function and promoting autophagic process in the liver.

4. Discussion

Excessive fat intake can disrupt the metabolic homeostasis in farmed fish, leading to impaired growth and inferior feed utilization [34]. Studies have shown that the optimal dietary lipid level for spotted seabass is approximately 7.4-12.9% of the diet, and lipid levels exceeding 15% disrupt lipid metabolism [35,36]. Likewise, in this study feeding the HFD with 17% fat led to decreased WG, SGR and PER compared to the group fed the NFD with 11% fat. The growth-promoting effect of COQ10 observed in the present study is consistent with

findings from studies on European seabass (*Dicentrarchus labrax*) and grey mullet (*Liza ramada*) [28,37].

Previous investigations have established that the accumulation of SFAs in fish is detrimental to growth [38]. In this experiment, the assessment of total fatty acid composition revealed that HFD intake resulted in a marked increase in the deposition of SFAs, concomitant with a reduction in the MUFA ratio, aligning with findings from research on rice field eel (*Monopterus albus*) [39]. DHA and EPA are pivotal for the growth and lipid metabolism in fish [40]. Notably, this experiment demonstrated that HFD ingestion led to decreased DHA and EPA ratios in the whole-body of spotted seabass. However, supplementation with COQ10 appeared to mitigate this decline, suggesting that COQ10 may promote the utilization of DHA and EPA, thereby facilitating the growth of spotted seabass and alleviating disturbances in lipid metabolism. Research on largemouth bass has indicated that COQ10 can promote the absorption and utilization of DHA and EPA, effectively countering the suppression of growth performance induced by oxidized fish oil [41]. Additionally, a study on triploid brown trout (*Salmo trutta*) showed that HFD intake resulted in increased total and muscle fat contents [42]. Similarly, our findings indicated that HFD feeding significantly elevated total and muscle fat content; however, supplementation with COQ10 did not yield a significant change in total fat content. Conversely, muscle fat content experienced a notable increase, which may be attributed to the role of COQ10 in promoting muscle fat deposition. Furthermore, investigations on grass carp demonstrated that DHA and EPA can stimulate muscle fat deposition [43], which could also elucidate the mechanisms by which COQ10 enhances muscle fat content.

The liver serves as a critical organ in the regulation of lipid metabolism in fish. Among its various functions, the activities of ALT and AST are of paramount importance, as these intracellular enzymes play vital roles in hepatic function. Serum activity levels of ALT and AST are frequently used as significant indicators for assessing the health status and the functional integrity of the fish liver [44]. Our results demonstrated that feeding HFD increases the ALT and AST activities in serum, while the addition of COQ10 reduced the activity of these transaminases. Similarly, studies on Nile tilapia (*Oreochromis niloticus*) [45] and golden pompano (*Trachinotus ovatus*) [46] showed enhanced serum ALT and AST activities following

HFD administration. Furthermore, investigations on rainbow trout and largemouth bass indicated that COQ10 could alleviate liver damage caused by ammonia nitrogen and oxidized fish oil, subsequently reducing the serum transaminase levels [47,48]. The body's fat metabolism can be accurately represented by its lipid status. Abnormally elevated TAG and T-CHO concentrations in fish blood, as key components of lipid metabolism, often indicate a disorder in lipid metabolism [49]. The findings of this study demonstrated an increase in serum TAG and T-CHO concentrations in the HFD group, which is consistent with research on largemouth bass (*Micropterus salmoides*) [50] and rice field eel (*Monopterus albus*) [51]. Studies in mice have shown that the addition of COQ10, either alone or in combination with rosiglitazone, can effectively reduce the elevation of blood lipid levels induced by HFD [21,22]. COQ10 was also found to lower serum lipid levels and promote fat metabolism in European eel and Pacific white shrimp [28,37]. Our results similarly indicated that the addition of COQ10 lowered serum TAG and T-CHO levels, suggesting its beneficial effects on liver health and fat metabolism.

Liver steatosis is a significant manifestation of disordered fat metabolism. Alterations in TAG content within the liver are often regarded as key markers of metabolic dysfunction affecting multiple organs [52,53]. Moreover, as the severity of liver steatosis intensifies, the extent of damage to liver function also increases [52,54,55]. In this study, HFD intake led to excessive fat deposition in the liver of spotted seabass, evidenced by a significant increase in TAG and T-CHO levels. Concurrently, abdominal fat was also significantly increased, indicating a disorder in lipid metabolism. Oil red O staining of liver sections and the quantitative assessment of lipid droplet area confirmed the findings from the liver biochemical indicators. NEFAs, regarded as substrates of fatty acid oxidation, are often implicated as sources of lipotoxicity [13]. Excessive NEFAs can lead to cellular damage and apoptosis [13]. In this study, HFD consumption led to augmented NEFAs concentration in the liver, while COQ10 supplementation decreased their levels, suggesting that COQ10 alleviates lipid toxicity by activating fatty acid oxidation. Overall, the results of the liver biochemical indices and histological analyses in this study showed that COQ10 can mitigate fat deposition in the liver and reduce lipotoxicity. These findings are consistent with results from a study on Nile tilapia [7].

FAS and ACC serve as key enzymes in fatty acid synthesis, playing a crucial role in the process of generating new fatty acids. Their expression and activity are regulated by the sterol regulatory element-binding protein (SREBP) family, which are the primary regulators of lipid homeostasis, SREBPs control the transcription of genes involved in lipid biosynthesis and uptake, ensuring a balance between fatty acids synthesis and degeneration to maintain metabolic equilibrium[56]. ATGL is critical in the mammalian lipolysis process and in mobilization of lipid stores. It initiates the first step of TAG catabolism, and the lipolysis facilitated by ATGL may have significant implications for maintaining liver lipid homeostasis and influencing the progression of liver diseases. Downregulated expression of ATGL can lead to obesity and other metabolic complications due to impaired lipid mobilization [57–59]. Numerous studies have reported that HFD intake can upregulate the expression of FAS and downregulate the expression of ATGL [60–62] in mice and fish models. Similarly, feeding spotted seabass the HFD resulted in increased expression of *fas*, *acc*, *srebp-1c* and reduced expression of *atgl*, which corresponded with the observed FAS and ATGL enzymatic activities in the liver. These HFD-induced alterations in *fas*, *acc*, *srebp-1c* and *atgl* genes expression and their corresponding enzymatic activity in the liver were reversed by COQ10 supplementation, indicating that COQ10 can alleviate fat deposition by promoting fat breakdown and inhibiting fat synthesis. In addition to regulating hepatic de novo lipogenesis, the balance of hepatic triglycerides is also maintained through mitochondrial β-oxidation. In this pathway, PPAR-α, a nuclear hormone receptor activated by fatty acids, plays a critical role in the transcriptional regulation of lipid metabolism, particularly in promoting fatty acid oxidation [63]. Among its downstream molecular targets, carnitine palmitoyltransferase-1 (CPT-1α) is an important component, serving as the rate-limiting enzyme in the mitochondrial fatty acid β-oxidation pathway. Our results showed that COQ10 treatment increased the expression of *ppar-α* and *cpt-1α*, promoting fatty acid oxidation. As an energy sensor, AMP-activated protein kinase (AMPK) plays a critical role in maintaining metabolic homeostasis. Studies have shown that AMPKα1 is associated with the incidence of NAFLD and is involved in the liver lipid metabolism [64–66]. Our previous research demonstrated that activation of AMPKα1 can reduce fat deposition in the liver of blunt snout bream [67]. Moreover, studies have shown that activation of AMPKα1 can upregulate CPT-1α and

PPARα to promote fatty acid β-oxidation [21]. Our data suggest that HFD ingestion may lead to dysfunction in AMPKα1 activation, while COQ10 application could potentially restore AMPKα1 activation. This suggests that the AMPKα1 metabolic pathway is involved in the lipid-lowering effect of COQ10. COQ10 appears to alleviate liver fat deposition in spotted seabass by both inhibiting lipogenesis and promoting fatty acid oxidation, consistent with findings from a study on mice [23]. However, the underlying mechanisms require further investigation.

According to the two-hit hypothesis, the initial hit involves an increase in triglyceride accumulation in the liver, disrupting lipid metabolic balance. The second hit primarily arises from the excessive deposition of reactive oxygen species (ROS) due to oxidative stress, resulting in lipid peroxidation and subsequent impairment of cellular structure and function [68,69]. To counter oxidative stress, fish have evolved an antioxidant defense system, which includes enzymatic antioxidants such as SOD, CAT, GPX and GR, as well as non-enzymatic antioxidants such as GSH [16,70]. MDA, one of the stable end products of lipid peroxidation, is commonly used as a marker to evaluate oxidative stress and lipid peroxidation in aquatic animals [71]. In this study, the activity of liver antioxidant enzymes in the HFD group was significantly lower than in the NFD group, while the MDA level in the HFD group exhibited the opposite trend. Elevated MDA levels in fish fed HFD indicated an imbalance between ROS production and removal. These findings are consistent with result from studies on juvenile black carp (*Mylopharyngodon piceus*) [72], Nile tilapia [73], and largemouth bass [74] fed HFDs. Our results showed that supplementation with an appropriate dose of COQ10 in HFD could increase the activities of SOD, CAT and GPX in the liver of spotted seabass and reduce MDA level. COQ10, particularly in its reduced form (ubiquinol), functions as a potent antioxidant and free radical scavenger. It protects DNA, cell membranes, lipids, and proteins, mitigating the potential for oxidative damage. Additionally, it aids in the regeneration of vitamin E and sometimes referred to as a 'supervitamin' or 'vitamin Q' [75,76]. A previous study on tilapia showed that supplementation of 20-40 mg/kg of COQ10 can significantly increase the activities of CAT, SOD, and GPX, as well as expression of their genes in the liver and intestine. Studies on rainbow trout and largemouth bass also found that COQ10 can alleviate oxidative stress caused by oxidized fish oil and ammonia nitrogen stress [30,47,48].

Mitochondria are essential organelles present in most eukaryotic cells. They are the primary sites for physiological processes such as the tricarboxylic acid (TCA) cycle, oxidative phosphorylation, and fatty acid β-oxidation, all of which are closely associated with nutrient metabolism. Therefore, normal mitochondrial function is necessary for animals to maintain metabolic homeostasis and efficiently utilize nutrients [(77)]. However, in cases of overnutrition, such as excessive fat intake, mitochondria become susceptible to metabolic stress [(12)]. Numerous studies have shown that lipid metabolic disorders in fish are often accompanied by liver mitochondrial damage. For example, a study on zebrafish (*Danio rerio*) showed that the addition of the carnitine synthesis inhibitor midozide to the diet caused excessive liver fat deposition, accompanied by decreased mitochondrial fatty acid β-oxidation [(78)]. Another study on grass carp (*Ctenopharyngodon idella*) showed that feeding a HFD enhances blood lipid content, alters liver fatty acid composition, and reduces liver mitochondrial content and oxidative capacity [(79)]. CS, a key rate-limiting enzyme in the TCA cycle, catalyzes the condensation of acetyl CoA and oxaloacetic acid to form citric acid, regulating the entry into the TCA cycle. SDH serves as a key link between the TCA cycle and oxidative phosphorylation. Both CS and SDH are used as marker enzymes for assessing mitochondrial function [(80)]. In this study, feeding the HFD resulted in decreased CS and SDH activities, while COQ10 supplementation in the HFD significantly increased their activity. NAD^+ is the primary hydrogen receptor in glycolysis (EMP) and the TCA cycle. The NADH generated transfers electrons to oxygen via the electron transport chain (ETC). During ATP synthesis, ROS are produced as byproducts of electron transfer in the ETC, and NADH is regenerated into NAD^+. The oxidation of most large metabolites, such as sugars, fats, and proteins, is completed through this system. Therefore, the NADH/NAD^+ ratio is a key indicator of the state of glycolysis and TCA cycle. Elevated NADH levels and a higher NADH/NAD^+ ratio indicate increased oxygen consumption during cellular respiration and a state of peroxidation. Additionally, a surge in the NADH/NAD^+ ratio can impede both glycolysis and the TCA cycle. Our results showed that HFD intake enhances the NADH/NAD^+ ratio in the liver of spotted seabass, indicating inhibition of lipid peroxidation and TCA cycle; however, this ratio was significantly reduced by COQ10 supplementation. MDH is an enzyme involved in the TCA cycle that converts malate to oxaloacetate,

influencing the efficiency of the cycle. A reduction in MDH activity in the liver of cobia (*Rachycentron canadum*) with increasing dietary lipid level has been reported [81]. Similarly, we observed a decrease in MDH activity in the HFD group, suggesting inhibition of the mitochondrial TCA cycle and impairment of mitochondrial function. However, supplementation with COQ10 significantly mitigated this effect. Additionally, mitochondrial dysfunction can impair the electron transport chain, leading to reduced ATP production [82]. Our data indicated that COQ10 administration can restore ATP levels in the liver of spotted seabass affected by HFD feeding, affirming the positive impact of COQ10 on mitochondrial function.

Mitochondria are highly dynamic organelles that undergo continuous renewal under normal physiological conditions. This renewal involves the constant generation of new, functional mitochondria through mitochondrial biogenesis, along with the removal of aging and damaged mitochondria through mitophagy. These two biological processes are essential for maintaining proper mitochondrial function, and consequently, cellular homeostasis [83]. The transcription coactivators PGC-1α and PGC-1β play pivotal roles in regulating mitochondrial biogenesis by activating the expression of downstream transcription factors. Among these, NRF1 stimulates the expression of nuclear-encoded mitochondrial genes, promoting the transport and assembly of peptides and proteins necessary for mitochondrial function. TFAM, on the other hand, promotes the replication and transcription of mitochondrial DNA, facilitating the formation of mitochondrial respiratory chain complexes [84]. In this study, HFD was observed to notably suppress the expression of *pgc-1α*, *nrf-1* and *tfam*, while COQ10 administration significantly enhanced the expression of *pgc-1α*, *pgc-1β*, *nrf1*, and *tfam*. These results suggest that HFD impairs mitochondrial development in the liver of spotted seabass, while COQ10 stimulates mitochondrial formation. This finding aligns with observations from two investigations in mammalian models [85,86]. This effect may be attributed to mitochondrial biogenesis, a widely conserved process across species. Therefore, COQ10 may play a similar role in promoting mitochondrial biogenesis in different species. The removal of impaired mitochondria and their restoration through mitochondrial biogenesis are crucial aspects of the mitochondrial quality control mechanism. The PINK1-mediated mitophagy pathway is a key regulatory mechanism in this context [87]. Our

results showed that the expression levels of *pink1*, *mul1*, and *atg5* in the PINK1-mediated mitophagy pathway were significantly decreased in the HFD group, while COQ10 supplementation in the HFD stimulated the expression of these genes. Mitophagy and mitochondrial biogenesis are closely interacted, and dysregulation of mitophagy can impair mitochondrial formation [88]. Thus, COQ10 may enhance mitochondrial biogenesis and improve mitochondrial function by stimulating mitophagy. However, additional evidence, such as protein expression analyses and further validation in cellular models, is needed to confirm that COQ10 activates mitophagy and promotes mitochondrial biogenesis.

5. Conclusion

In conclusion, our findings indicate that feeding a HFD can induce lipid metabolism disorders, characterized by excessive lipid accumulation, oxidative stress, liver histopathological abnormalities, and dysregulation of lipid metabolism-related genes expression. The administration of 20-80 mg/kg COQ10 in the HFD improved fish growth, promoted lipid metabolism, strengthened antioxidant capacity, stimulated mitochondrial function, and reduced excessive lipid accumulation. The lipid-lowering mechanism of COQ10 is likely mediated through the activation of AMPK signaling pathway, upregulation of lipolysis-related genes, and the promotion of mitophagy and mitochondrial biogenesis. However, further research is needed to clarify the precise mechanisms through which COQ10 modulates mitochondrial function to facilitate lipid reduction.

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Author Contributions

The authors' contributions were as follows: K.L. designed the research; X.M. conducted the research, analyzed the date and wrote the article; X.L., L.W., C.Z., B.H., and S.R. contributed to the writing and revision of the manuscript. All authors reviewed and approved the final manuscript.

Conflict of interest

We declare that we have no financial and personal relationships with other people or organizations that might inappropriately influence our work, and there is no professional or other personal interest of any nature or kind in any product, service and/or company that could be construed as influencing the content of this paper.

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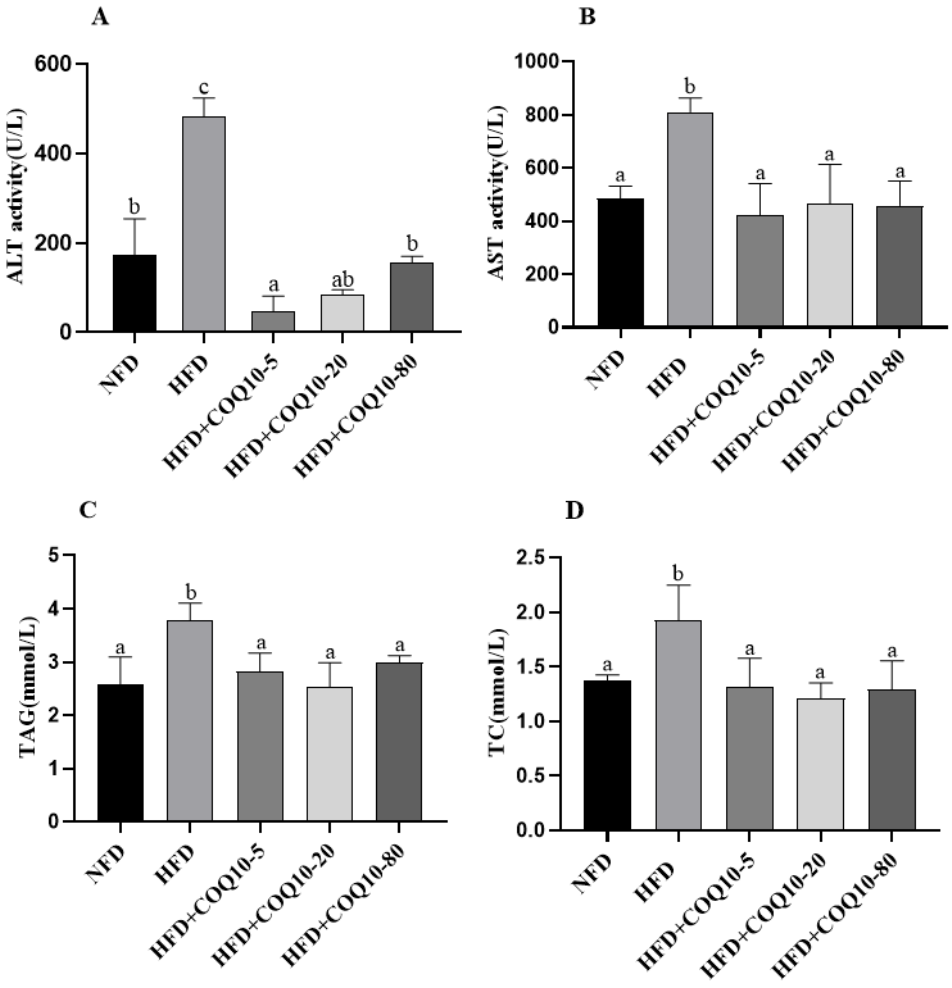

Fig. 1. Serum biochemical parameters of spotted seabass fed the experimental diets for 8 weeks (A: alanine aminotransferase activity (ALT), B: aspartate aminotransferase activity (AST), C: triacylglycerol level (TAG), D: total cholesterol level (TC)All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

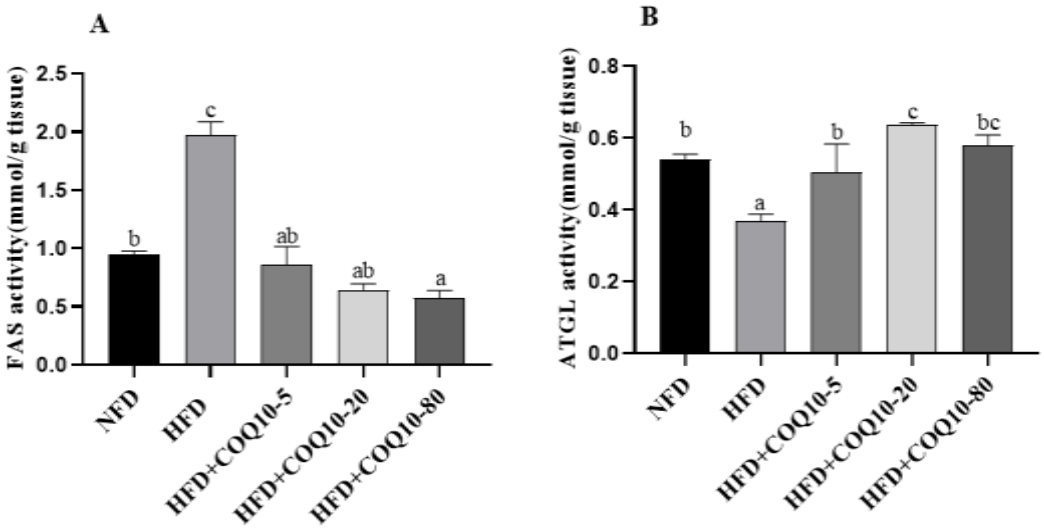

Fig. 2. Liver fat metabolism related enzymes activity in spotted seabass fed the experimental diets for 8 weeks (A: fatty acid synthase activity (FAS), B: triglyceride lipase activity (ATGL). All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

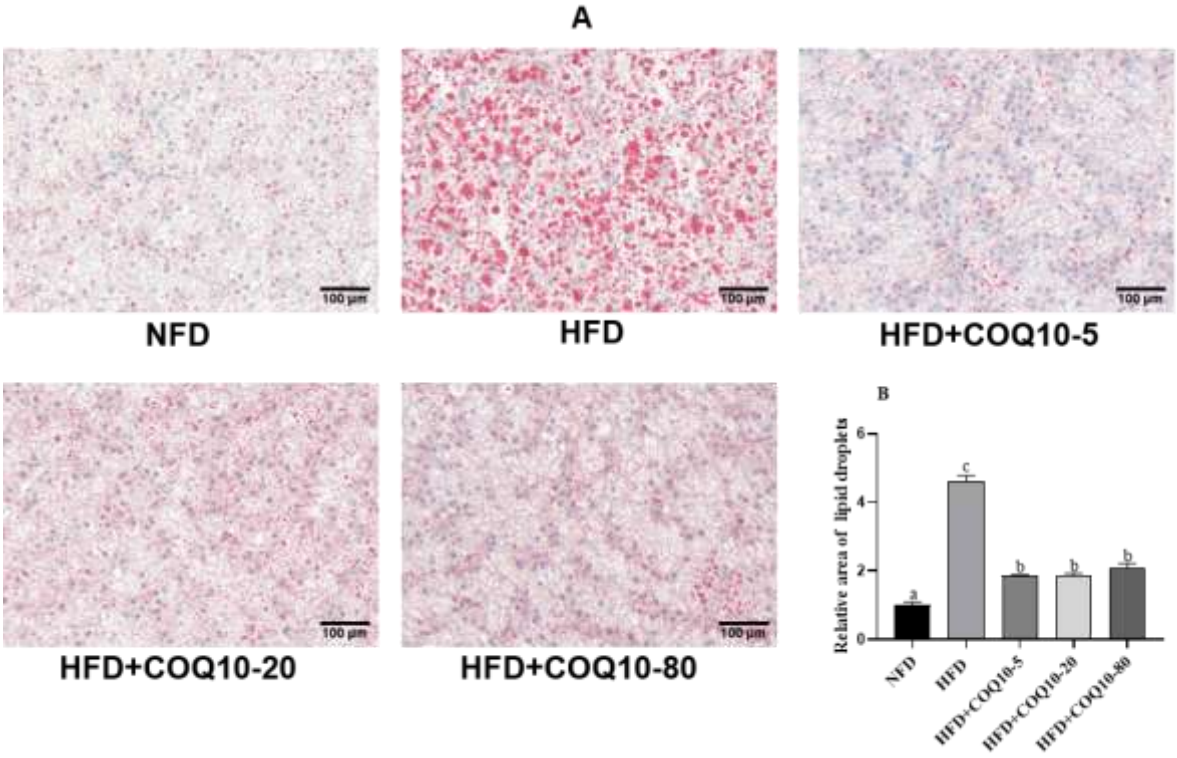

Fig.3. A: Liver histology (oil red O staining, scale = 100μm) of spotted seabass fed the experimental diets for 8 weeks. B: The relative area of red plaques (lipid droplets) after oil red O staining in each treatment group. All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

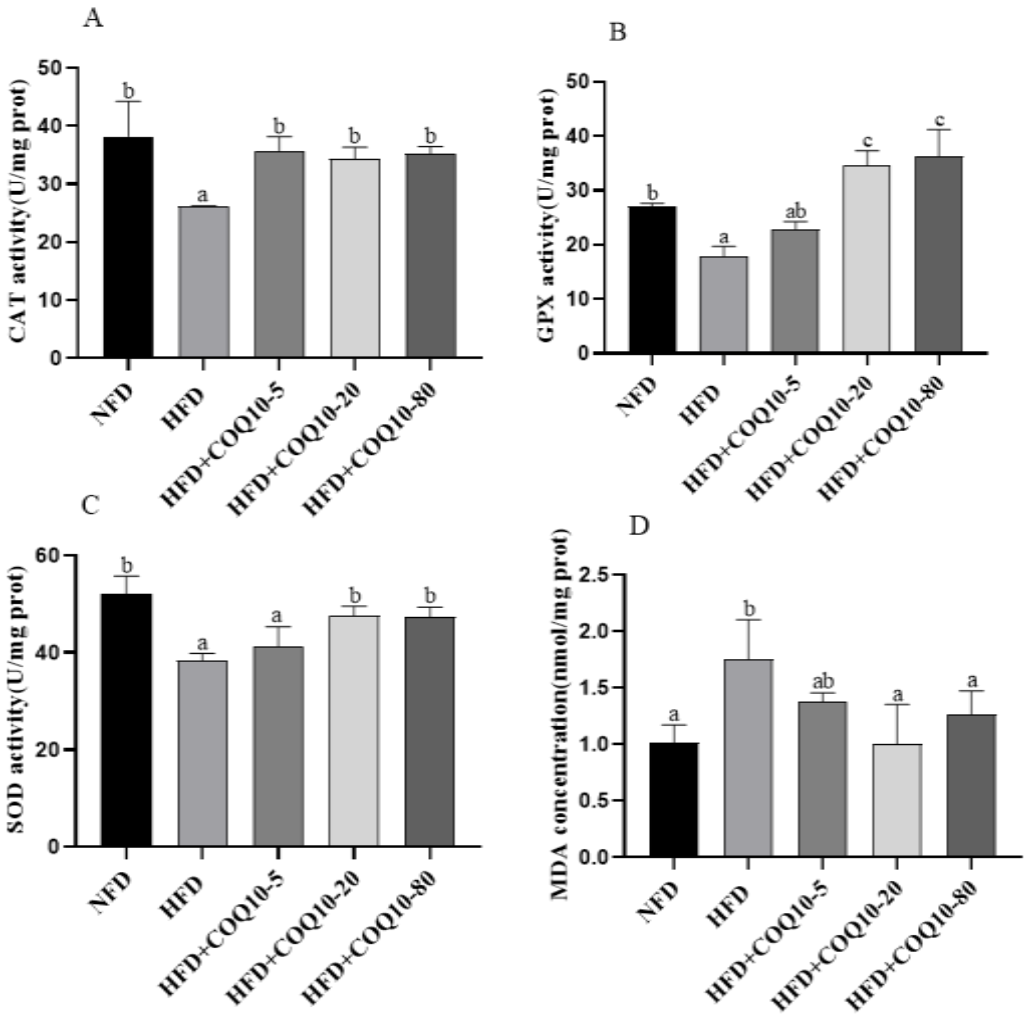

Fig. 4. Liver antioxidant capacity parameters of spotted seabass fed the experimental diets for 8 weeks (A: catalase activity (CAT), B: glutathione peroxidase activity (GPX), C: superoxide dismutase activity (SOD), D: malondialdehyde concentration (MDA). All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

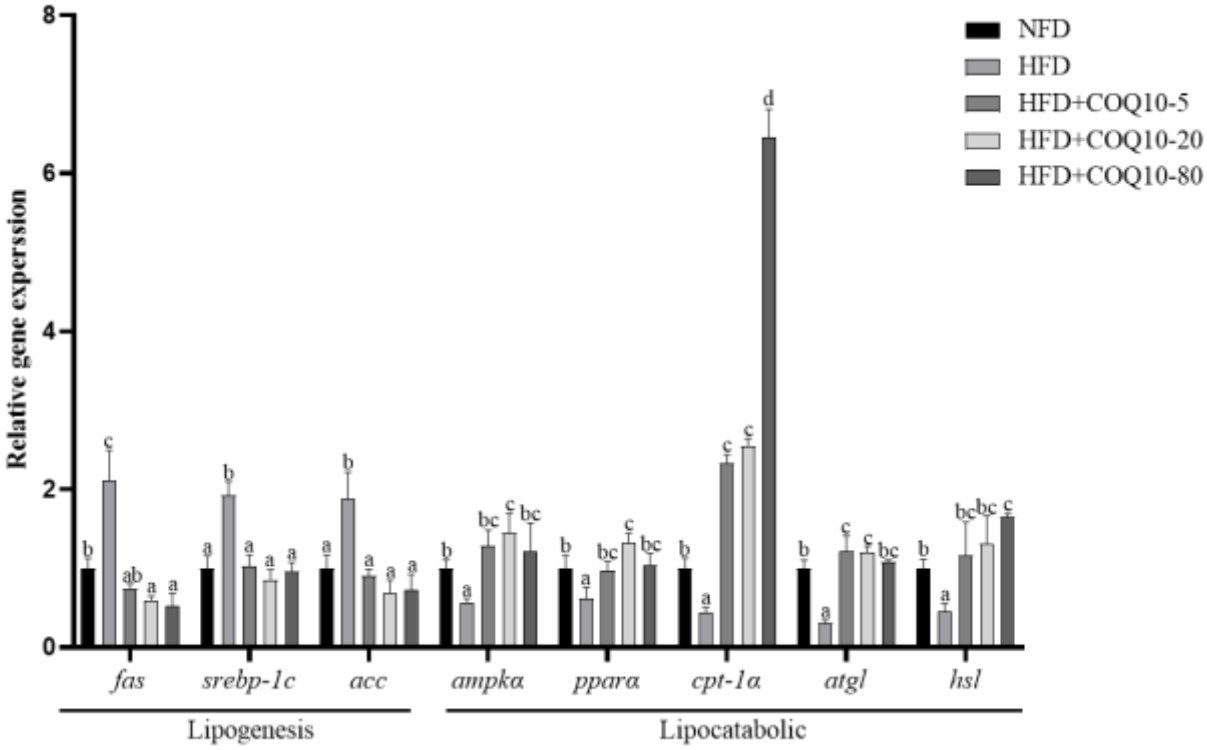

Fig.5. Expression of fat metabolism related genes in the liver of spotted seabass fed the experimental diets for 8 weeks. All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

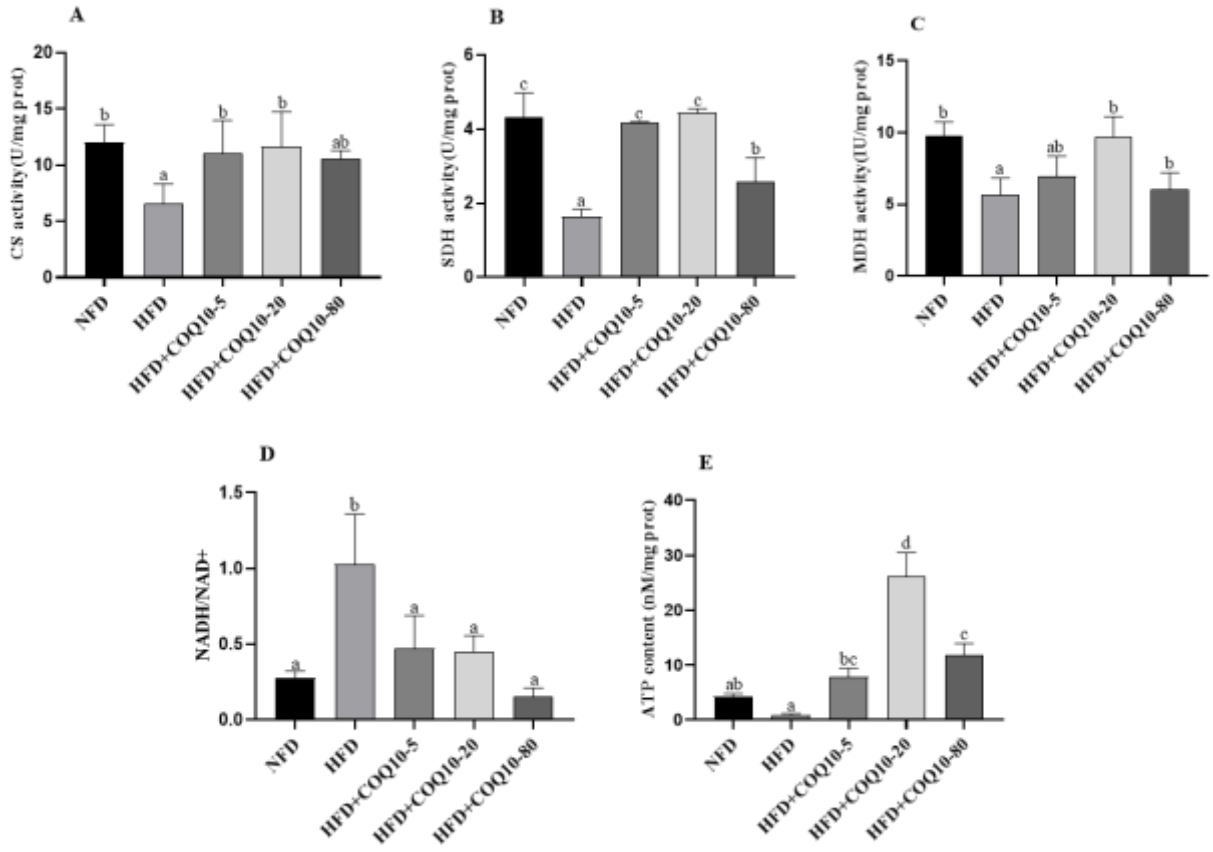

Fig.6. Mitochondrial citrate synthase (CS: A), succinate dehydrogenase (SDH: B), and malate dehydrogenase (MDH: C) activities, NAD + / NADH ratio (NAD + / NADH: D) and mitochondrial ATP content (E) in the liver of spotted seabass fed the experimental diets for 8 weeks. All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

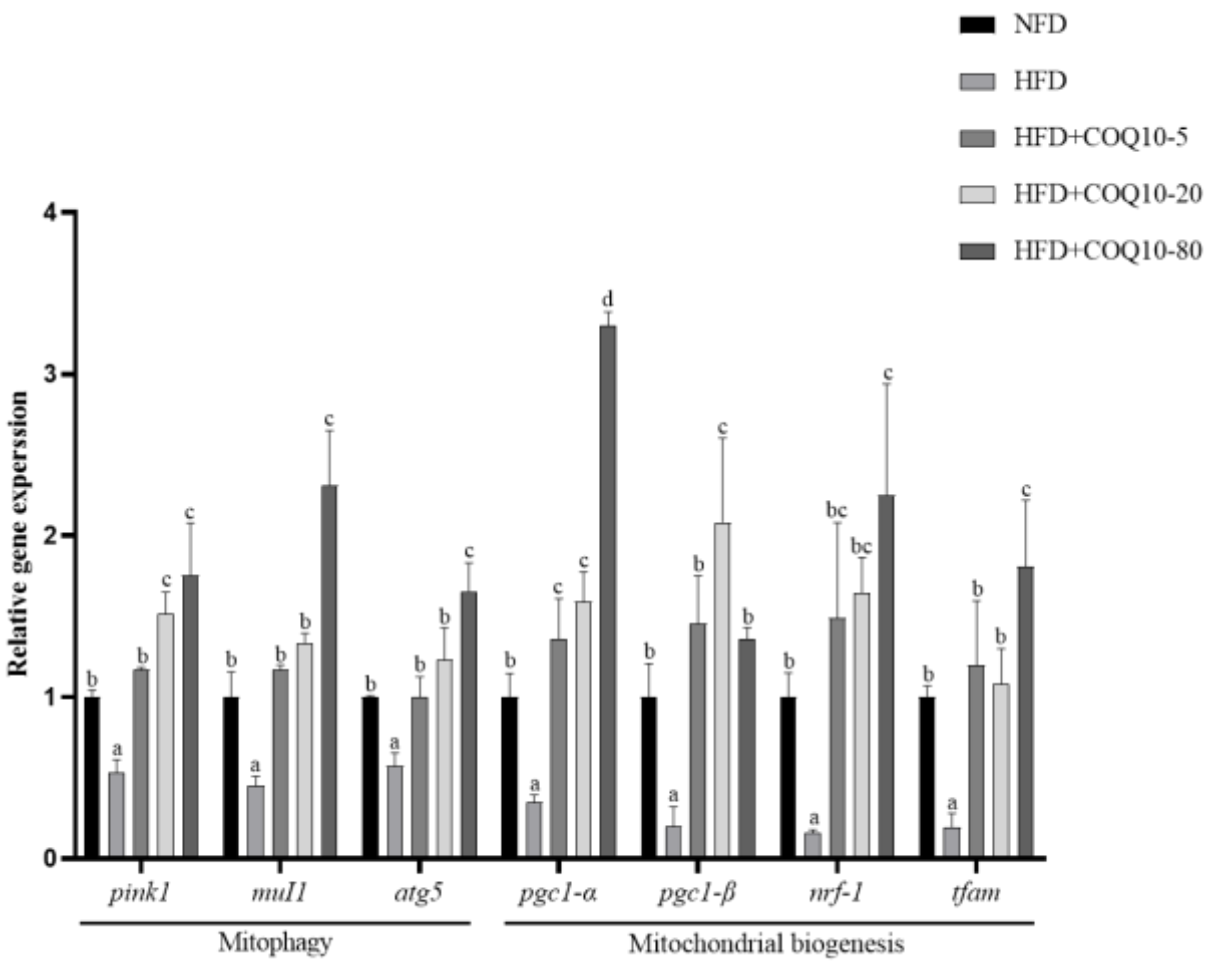

Fig. 7**.** Expressions of mitochondrial function related genes in the liver of spotted seabass fed the experimental diets for 8 weeks. All values are shown as mean ± SE. Bars with different letters are significantly different ($P < 0.05$).

Table 1. Formulation and chemical composition of the experimental diets (% dry matter).

	NFD	HFD	HFD+COQ10-5	HFD+COQ10-20	HFD+COQ10-80
Fish meal	35.00	35.00	35.00	35.00	35.00
Poultry by-product meal	12.39	12.39	12.39	12.39	12.39
Wheat gluten meal	7.35	8.78	8.78	8.78	8.78
Soybean meal	13.20	13.20	13.20	13.20	13.20
α-starch	3.00	3.00	3.00	3.00	3.00
Wheat flour	19.630	12.000	12.000	11.998	11.992
Fish oil	2.00	5.10	5.10	5.10	5.10
Soybean oil	2.00	5.10	5.10	5.10	5.10
Lecithin	2.00	2.00	2.00	2.00	2.00
Vitamin C	0.05	0.05	0.05	0.05	0.05
Vitamin premix	0.30	0.30	0.30	0.30	0.30
Mineral premix	0.50	0.50	0.50	0.50	0.50
Choline chloride	0.50	0.50	0.50	0.50	0.50
Calcium biphosphate	2.08	2.08	2.08	2.08	2.08
Coenzymum Q10	0	0	0.0005	0.002	0.008
Proximate composition (%)					
Dry matter	90.78	91.12	90.51	91.45	91.11
Crude protein	46.88	46.86	46.84	46.86	46.84
Crude lipid	11.62	17.41	17.42	17.56	17.52
Ash	11.00	10.92	11.20	10.83	10.93

Vitamin premix (g or mg per kg diet): Zoelite, 4.582 g; Thiamin, 10 mg; Riboflavin,8 mg; Pyridoxine HCl, 10 mg; Vitamin B12, 0.2 mg, Vitamin K3, 10 mg; Inositol,100 mg; Pantothenic acid, 20 mg; Niacin acid, 50 mg; Folic acid, 2 mg; Biotin,2 mg; Retinol acetate, 400 mg; Cholecalciferol, 5 mg; alpha-Tocopherol,100 mg; Eethoxyquin, 150 mg; Wheat middling, 1.1328 g.

Mineral mix (mg kg−1diet): NaF, 2 mg; KI, 0.8 mg; CoCl2·6H2O (1%), 50 mg;CuSO4·5H2O, 10 mg; FeSO4·H2O, 80 mg; ZnSO4·H2O, 50 mg; MnSO4·H2O,25 mg; MgSO4·7H2O, 200 mg.

Table 2. Fatty acid composition of feed (percentage of total fatty acids)

	NFD	HFD
14:00	1.17	1.51
16:00	15.99	16.88
18:00	4.71	5.02
20:00	0.26	0.25
∑SFA	22.13	23.66
16:1n-7	2.46	2.85
18:1n-9	28.43	26.51
∑MUFA	30.89	29.36
18:2n-6	36.00	33.66
20:4n-6	0.51	0.78
∑n-6 PUFA	36.51	34.44
18:3n-3	4.08	3.83
20:5n-3	1.26	2.13
22:6n-3	2.26	3.77
∑n-3PUFA	7.60	9.73
n-3/n-6 PUFA	0.21	0.28

Table 3. Sequences of primers used for RT-PCR.

Target genes[a]	primer sequence (5-3)	Annealing temperature (◦C)	Product size(bp)	GeneBank Number
pgc-1α	AACCCGACTCTTATCCCTCC CGTATCAACGCCACAGCAC	60	172	[1]
pgc-1β	AGGCAGGCTCGCTTTTCG GGCGGCTCCTTCTCGGTT	60	154	[1]
nrf1	GCCTTTCCACCTCTGACTG ACTCCTGCTTTCGCTTCC	60	102	[1]
tfam	GGTCAGACATTTCACTGGGTT G GCGGCTCTAATGCGTGAAT	60	131	[1]
pink1	CTGTGAAAGCCCGGTACACT TGATGTGGAACTTTGGGGCA	60	169	[1]
mul1	GCTGCCGTGATACGAGTCAT ACGTTGGACAAGGACTGGAC	60	216	[1]
atg5	TCAGTCGCTGCCATTAGAGC TCTCGTCACCTGCGAAAACT	60	207	[1]
ampkα1	CGCAGGGAGATCCAAAACCT GCTCGCCTCCTGAGACATAC	60	186	[1]
atgl	CTTCCTCTCCGCAACAAGTC TGGTGCTGTCTGGAGTGTTC	60	211	[1]
hsl	CGAAACACAGAGACGGTCCA TCATGACATCTACCAGCCGC	60	228	[1]
pparα	CCGTGCGTGTTTTCACCATT AGACCAAATACATCGCCCCC	60	193	[1]
cpt-1α	CCTCAATGATACATCGGAACC C	60	115	[1]

fas	CTGCGGCTCATCATCTAACG AAACTGAAGCCCTGTGTGCC ACCCTGCCTATTACATTGCTC	60	131	[1]
srebp-1c	CCTCACTCTGCAGCCAATCA CGTAGTCCCACCCTCAAACC	60	169	[1]
acc	AAGGCGGTGGTGATGGATTT GGCCATGTCGCCTTTGTTTT	60	174	[1]
β-action[b]	TCGAGCACGGTATTGTGACC TCAGGTGCAACTCTCAGCTC	60	135	MH181804.1

Pgc1α/β: Peroxisome proliferators activated receptor γ coactivator-1 α/β; *nrf1*: Nuclear respiratory factor 1; *tfam*: Mitochondrial transcription factor A; *pink1*: PTEN-induced putative kinase 1; *mul1*:mitochondrial E3 ubiquitin ligase 1b; *atg5*: autophagy protein 5; ampkα*1*:AMP-activated protein kinase; *atgl*: triglyceride lipase; *hsl*: Hormone sensitive Lipase; *pparα*: peroxisome proliferator-activated receptors;*cpt-1α*: Carnitine palmitoyltransferase-1; *fas*: fatty acid aynthase; *srebp-1c*: sterol regulatory element binding protein-1c; *acc*: acetyl coA carboxylase.

[a]The sequences of target genes were obtained from transcriptomic data in our previous study (28)

[b]Reference gene.

[1] According to the transcriptome data in our previous study

Table 4. Growth, feed utilization and survival of spotted seabass fed the experimental diets for 8 weeks.

	NFD	HFD	HFD+COQ10-5	HFD+COQ10-20	HFD+COQ10-80
IBW	12.00±0.04	12.02±0.05	11.98±0.04	12.01±0.06	11.97±0.08
FBW	129.45±0.93^{c}	112.05±0.96^{a}	123.10±0.74^{b}	128.28±1.26^{bc}	133.10±2.10^{c}
WG[1]	978.72±7.76^{c}	833.80±7.98^{a}	925.80±6.14^{b}	968.98±10.51^{bc}	1009.15±17.45^{c}
SGR[2]	4.49±0.01^{c}	4.21±0.02^{a}	4.39±0.01^{b}	4.47±0.02^{bc}	4.54±0.03^{c}
FCR[3]	1.08±0.01^{b}	1.20±0.05^{c}	1.04±0.01^{ab}	0.98±0.01^{a}	1.02±0.01^{ab}
FI[4]	124.71±3.09	119.83±0.93	115.04±0.92	111.54±2.63	117.16±8.69
PER[5]	2.01±0.07^{ab}	1.92±0.12^{a}	2.10±0.03^{ab}	2.27±0.03^{b}	2.27±0.14^{b}
IPF[6]	4.95±0.14^{a}	7.78±0.01^{c}	6.97±0.06^{b}	7.02±0.16^{b}	7.16±0.15^{b}
Survival (%)	98.33±1.67	100±0.00	100±0.00	100±0.00	100±0.00

Values are presented as mean ± SEM. The values with different superscript letters in the same row are significantly different ($P < 0.05$).

[1]Weight gain (%) = [(Final body weight – initial body weight) / initial body weight] × 100.

[2]Specific growth rate (%/d) = [(Ln final body weight – Ln initial body weight)/days] × 100.

[3]Feed conversion ratio = dry feed fed / wet weight gain.

[4]Feed intake (g/fish) = feed consumed / number of experimental fish.

[5]Protein efficiency ratio = wet weight gain / total protein given.

[6] Intraperitoneal fat ratio (%) = final intraperitoneal fat / body weight.

Table 5. Whole-body and muscle composition of spotted seabass fed the experimental diets for 8 weeks (% wet weight).

	NFD	HFD	HFD+COQ10-5	HFD+COQ10-20	HFD+COQ10-80
Whole-body					
Moisture	68.02±0.39	66.88±0.39	66.22±1.04	66.89±0.47	66.87±0.57
Protein	17.04±0.11	16.90±0.10	17.33±0.65	16.73±0.12	17.03±0.27
Lipid	5.94±0.31[a]	7.52±0.26[b]	7.41±0.35[b]	7.65±0.51[b]	7.57±0.71[b]
Ash	4.53±0.08	4.49±0.05	4.64±0.10	4.50±0.06	4.44±0.14
Muscle					
Moisture	77.62±0.32	77.29±0.45	77.45±0.09	77.62±0.06	77.18±0.10
Protein	20.43±0.20	20.69±0.40	20.65±0.04	20.59±0.07	20.84±0.08
Lipid	1.67±0.15[a]	2.05±0.13[ab]	2.30±0.08[b]	2.24±0.04[b]	2.19±0.21[b]
Ash	1.20±0.01	1.21±0.03	1.19±0.01	1.16±0.02	1.22±0.02

Values are presented as mean ± SEM. The values with different superscript letters in the same row are significantly different ($P < 0.05$).

Table 6. Whole-body fatty acid profile of spotted bass (percentage of total fatty acids) fed the experimental diets for 8 weeks.

	NFD	HFD	HFD+COQ10-5	HFD+COQ10-20	HFD+COQ10-80
14:00	2.45±0.04	2.53±0.07	2.42±0.02	2.51±0.04	2.47±0.04
16:00	18.58±0.33^{a}	21.23±0.3^{b}	18.07±0.23^{a}	19.01±0.06^{a}	18.84±0.60^{a}
18:00	3.68±0.03^{ab}	4.15±0.07^{c}	3.48±0.09^{a}	3.56±0.03^{ab}	3.71±0.08^{b}
20:00	0.21±0.01	0.19±0.01	0.20±0.01	0.20±0.01	0.21±0.01
∑SFA	24.92±0.39^{a}	28.11±0.35^{b}	24.16±0.31^{a}	25.28±0.08^{a}	25.23±0.71^{a}
16:1n-7	7.00±0.27	5.78±0.10	5.80±0.10	6.13±0.10	5.97±0.19
18:1n-9	30.00±0.33	28.65±0.27	28.37±0.11	29.07±0.21	28.98±0.44
∑MUFA	37.00±0.29^{c}	34.06±0.06^{a}	34.17±0.09^{a}	35.20±0.14^{b}	34.95±0.06^{b}
18:2n-6	22.17±0.26^{a}	26.00±0.05^{c}	25.08±0.21^{b}	24.76±0.07^{b}	24.78±0.28^{b}
20:4n-6	0.48±0.01	0.52±0.01	0.52±0.01	0.51±0.01	0.50±0.02
∑n-6 PUFA	22.65±0.26^{a}	26.53±0.04^{c}	25.60±0.21^{b}	25.27±0.27^{b}	25.28±0.26^{b}
18:3n-3	2.53±0.06^{a}	3.60±0.03^{b}	3.43±0.07^{b}	3.32±0.04^{b}	3.40±0.15^{b}
20:5n-3(EPA)	2.33±0.06^{ab}	2.42±0.05^{b}	2.40±0.04^{ab}	2.21±0.04^{a}	2.23±0.09^{ab}
22:6n-3(DHA)	3.39±0.11^{ab}	3.67±0.02^{b}	3.26±0.01^{a}	3.21±0.08^{a}	3.19±0.16^{a}
∑n-3PUFA	8.25±0.16^{a}	9.69±0.08^{c}	9.09±0.12^{bc}	8.74±0.12^{ab}	8.82±0.39^{ab}
n-3/n-6 PUFA	0.36±0.01	0.37±0.01	0.36±0.01	0.34±0.01	0.34±0.02

Values are presented as mean ± SEM. The values with different superscript letters in the same row are significantly different ($P < 0.05$).

Table 7. Triacylglycerol (TAG), total cholesterol (TC), and non-esterified free fatty acids (NEFA) concentrations in liver of spotted seabass fed the experimental diets for 8 weeks.

Item	Test diets				
	NFD	HFD	HFD+COQ10-5	HFD+COQ10-20	HFD+COQ10-80
TAG （mmol/g）	1.39±0.11[a]	5.70±0.64[c]	2.12±0.29[a]	3.78±0.70[b]	3.61±0.19[b]
T-CHO (mmol/g)	4.52±0.41[a]	7.46±0.44[b]	5.55±0.21[a]	4.86±0.38[a]	5.45±0.65[a]
Liver NEFA (mmol/g)	0.17±0.01[a]	0.38±0.01[b]	0.23±0.07[a]	0.21±0.03[a]	0.28±0.02[ab]

Values are shown as mean ± SE. The values with different superscript letters in the same row are significantly different ($P < 0.05$).