


Effects of alternative dietary oils on lipid metabolism and related gene expression in hybrid grouper (♀*Epinephelus fuscoguttatus* × ♂*E. lanceolatu*)

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Abstract

An 8-week growth trial was conducted to evaluate effects of dietary oil sources on growth, enzymes activity and genes expression levels related to lipid metabolism of hybrid grouper (♀*Epinephelus fuscoguttatus* × ♂*E. lanceolatu*) juveniles. Seven iso-lipid (97 g/kg of dry matter) and iso-protein (503.5 g/kg of dry matter) experimental diets were formulated containing 50 g/kg fish oil (FO; acting as controls) or various vegetable oils (VOs): corn oil (CO), sunflower oil (SO), tea oil (TO), olive oil (OO), rice oil (RO) and mixed oil (MO; comprising equal amounts of these oils). Each diet was fed to triplicate groups of 40 fish for per repetition (15.09 ± 0.01 g) for 56 days. The results show that (a) alternative dietary oils had no significant effects on final weight compared with control group ($p > .05$); (b) compared with FO group, VOs significantly changed the contents of serum lipoproteins, cholesterol, triglycerides and the activity of liver lipid-metabolizing enzymes ($p < .05$); (c) CO group had the least effect on the serum lipoproteins, triglycerides and cholesterol of grouper compared with control; the activity of liver lipid-metabolizing enzymes in RO and control group was the closest; (d) the mRNA levels of $\Delta 6$ Fatty acid desaturase ($\Delta 6$ Fad), hormone-sensitive lipase (HSL) and lipoprotein lipase (LPL) were not significantly effected by lipid sources, but CO, TO, OO and MO significantly down-regulated the expression of fatty acid synthetase (FAS) mRNA level in liver, while RO opposite ($p < .05$); (e) vegetable oil significantly up-regulated peroxisome proliferator-activated receptor α (PPAR α) and peroxisome proliferator-activated receptor β (PPAR β) mRNA levels, while TO and RO down-regulated peroxisome proliferator-activated receptor γ (PPAR γ) mRNA levels ($p < .05$); and 6) MO significantly increased the mRNA levels of heart-type fatty acid-binding protein (H-FABP) and adipocyte-type fatty acid-binding protein (A-FABP) ($p < .05$), while other VOs had no effect on them ($p > .05$). In conclusion, dietary substitution of FO by VO in diet affected lipid metabolism of grouper, which may be regulated by PPARs.

KEYWORDS

fish oil, hybrid grouper, lipid metabolism, vegetable oil



1 | INTRODUCTION

Fresh water fish can convert C18-unsaturated FAs into long-chain polyunsaturated FAs (LC-PUFA), while sea water fish lack of this transformation ability (Ghioni et al., 1999; Tocher & Ghioni, 1999); therefore, a certain amount of LC-PUFA must be added to the diets of sea water fish (Bostock et al., 2010; Tidwell & Allan, 2015). Fish oil (FO) is an important high-quality lipid source for aquatic animals due to its high level of n-3 high unsaturated fatty acid (HUFA) (Calder, 2012). However, the demand for FO is increasing with the rapid development of the aquaculture industry, and the price of FO is rising gradually, which makes the cost of aquaculture keep rising. It has become one of the hotspots in the field of aquatic animal nutrition and feed science to find the substitute of FO. Vegetable oils (VO) have the advantages of high yield, wide source and low price, which make it become the preferred source substitute for FO. At present, corn oil (Lin & Shiau, 2007), sunflower oil (Bransden et al., 2003), tea seed oil (Han et al., 2013), olive oil (Li, et al., 2019) and rice oil (Gandomkar et al., 2013) have been used in aquatic animal feed production. Nevertheless, due to the large amount of linoleic acid (c18:2n-6) and linolenic acid (c18:3n-3) in VO, and the relative lack of LC-PUFA, replacing FO with VO will lead to the decrease of the content of LC-PUFA in diets (Yildiz et al., 2018), which will affect the lipid metabolism of fish, and further affect the antioxidant and anti-stress ability of fish (Peng et al., 2016).

The genome-wide expression analysis showed that peroxisome proliferator-activated receptors (PPARs) is a ligand-dependent transcription factor regulating genes related to lipid metabolism (Cunha et al., 2015). And LC-FA including n-3 HUFA are ligands of PPARs (Schoonjans et al., 1996). The liver is the most important site for vertebrates to metabolic FAs (FAs) from food, and it is also the main site for the enhancement of β -oxidation of FAs (Lock et al., 1989). Fatty acid-binding protein (FABP) can transport FAs to different sites for metabolism or storage. FABP is widely distributed in tissues and has a high affinity for fatty acids. It can transport FA from cell membrane to intracellular utilization site and plays an important role in FA metabolism (Di Pietro & Santomé, 2001). However, there are few studies on the effects of lipid sources on lipid metabolism and PPARs or FABP family genes in fish (Saramah et al., 2019).

Groupers are an important aquaculture species in coastal areas of China. The hybrid grouper (*♀Epinephelus fuscoguttatus* × *♂E. lanceolatu*) is a marine carnivorous fish which has the high economic and nutritional value and excellent taste (Wu et al., 2017). Studies have shown that the hybrid grouper has better growth performance and resistance compared with its parental fish (Faudzi et al., 2018). Meanwhile, the convenience of transportation makes it one of the most important species in China aquaculture markets. At present, there are many researches on the nutrition of juvenile hybrid grouper (Jiang et al., 2016; Wu et al., 2017; Yin et al., 2018), but the research on the relationship between lipid

source and lipid metabolism is limited (Li, et al., 2019). Therefore, the present study aimed to compare effects of VO substitute for FO on liver enzymes activity and gene expression related to lipid metabolism of juvenile hybrid grouper (*♀Epinephelus fuscoguttatus* × *♂E. lanceolatu*).

2 | MATERIAL AND METHODS

2.1 | Experimental diets

Seven iso-lipid and iso-protein diets were formulated containing 50 g/kg FO (acting as controls), corn oil (CO), sunflower oil (SO), tea oil (TO), olive oil (OO), rice oil (RO) and mixed oil (MO; comprising equal amounts of these oils), respectively. All ingredients were crushed and sieved through a sixty mesh sieve, then thoroughly mixed using the progressive enlargement method, as described by Ayisi and Zhao (2017). Then added oil and lecithin, rubbed them manually, putted them into V-type vertical mixer after sieving and mixed them evenly, and then added distilled water (300–400 ml/kg) to mix them evenly. The diets were processed into 2.0 mm and 2.5 mm diameter pellets by a twin screw extruder (F-26, South China University of Technology, Guangdong Province, China), air-dried to about 100 g/kg of feed moisture content at room temperature, then ground and sieved to an appropriate size and stored in ziploc bags at -20°C until use. The ingredients and approximate compositions of the trial diets were shown in Tables 1 and 2.

2.2 | Fish and feeding trial

All animal experiments were conducted strictly based on the recommendations in the “Guide for the Care and Use of Laboratory Animals” set by the National Institutes of Health. The animal protocols were approved by the Animal Ethics Committee of Guangdong Ocean University (Zhanjiang, China). Hybrid groupers (*♀Epinephelus fuscoguttatus* × *♂E. lanceolatu*) were purchased from a local hatchery at Nanshan Island (Zhanjiang China) and acclimatized to the experimental conditions for one week while being fed with a commercial diet at the Donghai Island Breeding base of Guangdong Ocean University (Zhanjiang China). After fasting for 24 hr, 840 hybrid groupers (mean initial body weight \pm standard error = 15.09 ± 0.01 g) were randomly distributed into 21 tanks (1,000 L; 0.8 m in water depth). Each type of experimental feed was fed to triplicate groups of fish twice daily (08:00 and 16:00) until apparent satiation was observed. The amount of food ingestion was recorded for 8 weeks. About 500 L water was exchanged to maintain water quality every day. Each tank was provided with one piece of polyvinylchloride (PVC) pipe of 20.0 cm (diameter) × 30.0 cm (length) as shelter for the fish (Lin et al., 2007). The temperature of the water ranged from 29–32°C, salinity was 28, dissolved oxygen was >7 mg/L, while nitrates remained <0.03 mg/L.

TABLE 1 Composition and nutrients levels of the test diets (air dry matter g/kg)

Ingredients	Test diets						
	FO	CO	SO	TO	OO	RO	MO
Fish meal	430.0	430.0	430.0	430.0	430.0	430.0	430.0
Soybean meal	50.0	50.0	50.0	50.0	50.0	50.0	50.0
Soybean protein concentrate	60.0	60.0	60.0	60.0	60.0	60.0	60.0
Casein	60.0	60.0	60.0	60.0	60.0	60.0	60.0
Wheat gluten	130.0	130.0	130.0	130.0	130.0	130.0	130.0
Wheat flour	150.0	150.0	150.0	150.0	150.0	150.0	150.0
Phospholipid	15.0	15.0	15.0	15.0	15.0	15.0	15.0
Fish oil	50.0	-	-	-	-	-	-
Corn oil	-	50.0	-	-	-	-	-
Sunflower oil	-	-	50.0	-	-	-	-
Tea oil	-	-	-	50.0	-	-	-
Olive oil	-	-	-	-	50.0	-	-
Rice oil	-	-	-	-	-	50.0	-
Mixture oil	-	-	-	-	-	-	50.0
Vitamin premix ^a	2.0	2.0	2.0	2.0	2.0	2.0	2.0
Mineral premix ^a	5.0	5.0	5.0	5.0	5.0	5.0	5.0
Calcium monophosphate	15.0	15.0	15.0	15.0	15.0	15.0	15.0
Antioxidant	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Attractant	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Choline chloride	5.0	5.0	5.0	5.0	5.0	5.0	5.0
Sodium carboxymethyl cellulose	10.0	10.0	10.0	10.0	10.0	10.0	10.0
Cellulose microcrystalline	16.5	16.5	16.5	16.5	16.5	16.5	16.5
Total	1,000.0	1,000.0	1,000.0	1,000.0	1,000.0	1,000.0	1,000.0
Proximate composition							
Moisture ^b	99.5	99.3	97.4	99.0	98.8	98.2	98.8
Crude protein ^b	507.5	504.7	504.9	506.7	504.5	508.9	505.6
Crude lipid ^b	96.2	98.1	96.8	95.5	95.6	94.7	98.2

^aVitamin and mineral premix were obtained from Qingdao Master Biotechnology Co, Ltd (Qingdao, China).

^bMeasured value.

2.3 | Sample collection

At the end of the 8-week period, the fish were fasted for 24 hr before collecting samples. All fish were collectively weighed and record final weight. After weighing, four fish from each tank were randomly selected for blood collection by 1-ml sterile syringes. Blood was placed in 1.5-ml microcentrifuge tubes and stored at 4°C for 12 hr. The blood was later centrifuged (4 000 rpm for 15 min at 4°C) and the serum collected and stored at -20°C for enzyme activity analysis. The liver and intestine of another three fish were collected randomly to analyse enzyme activity. Then, liver of another three fish from each tank were immediately separated and loaded in 2-ml enzyme-free centrifuge tubes containing RNAlater, after then stored at -80°C for subsequent analysis of relative gene expression.

2.4 | Methods of analysis

The contents of total cholesterol (TC), triglyceride (TG), very low-density lipoprotein (VLDL) and high-density lipoprotein (HDL) and the activities of FA decompose enzyme (FADE), lipoprotein lipase (LPL), hepatic lipase (HL), carnitine acyltransferase 1 (CACT1), adipose triglyceride lipase (ATGL) and FA synthetase (FAS) were analysed using commercial ELISA kits (Shanghai Enzyme-linked Biotechnology Co., Ltd., Shanghai, China). FA composition of diets was determined from the total lipid extract. FA methyl esters were prepared by acid-catalysed transmethylation of total lipids using boron trifluoride-methanol according to Shantha and Ackman (1990) and were analysed in a gas chromatograph (7890A, Agilent Technologies Inc. US).



Fatty acids	FO	CO	SO	TO	OO	RO	MO
C14:0	1.61	0.96	0.94	0.95	0.92	1.07	1.06
C15:0	0.22	0.1	0.09	0.14	0.09	0.11	0.12
C16:0	14.47	14.37	12.20	10.63	13.86	16.90	13.61
C17:0	0.57	0.25	0.24	0.13	0.09	0.16	0.32
C18:0	5.15	2.72	2.89	4.01	3.63	2.61	3.35
C20:0	0.54	0.41	0.16	0.28	0.43	0.50	0.37
C22:0	0.21	0.17	0.10	0.57	0.17	0.22	0.24
C24:0	0.00	0.15	0.00	0.21	0.10	0.24	0.14
∑SAFA ^a	22.77	19.13	16.62	16.92	19.29	21.81	19.21
C16:1n7	3.58	1.55	1.54	1.51	1.91	1.61	1.86
C17:1n7	0.31	0.09	0.10	0.09	0.08	0.08	0.12
C18:1n9	23.75	25.48	58.00	22.60	54.70	33.29	36.76
C20:1n9	3.72	1.55	1.56	1.44	1.49	1.78	1.85
C22:1n9	0.49	0.27	0.28	0.26	0.25	0.29	0.30
C24:1n9	0.47	0.22	0.25	0.21	0.20	0.22	0.26
∑MUFA ^b	32.32	29.16	61.73	26.11	58.63	37.27	41.15
C18:2n6	13.05	43.73	14.62	49.94	14.81	32.68	28.59
C18:3n6	0.20	0.00	0.00	0.00	0.00	0.13	0.06
C20:4n6	1.59	0.27	0.24	0.24	0.25	0.26	0.44
∑n-6PUFA ^c	14.84	44	14.86	50.18	15.06	33.07	29.09
C18:3n3	2.34	1.37	1.14	1.05	1.32	1.70	1.45
C20:5n3	14.90	3.08	2.75	2.78	2.77	2.99	4.60
C22:6n3	12.12	3.18	2.90	2.95	2.89	3.12	4.47
∑n-3PUFA ^d	29.36	7.63	6.79	6.78	6.98	7.81	10.52
∑n-3HUFA ^e	27.02	6.26	5.65	5.73	5.66	6.11	9.07

^aSaturated fatty acids.

^bMonounsaturated fatty acids.

^c18:2n-6, 18:3n-6 and 20:4n-6.

^d18:3n-3, 20:5n-3 and 22:6n-3.

^e20:5n-3 and 22:6n-3.

2.5 | RNA extraction and cDNA synthesis

TransZol UP (TransGen Biotech, Beijing, China) of 1 ml was added to the samples, and the total RNA was extracted according to the manufacturer's protocol. The quantity and quality of isolated RNA were detected at 260 and 280 nm using a NanoDrop 2000 spectrophotometer (Gene Company Limited, Guangzhou, China) and by electrophoresis in 1% agarose gel, respectively. The first-strand cDNA was synthesized using PrimeScript™ RT Reagent Kits with cDNA Eraser (Takara, Japan) according to the manufacturer's instructions. The cDNA was stored at -20°C for real-time quantitative polymerase chain reaction (RT-qPCR).

2.6 | Real-time quantitative polymerase chain reaction (RT-qPCR)

Real-time quantitative polymerase chain reaction (RT-qPCR) was performed in a 384-well plate with a 10 µl reaction volume

TABLE 2 Fatty acid composition of the experimental diets (% total fatty acids)

containing 5 µl of SYBR® Green Real-time PCR Master Mix, 0.8 µl of each primer, 1 µl of cDNA sample and 3.2 µl of RNase Free dH₂O. The PCR conditions were set using a thermal programmer at 95°C for 30 s, 40 cycles of 95°C for 5 s and 60°C for 34 s. Each sample was tested in triplicate. Primers of the reference gene (β-actin) and target gene were designed according to published sequences of groupers (Table 3). Threshold cycle (Ct) values were collected from each sample after finishing the process. The relative expression levels were calculated using the $2^{-\Delta\Delta Ct}$ method (Livak & Schmittgen, 2001).

2.7 | Statistical analysis

All data were firstly examined for homogeneity of variance using SPSS version 20.0 (SPSS Inc., USA). The results were analysed by one-way ANOVA and Tukey test, and $p < .05$ was deemed to be statistically significant. The results are presented as means ± standard error (SEM).

TABLE 3 Primers used RT-qPCR

Primers names	Forward and reverse primers sequence (5' to 3')	Genbank accession No.
$\Delta 6$ Fad-F/R	CCTTTGTTCTTCTGCCTCC/ AAGCGTCAGTATCCAGTTAGTT	KP295471.1
FAS-F/R	GGCGGCATTGTAGGCATTA/ CAATCAAAGTGTAGCCTCGGTAG	FJ196231.1
HSL-F/R	TGCTCCGAGATTTCGACAG/AGGATGCCTCCGAAATGC	KF049203.1
LPL-F/R	CCACCTGTTCATCGACTCCC/ TCGGACGGACCTTGTGAT	EU683732.1
PPAR α -F/R	AAAAGCACGGCTCATACTCAC/ GCTCTGGCAGCAGTGGAA	FJ196235.1
PPAR β -F/R	GCTACAGAGCAGCAGACA/CTCCTCATCTTCGCTTTC	DQ232867.1
PPAR γ -F/R	ACCGCAGCACGAAGAACAAC/ TGGACGCCATAGTGAACCC	KM052849.1
L-FABP	TCCCAGGAGAACTACGAGG/ TGCCGATGGTAAAGGAGTTG	GU982566.1
H-FABP	GTGGATGGCGACAAGGTGAC/ TTCCGTTGACTTCCTGACC	MF034870.1
A-FABP	ACTCAAACCTGGCGAGGAG/ GCCTTCTCATAGTGCGTGT	EU042103.1
β -Actin -F/R	ACTGCTGCCTCCTTCATC/ ACCGCAAGACTCCATACCAA	KU746361.1

Abbreviations: A-FABP, adipocyte-type fatty acid-binding protein; FAS, fatty acid synthetase; H-FABP, heart-type fatty acid-binding protein; $\Delta 6$ Fad, $\Delta 6$ Fatty acid desaturase; HSL, hormone-sensitive lipase; L-FABP, liver-type fatty acid-binding protein; LPL, lipoprotein lipase; PPAR α , peroxisome proliferator-activated receptor α ; PPAR β , peroxisome proliferator-activated receptor β ; PPAR γ , peroxisome proliferator-activated receptor γ .

TABLE 4 Growth performance of hybrid grouper fed different diets

Diet	FO	CO	SO	TO	OO	RO	MO
IW (g)	15.09 \pm 0.01	15.08 \pm 0.01	15.10 \pm 0.01	15.09 \pm 0.01	15.09 \pm 0.01	15.10 \pm 0.01	15.10 \pm 0.04
FW (g)	73.97 \pm 1.22	77.80 \pm 3.11	69.68 \pm 3.70	73.13 \pm 3.06	76.05 \pm 1.72	71.71 \pm 1.14	70.86 \pm 3.66

Note: Values are means \pm SE ($n = 3$).

Abbreviations: FW, final weight; IW, initial weight.

3 | RESULTS

3.1 | Growth performance

The initial weight and final weight are shown in Table 4. As we can see, alternative dietary oils had no significant effects on the final weight compared with the control group ($p > .05$).

3.2 | Biochemical indices and lipid metabolism enzyme activities in serum

The results for these parameters are shown in Table 5. Compared with the control group, FADE was significantly higher except the SO and TO groups ($p < .05$); furthermore, the maximum value appeared in the MO group and was significantly higher than that of other groups ($p < .05$). The LPL value of the RO and MO groups was not significantly different ($p > .05$), but was significantly higher than

that of other groups ($p < .05$). The LPL of the CO and SO groups was not significantly different compared with the control group ($p > .05$). Compared with the control group, the TC of the SO and TO groups was significantly higher ($p < .05$), while that of the OO and MO groups were significantly lower ($p < .05$). The TG and VLDL levels decreased significantly after alternative feeding, except in the CO group ($p < .05$). In contrast, the HDL level increased significantly after alternative feeding, except in the CO group ($p < .05$).

3.3 | Lipid metabolism enzyme activities in liver and intestine

The lipid metabolism enzyme activities in the liver are shown in Table 6. It was observed that, compared with the control group, the liver LPL content of the SO and MO groups was significantly higher ($p < .05$), with the MO group having the highest value. However, the CO group had a significantly lower value than control ($p < .05$).

**TABLE 5** Biochemical indices and lipid metabolism enzymes activities in serum of hybrid grouper fed different diets

Diets	FADE U/L	LPL U/L	TC nmol/L	TG nmol/L	VLDL nmol/L	HDL mg/dL
FO	476.97 ± 5.48 ^a	269.70 ± 11.78 ^a	6.81 ± 0.31 ^c	7.34 ± 0.12 ^c	12.78 ± 0.10 ^d	33.04 ± 1.42 ^{ab}
CO	576.55 ± 2.57 ^b	248.26 ± 11.53 ^a	7.01 ± 0.02 ^{cd}	7.60 ± 0.14 ^c	13.05 ± 0.07 ^d	31.05 ± 0.27 ^a
SO	473.48 ± 9.56 ^a	267.87 ± 2.92 ^a	7.69 ± 0.10 ^e	5.42 ± 0.03 ^{ab}	11.90 ± 0.10 ^c	42.67 ± 0.34 ^c
TO	473.81 ± 6.62 ^a	421.64 ± 3.78 ^c	7.51 ± 0.06 ^{de}	5.11 ± 0.10 ^{ab}	10.82 ± 0.13 ^b	51.43 ± 0.56 ^d
OO	571.02 ± 4.14 ^b	356.28 ± 23.32 ^b	5.31 ± 0.06 ^b	5.15 ± 0.36 ^{ab}	10.14 ± 0.20 ^a	37.28 ± 0.88 ^{bc}
RO	585.56 ± 1.71 ^b	527.53 ± 10.25 ^d	6.92 ± 0.01 ^{cd}	4.62 ± 0.18 ^a	10.19 ± 0.08 ^a	57.65 ± 0.80 ^e
MO	706.97 ± 6.15 ^c	516.22 ± 17.78 ^d	4.44 ± 0.12 ^a	5.84 ± 0.39 ^b	9.84 ± 0.10 ^a	53.06 ± 2.72 ^{de}

Note: Values are means ± SE (n = 3). Values with different superscripts in the same column are significantly different (p < .05).

Abbreviations: FADE, fatty acid decompose enzyme; HDL, high-density lipoprotein; LPL, lipoprotein lipase; TC, total cholesterol; TG, triglyceride; VLDL, very low-density lipoprotein.

TABLE 6 Lipid metabolism enzymes activities in liver of hybrid grouper fed different diets

Diets	LPL (U/mg.pro)	ATGL (mIU/mg.pro)	CACT1 (U/mg.pro)	FAS (U/mg.pro)	HL (U/mg.pro)
FO	0.35 ± 0.02 ^b	423.09 ± 4.32 ^d	1.02 ± 0.02 ^b	2.35 ± 0.03 ^d	35.68 ± 0.94 ^a
CO	0.24 ± 0.01 ^a	352.74 ± 5.48 ^{bc}	0.66 ± 0.04 ^a	1.71 ± 0.13 ^{abc}	34.48 ± 0.14 ^a
SO	0.56 ± 0.02 ^c	373.91 ± 10.61 ^c	1.03 ± 0 ^b	2.19 ± 0.07 ^d	53.64 ± 1.60 ^{cd}
TO	0.34 ± 0.03 ^b	316.74 ± 6.43 ^a	1.09 ± 0.01 ^{bc}	1.49 ± 0.03 ^{ab}	49.42 ± 0.33 ^c
OO	0.35 ± 0.02 ^b	325.48 ± 5.50 ^{ab}	1.21 ± 0.04 ^c	1.72 ± 0.02 ^{bc}	57.42 ± 1.52 ^d
RO	0.40 ± 0.02 ^b	361.31 ± 3.46 ^c	0.95 ± 0.04 ^b	2.05 ± 0.12 ^{cd}	43.57 ± 0.51 ^b
MO	0.65 ± 0.02 ^c	340.57 ± 11.47 ^{abc}	0.73 ± 0.02 ^a	1.36 ± 0.01 ^a	50.86 ± 0.25 ^c

Note: Values are means ± SE (n = 3). Values with different superscripts in the same column are significantly different (p < .05).

Abbreviations: ATGL, adipose triglyceride lipase; CACT1, carnitine acyltransferase; FAS, fatty acid synthetase; HL, hepatic lipase; LPL, lipoprotein lipase.

ATGL and FAS levels were significantly lower in all groups than those in controls, except for the FAS of the SO and RO groups (p < .05). However, HL levels were significantly higher, except in the CO group (p < .05). Compared with the control group, the CACT1 level of the OO group were higher (p < .05), but that of the CO and MO groups were lower (p < .05), there were no significant differences among other groups (p > .05).

The effects of the experimental diets on intestinal FADE activity are shown in Figure 1. Compared with the control group, the CO, SO, TO and OO groups were not significantly different (p > .05), while the RO and MO groups had higher FADE activity (p < .05).

3.4 | Gene expression related to lipid metabolism

Relative gene expression of lipid metabolism-related genes for liver are presented in Figure 2. Compared with control, CO significantly up-regulated $\Delta 6$ Fad mRNA expression level (p < .05) and there is no significant difference among the other groups (p > .05). Compared with control, CO, TO, OO and MO groups significantly down-regulated FAS mRNA expression level (p < .05) and RO group was opposite. MO group significantly up-regulated HSL mRNA expression level, and OO group significantly up-regulated LPL mRNA expression level (p < .05); there were no significant differences in

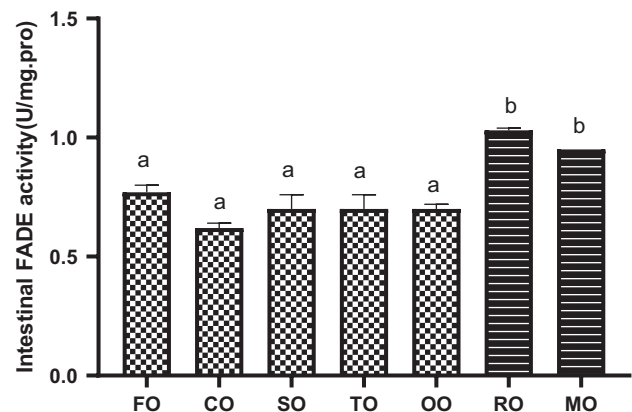


FIGURE 1 Intestinal FADE activity of hybrid grouper in different treatments. Values are means ± SEM (n = 3). Different letters assigned to the bars represent significant differences using Tukey's test (p < .05). FADE, fatty acid decompose enzyme

the other groups for HSL and LPL mRNA expression levels (p > .05). Compared with control, CO, OO and RO groups significantly up-regulated the PPAR α mRNA expression levels (p < .05); CO, SO and RO groups significantly up-regulated the PPAR β mRNA expression levels (p < .05); however, TO and RO groups significantly down-regulated the PPAR γ mRNA expression levels (p < .05). Meanwhile, CO,

TO and RO groups significantly down-regulated the L-FABP mRNA expression levels ($p < .05$); MO group significantly up-regulated the H-FABP and A-FABP mRNA expression levels compared with control ($p < .05$). There were no significant differences among the other groups for FABP family genes ($p > .05$).

4 | DISCUSSION

The results showed that dietary lipid source did not affect the FW of grouper after 8 weeks. A large number of studies have shown that VOs can completely or partially replace FO on the basis of meeting the essential FAs of marine fish (Fountoulaki et al., 2009; Yıldız et al., 2018). In this paper, 430 g/kg fish meal was added to the feed formula design, so that the fatty acids in the feed can meet the needs of grouper juveniles. This was consistent with previous study (Huang et al., 2016; Larbi et al., 2018; Peng et al., 2016).

In the study of fish oil substitution, increasing attention has been paid to changes in FAs (Fountoulaki et al., 2009; Jordal et al., 2007), because they also play essential roles in the digestion, absorption and synthesis of oils and lipids (Li et al., 2016; Monge-Ortiz et al., 2017). The primary pathways of lipid metabolism usually include digestion and absorption, lipid transport, lipid production and β -oxidation (NRC, 2011). Fish blood is closely related to metabolism, nutritional status and disease. When the fish body is affected by external factors and changes in physiology or pathology, this is primarily reflected in blood indicators. Blood lipid content is only a tiny fraction of the total body lipid content but it is very active in metabolism (Nakagawa, 1978). Exogenous food lipids absorbed by the intestinal tract, endogenous lipids synthesized by the liver, and mobilized adipose tissue must first pass through the blood to other tissues, and the transportation of fish lipid mainly depends on plasma (Hiraoka et al., 1979). Thus, blood lipid levels can reflect whole-body

lipid metabolism. In studies on *Dicentrarchus labrax* and *Oncorhynchus mykiss* (Figueiredo-Silva et al., 2015) and hybrid sturgeon (Liu et al., 2018), TG content decreased and TC content increased when FO was replaced with soybean or linseed oils. Previous studies on trout show that total replacement of FO with VOs leads to a decrease in plasma cholesterol (Luo et al., 2014; Richard et al., 2006), which is consistent with the case of the OO and MO groups in the present study. It is reported that HDL and VLDL levels indicate metabolic transport activity involving lipids (Ma et al., 2015). In this study, VLDL was significantly decreased and HDL was significantly increased by using VOs diet, except CO diet. Elevation of HDL may clean up excessive cholesterol.

Dietary lipid types not only affect the serum biochemical parameters of grouper, but also significantly affect the activities of LPL, HL, ATGL, CACT1 and FAS in liver. The liver is the main organ of FA β -oxidation and lipid synthesis in fish. Lipase mainly includes LPL and HL, collectively known as total lipase. LPL can catalyse the hydrolysis of TG carried by VLDL and chyle particles into glycerol and FAs for tissue storage and utilization (Feoli-Fonseca et al., 1998; Huang et al., 2017). HL has a variety of lipase activities and can be used as ligands to promote the entry of LDL and chyle particles into hepatocytes and directly participate in the reversal of HDL cholesterol and the decomposition of HDL cholesterol. It is also one of the enzymes related to endogenous TG metabolism in blood circulation, which has similar functions to LPL. It mainly acts on small granular lipoproteins and represents a major determinant of plasma HDL concentration (Cohen et al., 1999; Zamboni et al., 1993). The activity of HL influences HDL cholesterol and generates small dense LDL cholesterol, which implies a role for HL in atherosclerosis (Schiekofer et al., 2017). ATGL is a rate-limiting enzyme for hydrolysis of TC (Smirnova et al., 2006), and lack of ATGL will lead to hepatic steatosis. CACT plays an important role in transporting FAs through the mitochondrial inner membrane to produce energy (Vitoria

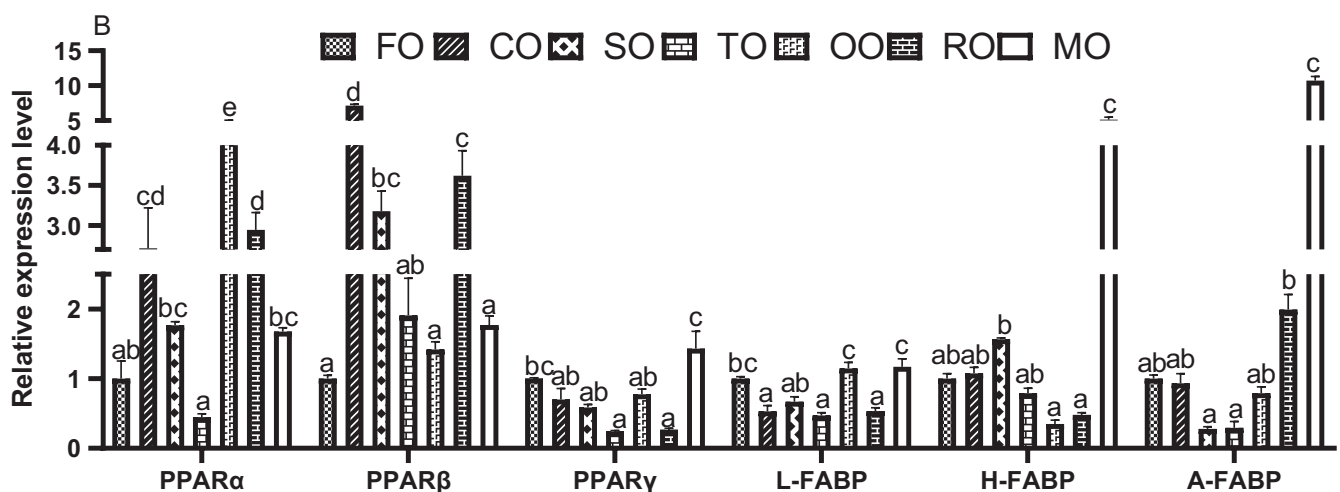


FIGURE 2 Relative expression of lipid metabolism-related genes for liver of hybrid grouper in different treatments. Values are means \pm SEM ($n = 3$). Different letters assigned to the bars represent significant differences using Tukey's test ($p < .05$). $\Delta 6$ Fad, $\Delta 6$ Fatty acid desaturase; FAS, fatty acid synthetase; HSL, hormone-sensitive lipase; LPL, lipoprotein lipase; PPAR α , peroxisome proliferator-activated receptor α ; PPAR β , peroxisome proliferator-activated receptor β ; PPAR γ , peroxisome proliferator-activated receptor γ ; L-FABP, liver-type fatty acid-binding protein; H-FABP, heart-type fatty acid-binding protein; A-FABP, adipocyte-type fatty acid-binding protein



et al., 2014). FAS is a key enzyme involved in the ab initio synthesis of FAs in animals. In teleosts, FAS exhibits a ubiquitous tissue-specific expression pattern, being higher in liver and adipose tissues (Liu et al., 2010). The results of the present study show that HL levels increased after dietary VO replacement (except in the CO group). This may be due to the fact that VO substitution increased the content of Σ MUFA in feed, and the fish can digest and absorb SAFA and MUFA preferentially (Rainuzzo et al., 1994), which increased the digestible FA content of the diet and promoted HL activities. However, ATGL and FAS levels were lower after replacement, which was related to the lower TG content of the VO groups and the inability to synthesize LC-PUFA from scratch. In addition, the results of LPL and CACT1 were different when FO was replaced by different VO, so enzyme activity may not be a sensitive evaluation index. Thus, the effect of lipid types on the lipid metabolism mechanism of groupers requires further study.

The regulation of lipid tissue synthesis and catabolism in animals is mainly through the regulation of the content and activity of key enzymes in lipid metabolism, and the level of gene expression of key enzymes determines the amount and activity of enzyme proteins (Yue et al., 2012). FAS activity and gene expression determine the speed of FA synthesis. It is generally believed that the determination of HSL activity in lipid and the concentration of FAs in blood can reflect the situation of lipid decomposition, and the expression and activity of HSL gene are affected by energy level, lipid type and fasting (Awad & Chattopadhyay, 1986; Stich et al., 1997; Sztalryd & Kraemer, 1994). LPL can catalyse the decomposition of triglycerides linked to proteins into glycerol and free FA, which play a key role in the metabolism of triglycerides (Yue et al., 2012). In this study, the substitution of vegetable oil for fish oil had no significant effect on HSL and LPL, but MO and OO significantly up-regulated the HSL and LPL gene expression level, respectively. These indicated that MO FAs was more balanced after various oils was mixed, which was conducive to the decomposition of lipid, while OO may be rich in some factors (antioxidant squalene) that promote the decomposition of lipid and TC. In addition, CO, TO, OO and MO significantly inhibited the FAS gene expression. However, Blake and Clarke (1990), Xu et al. (1999) indicated that PUFA can inhibit the expression of FAS mRNA in mouse liver, and the inhibition effect of n-3 PUFA was stronger than that of n-6 PUFA (Clarke et al., 1990). This was contrary to some results of this experiment, which may be due to the lipid deposition in liver after vegetable oil instead of fish oil (Yan et al., 2020).

PPARs family is an important transcription factor regulating metabolic balance, glucose, lipid and energy metabolism, insulin sensitivity, etc (Gross et al., 2017). In present study, differences in PPARs expressions were also affected among treatments, which likely resulted in different efficiency of lipid metabolism (Saramah et al., 2019). This was indicated that PPARs genes were highly influenced by dietary lipid sources. After replacing FO with VOs, the expression levels of PPAR α in CO, OO and RO groups and PPAR β in CO, SO and RO groups were significantly up-regulated. On the one hand, this may be related to the fact that the VOs up-regulated

the expression of pro-inflammatory factors in grouper tissues in our another paper (Yan et al., 2020), which was one of the targets of PPARs (Derosa et al., 2018). After PPARs is activated, the production of chemokines, cytokines and adhesion molecules will be reduced and anti-inflammatory effect will be produced by acting on inflammation-related transcription factors, so as to reduce tissue damage (Palomer et al., 2013). On the other hand, the reduction of dietary Σ n-3PUFA, Σ n-3/ Σ n-6PUFA and EPA/DHA, resulting from the substitution of dietary FO with VOs, may also be the reason for changing PPARs mRNA levels in grouper. Intracellular FAs and their metabolites can coordinate physiological processes through transcription factors, which are activated or inhibited by different FAS, thus controlling energy metabolism (Desvergne et al., 2006). However, the PPAR γ expression levels in TO and RO groups significantly down-regulated, which probable owing to different PPAR subtypes play different roles in adipocyte differentiation (Oku & Umino, 2008). PPAR α mainly regulates lipid metabolism by regulating FA metabolism-related genes, including FA β -oxidation and transport process, so as to reduce TG, free FA and VLDL synthesis. PPAR β -regulated gene expression is involved in cell energy metabolism, lipid and glucose utilization, maintaining energy balance. PPAR γ regulates the transcription of multiple genes involved in the differentiation of lipid precursor cells, regulates the glucose uptake of insulin-mediated peripheral tissues and increases insulin sensitivity (Ren et al., 2018). At the same time, PPARs expression also has tissue specificity (Shi et al., 2002) and plays different roles in lipid and energy dynamics and has different expression patterns (Saramah et al., 2019). In addition, the concentration and proportion of FAs in feedstuffs from different oil sources were different in present study, which had different effects on various PPAR subtypes. However, the effects of different concentrations and proportions of FAs on PPARs transcription in fish need further study.

FABPs can increase the solubility of FAs, transport FAs from lipid membrane to FA oxidation site, to triglyceride or phospholipid site, and enter into the nucleus to play its regulatory role (Di Pietro & Santomé, 2001). L-FABP mainly promotes the absorption, diffusion and metabolism of FA (Her et al., 2003); H-FABP mainly promotes FA binding and transport (Binas et al., 2003); A-FABP mainly regulates the oxidative energy supply of FAs and the metabolism of phospholipids and triglycerides (Chmurzyńska, 2006). In this study, CO, TO and RO significantly down-regulated the L-FABP, while MO significantly up-regulated the H-FABP and A-FABP. However, there was study shown that the expression of FABP3 (H-FABP) and FABP11 (the function is similar to A-FABP) in the white muscle of Atlantic salmon was significantly reduced after replacing FO with mixed VO (55 g/kg rapeseed oil, 30 g/kg palm oil and 15 g/kg linseed oil) (Torstensen et al., 2009), this is due to that the total replacement of FO with pure VOs reduced the absorption and transport of FAs in fish, while the MO group in this study was composed of FO and 5 kinds VOs to made its FAs complete, balanced and rich in special substances such as tea polyphenols, squalene and β -sitosterol, which are easy to lipid metabolism. Meanwhile, MO had no significant effect on L-FABP, but the ratio of MO to other group was the

largest. Under the mediation of these three genes, the serum TC and TG contents in MO group were significantly reduced compared with FO group.

5 | CONCLUSION

In summary, VOs changed serum biochemistry, lipoprotein level and liver lipid-metabolizing enzyme activity of grouper and also affected PPARs mRNA expression levels. We speculate that VOs may affect lipid metabolism of grouper by activating or inhibiting PPARs, and the concentration and/or proportion of FAs may be the activator or inhibitor of lipid metabolism process. The regulation of lipid metabolism pathway by FAs on PPARs needs to be further explored.

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CONFLICT OF INTEREST

The authors declare that there are no potential conflicts or competing of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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