

# Modification of Fillet Composition and Evidence of Differential Fatty Acid Turnover in Sunshine Bass *Morone chrysops* × *M. saxatilis* Following Change in Dietary Lipid Source

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**ABSTRACT:** Marine oil-based finishing diets have been used to restore fillet FA profile in several “medium-fat” fleshed aquaculture species, and a simple dilution model describing FA turnover has been established to predict and tailor final fillet composition. We evaluated finishing diet efficacy and suitability of the dilution model to describe patterns of FA change in a lean-fleshed model, sunshine bass. Two practical diets (45% crude protein, 15% crude lipid) were formulated, respectively containing corn oil (CO) or menhaden oil (MO) as the primary lipid sources. Sunshine bass (age 1 [~14 mo], 347 ± 8.6 g, mean individual weight ± SEM) were stocked in a recirculating system and fed the diets according to different feeding regimens during the final 28 wk of the production cycle. Control groups were fed the CO or the MO feeds exclusively; whereas, the remaining treatment groups were transitioned from the CO diet to the MO diet at 4-, 8-, or 12-wk intervals. Upon completion of the feeding trial, fish were harvested, and production performance and fillet composition were assessed. Replacing MO with CO as the primary lipid source in sunshine bass diets yielded fillets with distinctly different FA profiles; however, finishing with a MO-based diet offered significant compensation for CO-associated reductions in fillet long-chain highly unsaturated FA (LC-HUFA). Although complete restoration was not observed, we achieved significant augmentation of endogenous n-3 FA within 4 wk of feeding the MO diet, and observed a significant increase in LC-HUFA and a beneficial shift in n-3:n-6 FA ratio after 8 weeks. Simple dilution accurately predicted tissue composition for most FA; however, deviations from the model were noted, suggesting selective retention of n-3, PUFA, and LC-HUFA and preferential catabolism of saturates. We conclude marine oil-based finishing diets can rapidly augment beneficial FA levels in sunshine bass fillets; however, simple dilution models do not fully describe selective FA metabolism observed for this lean-fleshed fish.

Paper no. L10041 in *Lipids* 41, 1029–1038 (November 2006).

Marine oils derived from feed-grade, reduction fisheries often serve as the primary lipid constituents of aquaculture diets because of their high palatability to cultured animals, attractant properties, and historically widespread availability and competitive pricing. Unfortunately, exhaustive harvests and declining productivity of reduction fisheries (1) have caused marine oil prices to increase, along with pressure from conservationists to reduce use of marine animal-derived products (2). In addition to cost and availability issues, marine oils have recently been implicated as vectors of metals and various organic contaminants found in farm-raised fish (3), precipitating immense scrutiny of aquaculture from the scientific and lay communities. Although the validity of these concerns may be individually questioned (4,5), all professionals within fisheries and aquaculture recognize their cumulative impact and the limitations of capture fisheries in keeping pace with the growing demands of aquafeed production (5,6).

Sustainable expansion of aquaculture requires use of alternative lipid sources, but modified feed formulations may alter the final FA composition of cultured products and limit their nutritional value to human consumers. Marine oils contain substantial amounts of long-chain highly unsaturated FA (LC-HUFA, carbon chain length ≥20 and double bonds ≥3) that impart benefits beyond basic nutritive value (7,8) and have been shown to modulate a range of human health conditions (9,10,11,12). Tissue FA composition of fishes largely reflects the diet (13,14), and thus fillets of fish fed marine oil-based diets contain substantial amounts of bioactive LC-HUFA such as arachidonic (20:4n-6), eicosapentaenoic (20:5n-3), and docosahexaenoic (22:6n-3) acids. Conversely, oils derived from terrestrial plants do not contain these compounds, and reductions in LC-HUFA have been demonstrated following their incorporation in diets for sunshine bass *Morone chrysops* × *M. saxatilis* (15), rainbow trout *Oncorhynchus mykiss* (16), Atlantic salmon *Salmo salar* (17), gilthead seabream *Sparus aurata* (18), and red seabream *Pagrus auratus* (19). The functional nutritional value of these modified products is thereby reduced (20), linking alternative lipids with reductions in the nutritional benefit of consuming fillets from cultured fish.

To mitigate conflicting demands of sustainability and product value, aquaculture nutrition research groups have evaluated implementation of “finishing diets” at the end of the produc-

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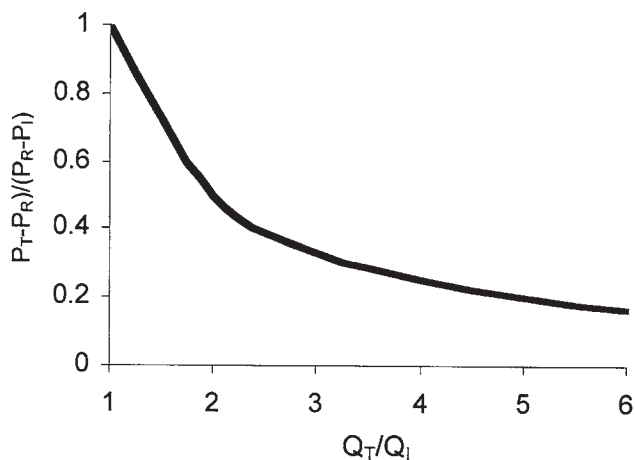
Presented at Aquaculture America 2006, February 13–16, 2006, Las Vegas, Nevada and Aqua 2006, May 9–13, 2006, Florence, Italy

Abbreviations: CO, corn oil; FCR, food conversion ratio; HSI, hepatosomatic index; IP, intraperitoneal; LC-HUFA, long-chain highly unsaturated FA; MO, menhaden oil.

tion cycle to restore LC-HUFA content to fillets of several aquaculture species (6). Partial restoration of fillet LC-HUFA content was achieved using finishing diets in “medium-fat” species (approximately 2–8% lipid in fillet, fresh-weight basis [21]) such as turbot *Psetta maxima* (22) and Atlantic salmon (23–25). A simple dilution model (Fig. 1) has been used to describe FA turnover following dietary modification in these species (14,26–28), and has been suggested as a means of gauging feed management and finishing strategies to tailor final FA composition of cultured products. Although alternative lipid sources have been widely researched in many aquaculture species, finishing diets and FA turnover have not previously been evaluated using a lean-fleshed model (generally <2% [21]). Sunshine bass are interspecific hybrids of female white bass *Morone chrysops* and male striped bass *M. saxatilis* (reciprocal cross hybrid striped bass) and are widely cultured in freshwater systems for their mild-flavored, lean flesh. Accordingly, our objectives were to evaluate production performance and fillet composition of sunshine bass fed a low LC-HUFA content (plant-derived lipid) diet, tissue FA composition and turnover following implementation of a high-LC-HUFA content (marine-derived lipid) finishing diet, and the suitability of the established dilution model to describe patterns of FA change in this fish.

## EXPERIMENTAL PROCEDURES

**Diet preparation and analyses.** We formulated two isocaloric, isonitrogenous practical diets to contain 45% crude protein and 15% crude lipid (Table 1) and had them manufactured (extrusion processed, floating pellets) by a commercial aquafeed producer. Diets were formulated to meet all known nutritional requirements of growing sunshine bass (29) and differed only in lipid source. The formulations were designed to be generally characteristic of diets used in sunshine bass culture, but represent a plant-derived lipid “production diet” and a marine animal-derived lipid “finishing diet” to be evaluated during grow-out and at the end of the production cycle, respectively. The production diet utilized corn oil (CO) as the predominant lipid source, whereas the finishing diet contained menhaden (*Brevoortia* spp.) oil (MO), thus generating two distinct dietary FA profiles (Table 2). Although other plant-derived products such as canola and soybean oils possess greater 18-carbon n-3 FA content than corn oil, they do not provide LC-HUFA. We have previously observed the high levels of 18:3n-3 associated with these oils to complicate interpretation of fillet n-3 content with respect to the n-3 LC-HUFA of greatest functional nutritional value to human consumers (15). In this sense, corn oil serves as an excellent negative control with respect to n-3 FA content and was selected for its utility from a hypothesis-testing perspective. Proximate analyses of triplicate diet samples were conducted according to standard methods for analysis of animal feeds (30) for moisture (Official Method 930.15), crude protein (Official Method 954.01), and ash (Official Method 942.05). Crude lipid was determined gravimetrically according to the method of Folch *et al.* (31). Crude lipid samples were re-



**FIG. 1.** Theoretical model of FA dilution within fish tissues following dietary change, where  $(P_T - P_R)/(P_R - P_I)$  represents the ratio of relative change in fillet FA and  $Q_T/Q_I$  represents the relative change in total lipid (14).

served for subsequent FA analysis (see section on FA analyses). Mean diet composition was confirmed as 9.6% moisture, 45.2% crude protein, 14.5% crude lipid, and 7.4% ash (dry matter, Table 1).

**Experimental design and feeding trial.** Before the study, feed-trained sunshine bass were obtained as fingerlings (Keo Fish Farms, Inc., Keo, AR, USA) and reared in-house to sub-market size (age 1 [~14 months],  $347 \pm 8.6$  g, mean individual weight  $\pm$  SEM) on standard, commercial sunshine bass grow-out diets. The fish were then stocked into a water recirculation system consisting of 30 270-L tanks and associated mechanical and biological filtration units at six fish per tank.

The feeding trial (28-wk duration) consisted of five feeding regimen treatment groups using the CO diet, the MO diet, or temporal combinations of both diets (Fig. 2). To establish similar nutritional status and initial FA profiles, the fish were fed assigned diets for a 16-wk baseline period. After 16 wks, one fish was removed from each replicate tank, euthanized, and sampled to determine baseline FA profile. After collection of the baseline samples, the remaining 12 wk of the experimental period were divided into three 4-week intervals for finishing diet implementation. The positive control treatment was fed the MO diet and the negative control treatment was fed the CO diet for the duration of the 28-wk trial. Three interval treatment groups were initially fed the production diet, followed by implementation of the finishing diet at 4-, 8-, or 12-wk before harvest. The five treatments established over the 28-wk feeding trial—0 (CO control), 4, 8, 12, and 28 (MO control) wk of MO diet use—were each randomly assigned to six replicate tanks, with tanks serving as experimental units ( $N = 6$ ). Fish were fed the appropriate diets every other day to apparent satiation, and any pellets remaining 1 h after feeding were removed and enumerated.

Temperature, dissolved oxygen (YSI Model 55 Oxygen Meter, Yellow Springs, OH, USA), and pH (WTW Model PH315i Handheld pH Meter, Weilheim, Germany) were mea-

**TABLE 1**  
**Formulation and Proximate Composition of Experimental Diets**

	Dietary formulation	
	CO (production) diet	MO (finishing) diet
Ingredient <sup>a</sup>		
Menhaden meal <sup>b</sup>	500.0	500.0
Menhaden oil	—	85.0
Corn oil	85.0	—
Wheat flour	336.8	336.8
Corn gluten	64.2	64.2
Mineral premix	1.0	1.0
Vitamin premix	6.0	6.0
Vitamin C (Stay-C 35%)	1.0	1.0
Choline (70%)	6.0	6.0
Proximate composition <sup>c</sup>		
Moisture	9.7	9.5
Protein	44.7	45.6
Lipid	14.4	14.5
Ash	8.5	6.2

<sup>a</sup>Expressed as g kg<sup>-1</sup> feed, dry-matter basis.<sup>b</sup>Typically contains 7.7% crude lipid (44); sufficient to meet LC-HUFA requirements of sunshine bass at present inclusion rate.<sup>c</sup>Expressed as percent dry matter (except moisture).**TABLE 2**  
**Total Lipid FA Composition of Experimental Diets<sup>a</sup>**

	Dietary formulation	
	CO (production) diet	MO (finishing) diet
14:0	1.98	9.57
15:0	0.18	0.78
16:0	15.26	23.97
17:0	0.18	0.48
18:0	2.95	4.72
20:0	0.38	0.42
22:0	0.11	0.16
Saturates	21.06	40.09
16:1n-7	1.98	11.18
18:1n-9	23.84	8.50
18:1n-7	1.32	3.28
20:1n-9	0.42	0.67
22:1n-11	0.20	0.13
22:1n-9	0.11	0.09
Monoenes	27.86	23.86
18:2n-6	42.19	5.42
18:3n-6	0.03	0.19
20:2n-6	0.07	0.18
20:3n-6	0.05	0.18
20:4n-6	0.52	1.50
n-6	42.86	7.46
18:3n-3	0.98	1.41
18:4n-3	0.27	1.77
20:3n-3	0.02	0.11
20:4n-3	0.12	1.04
20:5n-3	3.03	11.80
22:5n-3	0.52	2.28
22:6n-3	3.27	10.11
n-3	8.21	28.53
PUFA <sup>b</sup>	51.08	36.00
LC-HUFA <sup>c</sup>	7.53	27.03
n-3:n-6	0.19	3.82

<sup>a</sup>Mean FA values (relative mol% of total FAME) of triplicate samples. Totals and ratios of relevant FA classes are also provided.<sup>b</sup>Includes FA with double bonds  $\geq 2$ .<sup>c</sup>Includes FA with carbon chain length  $\geq 20$  and double bonds  $\geq 3$ .

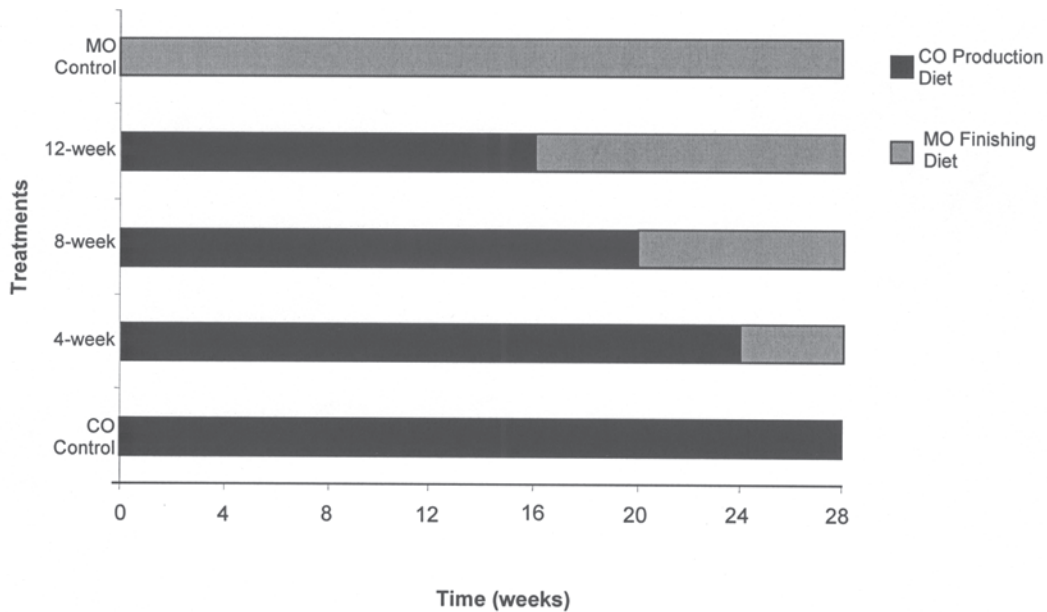


FIG. 2. Schematic representation of feeding regimen treatments with respect to timing of finishing diet implementation.

sured periodically and maintained at  $24.0 \pm 0.5^\circ\text{C}$ ,  $7.7 \pm 0.2 \text{ mg L}^{-1}$ , and  $7.5 \pm 0.3$ , respectively. Alkalinity ( $\text{mg CaCO}_3 \text{ L}^{-1}$ ), ammonia ( $\text{mg NH}_3\text{-N L}^{-1}$ ), nitrite ( $\text{mg NO}_2\text{-N L}^{-1}$ ), and nitrate ( $\text{mg NO}_3\text{-N L}^{-1}$ ) were measured weekly (DR/2010 spectrophotometer and digital titrator, Hach Company, Loveland, CO, USA). All water quality parameters were maintained within ranges suitable for sunshine bass culture (32). All culture and husbandry methods, as well as euthanasia and sample collection procedures described below, were conducted under the direction and approval of the Southern Illinois University Institutional Animal Care and Use Committee, protocol No. 04-016.

**Harvest, sample collection, and production performance.** Fish were harvested from tanks, weighed, euthanized by single pithing, and immediately packed in ice before processing. Livers and intraperitoneal (IP) fat masses were dissected from the viscera to calculate hepatosomatic (HSI; liver weight/whole body weight\*100) and liposomatic (IP fat weight/whole body weight\*100) indices. Survival, percent weight gain ( $[\text{average individual weight}_{\text{final}}/\text{average individual weight}_{\text{initial}}]*100$ ), and food conversion ratio (FCR; weight of food fed/weight gained) were calculated for each tank.

Fillets were harvested by one of four designated filleters, and dressout percentages were calculated as the ratio of the weight of skinless, boneless, J-cut fillets (without belly flap) to total weight of fish. One fillet from each fish was packaged in sterile, polyethylene bags (Whirl-pak<sup>®</sup>, Nasco, Fort Atkinson, WI, USA) and stored frozen ( $-80^\circ\text{C}$ ) before proximate and FA analyses.

**Proximate composition of fillet meat.** Fillet samples were analyzed using standard methods (30) for meat products to determine percent moisture (Official Method 950.46), crude protein (Official Method 981.10), and ash (Official Method 920.153). Crude lipid content was determined using the method of Folch

et al. (31). Crude lipid samples were reserved for subsequent FA analysis.

**FA analyses.** Crude lipid samples were subjected to acid-catalyzed transmethylation performed overnight at  $50^\circ\text{C}$  as described previously by Christie (33). The resultant FAME were separated using a Shimadzu GC-17A gas chromatograph (Shimadzu Scientific Instruments, Kyoto, Japan) equipped with a flame ionization detector (FID) fitted with a permanently bonded polyethylene glycol, fused silica capillary column (Omegawax 250,  $30 \text{ m} \times 0.25 \text{ mm i.d.}$ ,  $0.25 \mu\text{m}$  film). The injection volume was  $1.0 \mu\text{L}$ , helium was the carrier gas ( $30 \text{ cm/s}$ ,  $205^\circ\text{C}$ ), and the injector temperature was  $250^\circ\text{C}$ . A split-less injection technique (100:1) was used, and the temperature program was as follows:  $50^\circ\text{C}$  held for 2 min, increased to  $220^\circ\text{C}$  at  $4^\circ\text{C/min}$ , and held at  $220^\circ\text{C}$  for 15 min. Individual FAME were identified by reference to external standards (Supelco 37 Component FAME Mix, PUFA-1, and PUFA-3; Supelco, Bellefonte, PA, USA). All solvents used were of HPLC grade and obtained from Sigma Diagnostics Inc. (St. Louis, MO, USA).

**Evaluation of FA turnover and the dilution model.** The dilution equation suggested as a generalized model of FA turnover in fishes (14,26–28) may be expressed as

$$P_T = P_R + (P_R - P_I)/(Q_T/Q_I)$$

where  $P_T$  is the percentage of a FA in a test fillet at time  $T$  following dietary change,  $P_I$  and  $P_R$  are the percentages of the same FA initially (before dietary change) and in a reference fillet (fed the initial diet throughout), and  $Q_I$  and  $Q_T$  represent total lipid (total FA) initially and at time  $T$ , respectively. To test the suitability of the dilution model for sunshine bass, we compared actual FA composition with the fillet composition predicted by the generalized dilution model using baseline and

**TABLE 3**  
**Total Lipid FA Composition of Baseline Fillet Samples (Wk 16)<sup>a</sup>**

FA	Feeding regimen				
	CO control	4-wk	8-wk	12-wk	MO control
14:0	2.7 ± 0.2 <sup>b</sup>	2.3 ± 0.2 <sup>b</sup>	2.3 ± 0.2 <sup>b</sup>	2.6 ± 0.2 <sup>b</sup>	3.7 ± 0.2 <sup>a</sup>
16:0	19.2 ± 0.4 <sup>b</sup>	20.1 ± 0.4 <sup>b</sup>	20.4 ± 0.4 <sup>b</sup>	19.5 ± 0.4 <sup>b</sup>	21.3 ± 0.4 <sup>a</sup>
18:0	3.4 ± 0.3 <sup>a</sup>	3.8 ± 0.3 <sup>a</sup>	3.9 ± 0.3 <sup>a</sup>	3.4 ± 0.3 <sup>a</sup>	3.5 ± 0.3 <sup>a</sup>
Saturates <sup>b</sup>	31.2 ± 0.8 <sup>b</sup>	32.5 ± 0.8 <sup>b</sup>	32.5 ± 0.8 <sup>b</sup>	30.7 ± 0.8 <sup>b</sup>	37.2 ± 0.8 <sup>a</sup>
16:1n-7	6.0 ± 0.5 <sup>b</sup>	5.4 ± 0.5 <sup>b</sup>	3.6 ± 0.5 <sup>c</sup>	5.5 ± 0.5 <sup>b</sup>	8.1 ± 0.5 <sup>a</sup>
18:1n-9	26.3 ± 1.3 <sup>a</sup>	23.9 ± 1.3 <sup>a</sup>	24.5 ± 1.3 <sup>a</sup>	27.2 ± 1.3 <sup>a</sup>	24.1 ± 1.3 <sup>a</sup>
18:1n-7	2.3 ± 0.1 <sup>b</sup>	2.2 ± 0.1 <sup>b</sup>	2.1 ± 0.1 <sup>b</sup>	2.2 ± 0.1 <sup>b</sup>	2.9 ± 0.1 <sup>a</sup>
20:1n-9	1.4 ± 0.1 <sup>a</sup>	1.3 ± 0.1 <sup>a</sup>	1.2 ± 0.1 <sup>a</sup>	1.4 ± 0.1 <sup>a</sup>	1.5 ± 0.1 <sup>a</sup>
Monoenes <sup>c</sup>	36.2 ± 1.8 <sup>a</sup>	33.1 ± 1.8 <sup>a</sup>	31.8 ± 1.8 <sup>a</sup>	36.6 ± 1.8 <sup>a</sup>	37.0 ± 1.8 <sup>a</sup>
18:2n-6	19.5 ± 0.6 <sup>a</sup>	19.0 ± 0.6 <sup>a</sup>	20.4 ± 0.6 <sup>a</sup>	20.9 ± 0.6 <sup>a</sup>	10.0 ± 0.6 <sup>b</sup>
20:2n-6	0.9 ± 0.0 <sup>a</sup>	1.0 ± 0.0 <sup>a</sup>	0.9 ± 0.0 <sup>a</sup>	0.9 ± 0.0 <sup>a</sup>	0.6 ± 0.0 <sup>b</sup>
20:4n-6	1.2 ± 0.1	1.6 ± 0.1 <sup>a</sup>	1.4 ± 0.1 <sup>a</sup>	1.1 ± 0.1 <sup>a</sup>	1.5 ± 0.1 <sup>a</sup>
n-6 <sup>d</sup>	24.3 ± 0.6 <sup>a</sup>	23.8 ± 0.6 <sup>a</sup>	24.9 ± 0.6 <sup>a</sup>	25.7 ± 0.6 <sup>a</sup>	15.3 ± 0.6 <sup>b</sup>
18:3n-3	1.1 ± 0.1 <sup>a</sup>	1.0 ± 0.1 <sup>a</sup>	0.9 ± 0.1 <sup>a</sup>	1.0 ± 0.1 <sup>a</sup>	1.1 ± 0.1 <sup>a</sup>
20:5n-3	5.0 ± 0.4 <sup>b</sup>	5.4 ± 0.4 <sup>b</sup>	5.1 ± 0.4 <sup>b</sup>	4.3 ± 0.4 <sup>b</sup>	7.4 ± 0.4 <sup>a</sup>
22:5n-3	1.2 ± 0.1 <sup>b,c</sup>	1.3 ± 0.1 <sup>b</sup>	1.2 ± 0.1 <sup>b,c</sup>	1.0 ± 0.1 <sup>c</sup>	1.6 ± 0.1 <sup>a</sup>
22:6n-3	7.7 ± 1.1 <sup>a</sup>	9.5 ± 1.1 <sup>a</sup>	9.9 ± 1.1 <sup>a</sup>	6.7 ± 1.1 <sup>a</sup>	9.7 ± 1.1 <sup>a</sup>
n-3 <sup>e</sup>	4.2 ± 0.1 <sup>c</sup>	4.6 ± 0.1 <sup>b</sup>	4.2 ± 0.1 <sup>b,c</sup>	3.8 ± 0.1 <sup>c</sup>	5.0 ± 0.1 <sup>a</sup>
PUFA <sup>f</sup>	28.5 ± 0.5 <sup>a</sup>	28.3 ± 0.5 <sup>a</sup>	29.1 ± 0.5 <sup>a</sup>	29.6 ± 0.5 <sup>a</sup>	20.4 ± 0.5 <sup>b</sup>
LC-HUFA <sup>g</sup>	3.9 ± 0.2 <sup>b</sup>	4.5 ± 0.2 <sup>a</sup>	4.2 ± 0.2 <sup>a,b</sup>	3.6 ± 0.2 <sup>b</sup>	4.6 ± 0.2 <sup>a</sup>
n-3:n-6	0.2 ± 0.0 <sup>b,c</sup>	0.2 ± 0.0 <sup>b</sup>	0.2 ± 0.0 <sup>b,c</sup>	0.2 ± 0.0 <sup>c</sup>	0.3 ± 0.0 <sup>a</sup>
Bioactive					
LC-HUFA <sup>h</sup>	1.7 ± 0.1 <sup>b,c</sup>	1.9 ± 0.1 <sup>b</sup>	1.7 ± 0.1 <sup>b,c</sup>	1.5 ± 0.1 <sup>c</sup>	2.4 ± 0.1 <sup>a</sup>

<sup>a</sup>Mean values (relative mol% of total FAME) ± SEM of predominant muscle FA (≥1%) from replicate groups (1 fish subsampled from each of 6 replicate tanks per regimen treatment, N = 6) of sunshine bass according to feeding regimen. Totals and ratios of relevant FA classes and crude lipid composition are also provided. Note all treatment groups were fed the CO diet during the baseline period, except the MO control group, which was fed the MO diet throughout the feeding trial.

<sup>b</sup>Also includes 15:0, 17:0, 20:0, and 22:0.

<sup>c</sup>Also includes 22:1n-11 and 22:1n-9.

<sup>d</sup>Also includes 18:3n-6 and 20:3n-6.

<sup>e</sup>Also includes 18:4n-3, 20:3n-3, and 20:4n-3.

<sup>f</sup>FA with double bonds ≥2.

<sup>g</sup>FA with carbon chain length ≥20 and double bonds ≥3.

<sup>h</sup>Defined by authors as 20:4n-6, 20:5n-3, and 22:6n-3.

harvest data from the MO control and 12-wk MO treatments. The model was previously shown to be relatively robust to using whole body masses as surrogate measures of  $Q_T$  and  $Q_I$  when total adiposity changed little over time (14). As the proximate composition of fillets did not differ among treatment groups or change considerably over the 12-wk finishing period, we substituted average baseline body mass ( $Q_B$ ) and average mass at harvest ( $Q_H$ ) for  $Q_I$  and  $Q_T$ , respectively.

**Statistical analyses.** Production performance, fillet proximate composition, and FA profile data were subjected to ANOVA within the GLM framework of the Statistical Analysis System, version 9.1 (SAS Institute, Cary, NC, USA) to determine if differences existed among feeding regimen treatment groups. Actual and predicted FA profiles of the 12-wk MO group were similarly analyzed using ANOVA to determine if observed FA abundance differed significantly from predicted levels. For all statistical analyses, individual tanks were used as experimental units, and variation among tanks within treatments was used as the experimental error to test for significance. Differences were considered significant at  $P \leq 0.05$ .

## RESULTS

Feeding the CO diet during the baseline period significantly altered the FA profile of sunshine bass fillets, specifically reducing the level of n-3 and LC-HUFA in favor of n-6 and PUFA (double bonds ≥2), particularly 18:2n-6 (Table 3). After completion of the 16-wk baseline period, fillets of fish fed the CO diet (including CO control, 4-, 8-, and 12-week MO treatment groups) were significantly lower in 14:0, 16:0, 18:1n-7, 20:5n-3, and total saturates, and higher in 18:2n-6, total n-6, and total PUFA compared to fillets from fish that had been solely fed the MO diet (MO control group). Although some significant differences were observed among the CO fed treatment groups, that is, 16:1n-7, 22:5n-3, total n-3, total LC-HUFA, total bioactive LC-HUFA (20:4n-6, 20:5n-3, and 22:6n-3), and n-3:n-6 ratio; in general, these differences were numerically small and remained statistically distinct from the MO control group.

Implementation of the MO finishing diet during the final 12 wk of the experimental period significantly altered fillet FA composition, partially mitigating the effects of the CO diet on

**TABLE 4**  
**Total Lipid FA Composition of Harvest Fillet Samples (Wk 28)<sup>a</sup>**

FA	Feeding regimen				
	CO control	4-wk	8-wk	12-wk	MO control
14:0	2.3 ± 0.1 <sup>c</sup>	2.6 ± 0.1 <sup>b,c</sup>	2.7 ± 0.1 <sup>b</sup>	2.8 ± 0.1 <sup>b</sup>	3.4 ± 0.1 <sup>a</sup>
16:0	19.0 ± 0.3 <sup>b</sup>	19.4 ± 0.3 <sup>b</sup>	19.6 ± 0.3 <sup>b</sup>	19.6 ± 0.3 <sup>b</sup>	21.2 ± 0.3 <sup>a</sup>
18:0	3.4 ± 0.2 <sup>a</sup>	3.5 ± 0.2 <sup>a</sup>	3.6 ± 0.1 <sup>a</sup>	3.5 ± 0.2 <sup>a</sup>	4.0 ± 0.1 <sup>a</sup>
Saturates <sup>b</sup>	25.2 ± 0.4 <sup>c</sup>	26.1 ± 0.4 <sup>b,c</sup>	26.5 ± 0.4 <sup>b</sup>	26.8 ± 0.4 <sup>b</sup>	29.3 ± 0.4 <sup>a</sup>
16:1n-7	5.5 ± 0.2 <sup>c</sup>	5.8 ± 0.2 <sup>b,c</sup>	6.0 ± 0.2 <sup>b,c</sup>	6.3 ± 0.2 <sup>b</sup>	7.4 ± 0.2 <sup>a</sup>
18:1n-9	24.9 ± 0.6 <sup>a</sup>	23.9 ± 0.6 <sup>a</sup>	23.2 ± 0.6 <sup>a</sup>	24.1 ± 0.6 <sup>a</sup>	19.3 ± 0.6 <sup>b</sup>
18:1n-7	2.2 ± 0.1 <sup>c</sup>	2.4 ± 0.1 <sup>b,c</sup>	2.4 ± 0.1 <sup>b</sup>	2.5 ± 0.1 <sup>b</sup>	2.9 ± 0.1 <sup>a</sup>
20:1n-9	1.3 ± 0.0 <sup>d</sup>	1.4 ± 0.0 <sup>d</sup>	1.3 ± 0.0 <sup>d</sup>	1.4 ± 0.0 <sup>d</sup>	1.2 ± 0.0 <sup>d</sup>
Monoenes <sup>c</sup>	34.2 ± 0.8 <sup>a</sup>	33.8 ± 0.8 <sup>a</sup>	33.2 ± 0.8 <sup>a,b</sup>	34.5 ± 0.8 <sup>a</sup>	31.1 ± 0.8 <sup>b</sup>
18:2n-6	21.9 ± 0.8 <sup>a</sup>	18.8 ± 0.8 <sup>b</sup>	17.4 ± 0.7 <sup>b</sup>	17.3 ± 0.8 <sup>b</sup>	9.4 ± 0.7 <sup>c</sup>
20:2n-6	1.0 ± 0.0 <sup>d</sup>	0.8 ± 0.0 <sup>b</sup>	0.8 ± 0.0 <sup>b</sup>	0.8 ± 0.0 <sup>b</sup>	0.6 ± 0.0 <sup>c</sup>
20:4n-6	1.3 ± 0.1 <sup>c</sup>	1.4 ± 0.1 <sup>b,c</sup>	1.6 ± 0.1 <sup>b</sup>	1.4 ± 0.1 <sup>b,c</sup>	2.1 ± 0.1 <sup>a</sup>
n-6 <sup>d</sup>	24.6 ± 0.7 <sup>a</sup>	21.5 ± 0.8 <sup>b</sup>	20.2 ± 0.7 <sup>b</sup>	20.0 ± 0.7 <sup>b</sup>	12.4 ± 0.7 <sup>c</sup>
18:3n-3	1.0 ± 0.0 <sup>d</sup>	1.0 ± 0.0 <sup>d</sup>	1.0 ± 0.0 <sup>d</sup>	1.0 ± 0.0 <sup>d</sup>	1.1 ± 0.0 <sup>d</sup>
20:5n-3	4.8 ± 0.3 <sup>c</sup>	5.7 ± 0.3 <sup>b,c</sup>	6.3 ± 0.3 <sup>b</sup>	6.2 ± 0.3 <sup>b</sup>	8.9 ± 0.3 <sup>a</sup>
22:5n-3	1.2 ± 0.0 <sup>c</sup>	1.4 ± 0.0 <sup>b</sup>	1.5 ± 0.0 <sup>b</sup>	1.4 ± 0.0 <sup>b</sup>	1.9 ± 0.0 <sup>a</sup>
22:6n-3	8.3 ± 0.6 <sup>c</sup>	9.7 ± 0.6 <sup>b,c</sup>	10.2 ± 0.6 <sup>b</sup>	9.6 ± 0.6 <sup>b,c</sup>	13.9 ± 0.5 <sup>a</sup>
n-3 <sup>e</sup>	16.0 ± 0.9 <sup>c</sup>	18.7 ± 0.9 <sup>b</sup>	20.1 ± 0.8 <sup>b</sup>	19.0 ± 0.9 <sup>b</sup>	27.2 ± 0.8 <sup>a</sup>
PUFA <sup>f</sup>	40.7 ± 0.6 <sup>a</sup>	40.1 ± 0.6 <sup>a</sup>	40.3 ± 0.6 <sup>a</sup>	39.0 ± 0.6 <sup>a</sup>	39.5 ± 0.6 <sup>a</sup>
LC-HUFA <sup>g</sup>	16.2 ± 1.0 <sup>c</sup>	18.9 ± 1.0 <sup>b,c</sup>	20.3 ± 1.0 <sup>b</sup>	19.1 ± 1.0 <sup>b</sup>	27.6 ± 0.9 <sup>a</sup>
n-3:n-6	0.7 ± 0.1 <sup>c</sup>	0.9 ± 0.1 <sup>b,c</sup>	1.0 ± 0.1 <sup>b</sup>	1.0 ± 0.1 <sup>b</sup>	2.3 ± 0.1 <sup>a</sup>
Bioactive					
LC-HUFA <sup>h</sup>	14.4 ± 0.9 <sup>c</sup>	16.8 ± 1.0 <sup>b,c</sup>	18.1 ± 0.9 <sup>b</sup>	17.1 ± 0.9 <sup>b,c</sup>	24.9 ± 0.9 <sup>a</sup>

<sup>a</sup>Mean values (relative mol% of total FAME) ± SEM of predominant muscle FA (≥1%) from replicate groups (5 fish sampled from each of 6 replicate tanks per regimen treatment, N = 6) of sunshine bass according to feeding regimen. Totals and ratios of relevant FA classes are also provided.

<sup>b</sup>Also includes 15:0, 17:0, 20:0, and 22:0.

<sup>c</sup>Also includes 22:1n-11 and 22:1n-9.

<sup>d</sup>Also includes 18:3n-6 and 20:3n-6.

<sup>e</sup>Also includes 18:4n-3, 20:3n-3, and 20:4n-3.

<sup>f</sup>FA with double bonds ≥2.

<sup>g</sup>FA with carbon chain length ≥20 and double bonds ≥3.

<sup>h</sup>Defined by authors as 20:4n-6, 20:5n-3, and 22:6n-3.

fillet FA profile (Table 4). Although complete restoration (statistically equivalent to MO control group) was not observed, fillet 18:2n-6, 20:2n-6, 22:5n-3, total n-6, and total n-3 FA were significantly altered to reflect a MO-associated FA profile after a finishing period of 4 wk. After an 8-wk finishing period, significant restorative effects were observed for 14:0, 18:1n-7, 20:4n-6, 20:5n-3, 22:6n-3, total saturates, LC-HUFA, bioactive LC-HUFA, and n-3:n-6 FA ratio (Table 4). Fillet 16:1n-7 content also was observed to change following finishing diet implementation; however, significance was only noted after a finishing period of 12 wk.

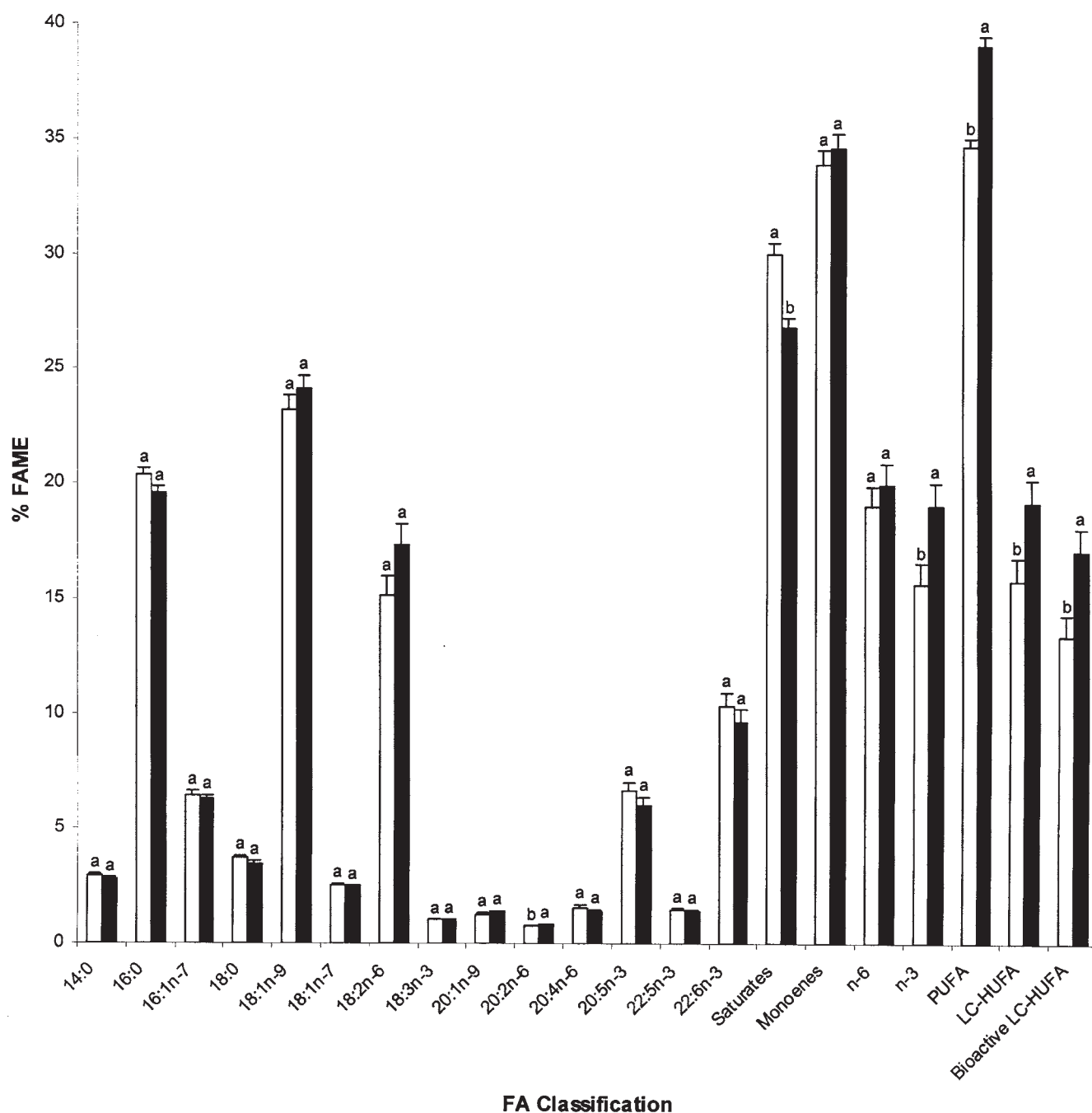
Comparison of actual FA profile of fillets from the 12-wk MO group with the profile predicted by the model indicated simple dilution adequately described turnover for a majority of the dominant fillet FA; however, significant deviation from predicted values were noted (Fig. 3). Actual abundance greater than predicted values was observed for 20:2n-6, n-3, PUFA, LC-HUFA, and bioactive LC-HUFA, indicating selective retention of these FA classes. Conversely, saturates were less abundant than predicted by the model, indicating selective catabolism of these FA.

Equivalent production performance was observed among all

treatment groups (Table 5). Survival (100 ± 0%, mean ± SEM), weight gain (206 ± 19%), food conversion ratio (1.7 ± 0.1), dressout (28 ± 0.4%), hepatosomatic (2.8 ± 0.1) and liposomatic (3.7 ± 0.5) indices were statistically equivalent among dietary groups and within acceptable ranges for sunshine bass production performance. Fillet moisture (75.3 ± 1.8%), crude protein (21.3 ± 1.2%), crude lipid (2.5 ± 0.5%), and ash (1.2 ± 0.1%) content were not affected by dietary treatment.

## DISCUSSION

Replacing MO with CO as the primary lipid source in sunshine bass diet yielded fillets with distinctly different FA profiles (Table 3). However, finishing with a MO-based diet offered partial compensation for CO-associated reductions in beneficial fillet FA (Table 4). Use of the CO diet increased fillet n-6 and PUFA content at the expense of n-3 and LC-HUFA. These fillets were significantly lower in saturates and higher in PUFA, but this is primarily due to an approximately twofold increase in 18:2n-6 content. High levels of 18:2n-6 and reduced n-3 FA incorporation skewed the n-3:n-6 FA ratio heavily in favor of n-6 FA. This suboptimal ratio, coupled with markedly lower



**FIG. 3.** Comparison of actual FA composition (relative mol%) of sunshine bass fillets (black bars) and predicted composition (white bars) based on the dilution model  $P_{12} = P_R + (P_R - P_0)/(Q_H/Q_B)$  where  $P_0$  and  $P_{12}$  are the percentages of a FA in the fillet before and after 12 wk of finishing diet implementation,  $P_R$  is the percentage of the FA in reference fillets from the MO control group, and  $Q_B$  and  $Q_H$  are the average body mass after completion of the baseline period and at harvest, respectively. Error bars represent  $\pm$ SEM, and columns within FA classifications with common superscripts are not significantly different ( $P \geq 0.05$ ).

levels of bioactive LC-HUFA, indicates these fillets would be of reduced functional nutritional value to human consumers. Implementation of the MO diet at the end of the production cycle had a restorative effect on fillet FA composition (Table 4), partially reversing the effects of using the CO diet. Significant restoration of endogenous n-3 FA was achieved within 4

wk of feeding the MO diet, and a significant increase in LC-HUFA and a beneficial shift in n-3:n-6 FA ratio was observed after 8 wk.

Finishing diets have been successfully used to augment MO-associated FA content of turbot (22) and Atlantic salmon (24,25) fed diets containing plant-derived lipids. Although the

**TABLE 5**  
**Production Performance and Fillet Proximate Composition<sup>a,b</sup>**

Parameter	Feeding regimen				
	CO control	4-wk	8-wk	12-wk	MO control
Production performance					
Survival	100 ± 0	100 ± 0	100 ± 0	100 ± 0	100 ± 0
Weight gain (%)	197 ± 19	199 ± 19	233 ± 19	212 ± 19	187 ± 19
Initial weight (g)	362 ± 19	343 ± 19	329 ± 19	333 ± 19	368 ± 19
Baseline weight (g)	490 ± 40	469 ± 40	482 ± 40	575 ± 40	608 ± 4
Harvest weight (g)	710 ± 23	660 ± 23	705 ± 23	707 ± 23	687 ± 23
FCR	1.7 ± 0.1	1.8 ± 0.1	1.6 ± 0.1	1.5 ± 0.1	1.8 ± 0.1
Dressout (%)	28 ± 0.4	27 ± 0.4	28 ± 0.4	27 ± 0.4	29 ± 0.4
HSI	3.0 ± 0.1	2.9 ± 0.1	2.8 ± 0.1	2.8 ± 0.1	2.6 ± 0.1
LSI	4.8 ± 0.5	3.8 ± 0.5	3.3 ± 0.5	3.1 ± 0.5	3.2 ± 0.5
Fillet proximate composition <sup>c</sup>					
Moisture (%)	75.9 ± 1.8	76.0 ± 1.8	73.4 ± 1.8	73.1 ± 1.8	78.3 ± 1.8
Protein (%)	21.7 ± 1.2	22.2 ± 1.2	21.8 ± 1.2	20.2 ± 1.2	20.6 ± 1.2
Lipid (%)	2.7 ± 0.5	2.2 ± 0.5	2.5 ± 0.5	3.2 ± 0.5	2.0 ± 0.5
Ash (%)	1.2 ± 0.1	1.2 ± 0.1	1.2 ± 0.1	1.3 ± 0.1	1.1 ± 0.1

<sup>a</sup>No significant differences were noted among feeding regimens for any of the parameters ( $P > 0.05$ ).

<sup>b</sup>Means ± SEM, 5 fish sampled from each of 6 replicate tanks per regimen treatment ( $N = 6$ ).

<sup>c</sup>Percent composition may not sum to 100 due to analytical margins of error and rounding.

negative effects of plant-derived lipid on fillet FA profile were partially reversed in these studies, the finishing period necessary to elicit significant compositional changes was longer (8–20 wk vs. 4–8 wk) for these species relative to our results. Moreover, many of these studies used diets containing in excess of 30% crude lipid, roughly twice the lipid content of the feeds we used to elicit similar composition changes.

Asymptotic dilution models suitably described FA turnover in Atlantic salmon (14,26), red seabream (27), and brown trout *Salmo trutta* (28), with rapid changes in fillet composition observed shortly after dietary modification giving way to diminishing effects over the growth period (Fig. 1). However, Jobling (14,26) cautioned the model, though apparently well-suited to medium-fat species, may not be appropriate for lean-fleshed fish. Structural phospholipids are dominant components of the lipid fraction in lean tissues, and it was suggested the relative unresponsiveness of the polar lipid fraction may cause FA turnover to deviate from the dilution model in these species (14,26). We found simple dilution accurately predicts tissue composition for most predominant FA, which are apparently deposited within muscle tissue with little-to-no specificity with respect to final tissue composition. However, deviations from the model were also noted, suggesting selective metabolism of certain FA classes (27). Specifically, we found total n-3 FA, PUFA, LC-HUFA, and especially bioactive LC-HUFA in greater than expected abundance, suggesting preferential retention of these FA; whereas actual levels of saturates were below predicted levels, suggesting preferential catabolism or deposition in other body compartments. Apparent processes of selective retention are further supported by differences in turnover rates observed for n-3, LC-HUFA, and bioactive LC-HUFA. Selective retention would imply faster turnover rates for FA selected for deposition compared to rates for other FA. Comparing the FA profiles of filets from the CO control and the 4-wk

MO treatments, the absolute percent change achieved after 4 wk of finishing diet use is consistently higher (mean 17%) for n-3, LC-HUFA, and bioactive LC-HUFA than other FA (mean 8%). Finally, it is important to note the preferentially retained FA classes were not those found in the greatest abundance in sunshine bass fillet polar fractions (namely 16:0, 18:1n-9, and 18:2n-6 [34]), and thus the selective processes we observed do not appear to be artifacts of greater total polar lipid. Accordingly, our results strongly suggest (1) n-3, PUFA, LC-HUFA, and bioactive LC-HUFA are selectively retained within sunshine bass muscle tissue; and (2) this process is functionally independent of changes in structural phospholipid elements during growth of muscle tissue.

Many fish species, including white bass *M. chrysops* (35), striped bass *M. saxatilis* (36), and their hybrids (37), have dietary requirements for 20:4n-6, 20:5n-3, and 22:6n-3 due to limited activity of appropriate enzymes to produce sufficient amounts of these bioactive LC-HUFA from 18-carbon precursors (38). Several groups have suggested limited endogenous and exogenous availability obliges moronids to conserve these FA (35,39–41). Our observation of bioactive LC-HUFA levels in excess of predicted values supports this hypothesis. The FA dilution model is adequate for estimating gross changes in fillet composition of fish species following dietary change; however, it does not appear to fully describe the pattern of FA turnover in lean-fleshed fish such as sunshine bass. Further experimentation carefully designed to address interspecific differences in biology, differences in gross dietary lipid content, and culture conditions is necessary to unequivocally define temporal patterns of FA change in fishes.

Nutritional and medical communities continue to recommend increasing human consumption of high-quality seafood to improve and maintain public health (42). With global seafood consumption at record highs and many food-grade

fisheries apparently static or in decline (1), aquaculture must assume a greater role in meeting seafood demand (43). Unfortunately, limited availability of high LC-HUFA-content feedstuffs places demands for increased quantity and quality of aquaculture products in juxtaposition. Partial or complete replacement of marine-derived lipid in aquafeeds reduces production costs, relieves harvest pressure on feed-grade fisheries, limits transfer and accumulation of contaminants, and reduces the environmental “footprint” of aquaculture. However, utilization of alternative lipids throughout the production cycle significantly alters fillet FA profile and reduces the functional nutritional value of cultured seafood products. By implementing finishing diets, aquaculturists may preserve or enhance the marketability of their products while decreasing production cost and dependence on finite resources. Although our results are promising, full realization of these goals will require the development of nutritional strategies to optimize fillet FA profile. Refining our understanding of FA turnover in fishes will provide the scientific foundation for successful application of these principles in aquaculture, and ultimately provide for optimal nutrition and management of aquatic livestock.

## ACKNOWLEDGMENTS

We thank Darren Ellison, Andrew Coursey, Adam Jarosinski, Craig Kasper, David Knuth, Heidi Lewis, Angela Merkel, Eve Poynter, Lance Schuler, and Bruce Tetzlaff for their help in data collection. We also thank Dr. Delbert Gatlin III for his comments and editorial suggestions provided during preparation of the manuscript. The material presented is based on work supported by the National Science Foundation under grant No. 0227925. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation. Funded by the National Science Foundation under grant No. 0227925.[EQ1]

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[Received July 18, 2006; accepted November 3, 2006]