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Growth response, plasma metabolites and intestinal brush border enzyme activity of sea bass fed diets including a blend of two marine microalgae

Maria Messina[1], Massimiliano Bruno[1], Gloriana Cardinaletti[1], Bianca Maria Poli[2], Graziella Chini Zittelli[3], Francesca Tulli[1] Emilio Tibaldi[1]

[1]Dipartimento di Scienze degli Alimenti, Università degli Studi di Udine, Italy
[2]Dipartimento di Scienze delle Produzioni Agro-Alimentari e dell'Ambiente, Università degli Studi di Firenze, Italy
[3]Istituto per lo Studio degli Ecosistemi, Consiglio Nazionale delle Ricerche, Sesto Fiorentino, (FI), Italy
Corresponding author: maria.messina@uniud.it

Microalgae have attracted increasing attention as animal feed supplements since they are natural sources of bioactive compounds which give them nutraceutical properties in addition to their basic nutritional value. More recently, dry microalgae biomass have also been proposed as raw materials in partial substitution for fish meal and oil in aquafeeds. The aim of this study was to evaluate the effects of including a blend of dried marine microalgae in low fish meal/fish oil diets on growth performance, levels of plasma metabolites and activity of brush border intestinal enzymes in adult European sea bass (*Dicentrarchus labrax*, L.). Two test diets (A1 and A2) were prepared by including a blend of Isochrysis galbana and Tetraselmis suecica dried biomass in a 2:1 w:w ratio to replace 15 and 45% fish meal protein and 10 and 30% fish lipid of a control diet (C) with a 50:50 fish to vegetable-protein-lipid ratio. One hundred eight fish (mean body weight 204±12.7 g) were randomly divided among 9 groups kept in a marine recirculating tank system ensuring nearly optimal water condition to sea bass (temperature 21°C, salinity 28‰). Fish were fed the test diets to visual satiety over 15 weeks according to a randomized design with 3 replicates per dietary treatment. At the end of the trial, final biomass, specific growth rate (SGR) and feed conversion ratio (FCR) were calculated per group and 6 fish per dietary treatment were sacrificed and immediately subjected to blood and intestine sampling for further analysis of plasma metabolite levels (glucose, cholesterol, triglyceride, total proteins and albumin levels) and activity of mucosal brush border enzymes in different sections. No diet-induced effects were noted in the final individual live weight, 420±14.5g, SGR, 0.68±0.003 and FCR, 1.7±0.11. Amongst plasma metabolites, only cholesterol and total proteins were affected by dietary treatments resulting in reduced levels only in fish given the diet highest in microalgae relative to controls (347.2 *vs.* 276.6 mg/dL and 5.90 *vs.* 5.37 mg/dl; respectively, P<0.05). The activity of the intestinal mucosal enzymes varied according to the different intestinal tracts but did not show major diet-dependent changes. This study suggests that a blend of dried marine microalgae biomass could further reduce reliance on fish meal and fish oil in practical diets for adult sea bass without adversely affecting growth response and digestive-absorptive functions.

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Dietary fish oil and stearate action on adipose lipid metabolism transcriptomics in periparturient dairy goats

Jessica Michela Caputo[1], Guido Invernizzi[1], Anna Campagnoli[1], Greta Farina[1], Mariella Ferroni[1], Alessandro Agazzi[1], Juan J. Loor[2], Giovanni Savoini[1]

[1]Dipartimento di Scienze veterinarie per la salute, la produzione animale e la sicurezza alimentare, Università degli Studi di Milano, Italy
[2]Department of Animal Sciences, University of Illinois at Urbana–Champaign, IL, USA
Corresponding author: jessica.caputo@unimi.it

The aim of this study was to evaluate the effects of saturated or unsaturated fatty acids on adipose mRNA level of genes involved in the major lipogenic metabolic pathways. Twenty-three second parity alpine dairy goats were assigned to three treatments: (C; n=8) fed a non fat-supplemented basal diet, (ST; n=7) fed a basal diet supplemented with stearic acid and (FO; n=8) fed a basal diet supplemented with fish oil. The supplementation started from the last week of gestation and lasted 21 days after kidding. Treatments supplied 30g/head/d extra fatty acids during the dry period and 50g/head/d during lactation. Individual blood samples were taken at 14, 7 and 2 days before the expected kidding day as well as 0, 2, 7, 14 and 21 DIM. Liver and adipose tissue biopsies from each experimental subject were harvested on days -7, +7 and +21 relative to parturition. Quantitative real-time RT-PCR of ADIPOQ, LPIN1, LPL, PPARG, SREBF1 and THRSP expression was performed. Data obtained were analyzed using the MIXED procedure of SAS. No differences were observed for milk production, milk composition, body weight and body condition score. Differences were detected for EB between C compared with ST and FO at day 7 (0.34 *vs.* -1.12 and 0.91 respectively; P,â§0.05). Serum cholesterol concentration was significantly higher in FO compared to C (P<0.01) and ST (P<0.05) at day 21. Fat supplementation significantly affected subcutaneous adipose genes involved in TAG synthesis (LPIN1), in the regulation of lipogenesis (THRSP) and nuclear receptor (SREBF1). No effects were observed for genes involved in LCFA uptake (LPL) and on the expression of the adiponectin (ADIPOQ). LPIN1 expression was significantly higher in the FO group compared with ST (1.46-fold *vs.* 0.59-fold; P<0.04) suggesting increased lipogenesis. THRSP (P=0.003) and SREBF1 (P=0.04) were up regulated before kidding and increasingly down regulated from 7 to 21 days postpartum. In conclusion, this study highlighted the important role of saturated or unsaturated fat administration in dairy goat diets to modulate mRNA expression of genes involved in TAG synthesis, regulation of lipogenesis and nuclear receptor.