TOWARDS A FREE WILD FISH AND SOY DIET FOR EUROPEAN SEABASS USING BY-PRODUCTS FROM FISHERY AND AQUACULTURE

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Introduction

The rapid development of aquaculture, in last decade, has made this sector one of the most important both at economic and social level gaining a main role in human nutrition, but this industry is severely limited by the lack of proteins intended for animal feed (as a competitor of human nutrition) (Wang et al. 2015). Fishery and aquaculture by-products can be considered as promising alternative feed ingredients in terms of nutritional quality and availability; however, these products are still underused resulting in economic and environmental issues (Gasco et al. 2020). At the same time, limiting the use of soy in fish diets has become necessary for the sustainability of aquaculture production. In past years, due to emerging health concern, gluten meal has become an even more significant cereal by-product of agriculture that is spreading thanks to its high protein content (Tapia-Hernández et al. 2019). The effects of total replacement of wild fish meal, (FM) fishoil (FO) and soy product (SP) by using fishery and aquaculture by-products and gluten were tested on the growth, gut health and fish quality parameters of European seabass.

Materials and Method

Five experimental diets (control C, 0FM100FO, 0FMFO, 0FMFO-50SP, 0FMFO-0SP) were formulated to totally replace wild fishmeal (FM), wild fish oil (FO) and soy protein using fisheries and aquaculture by-product, and gluten protein. 50 Sea bass individuals (initial weight: 75.96±6.99g) were reared in recirculated aquaculture system for 119 days, during the on-growing phase. Temperature was maintained constant at 22±0.5°, photoperiod was set on 12h day length through artificial light and water parameters, as salinity, dissolved oxygen and nitrogen compound were daily monitored. At the end of the trial, growth indexes, feed intake (FI), proximate composition, somatometric indexes, blood plasma biochemistry were detected. The assessment of gut microbiota (GM) was made by Next-generation sequencing. The assignment of all major NMR signals of the perchloric extracts was performed and a multivariate classification analysis was applied on the entire dataset to reveal metabolites important for characterizing samples according to the diets. Differences among treatments were considered significant at $P < 0.05$.

Results

Final body weight was significantly higher in diet C and 0FM100FO compared to other treatments. Specific growth rate and weigh gain were higher in C compared to 0FM100FO. 0FM0FO-50SP was lower than 0FM100FO, but meantime, 0FM0FO and 0FM0FO-0SP were lower compared to other treatments. FI values were significantly higher in 0FM0FO then 0FM0FO-0SP. FCR, was statistically lower in C compared to 0FM0FO, 0FM0FO-50SP and 0FM0FO-0SP. Values of proteins in 0FM100FO were significantly higher compared to 0FM0FO. Protein efficiency ratio was statistically higher in C then 0FM0FO, 0FM0FO-50SP and 0FM0FO-0SP, while 0FM0F0-0SP was higher than 0FM0FO and 0FM0FO-50SP. Gross protein efficiency was lower in 0FM0FO and 0FM0FO-50SP compared to C and 0FM100FO. Results of viscerosomatic index were statistically lower in diet C compared to 0FM0FO-0SP. 0FM0FO-0SP value of hepatosomatic index was higher compared to 0FM0FO-50SP, 0FM0FO and C, at the same time 0FM0FO-50SP was lower than 0FM0FO-0SP. Results of

Lipid efficiency rate and inorganic phosphorus shown a P-value lower than 0.05 but not specific difference among treatments was evaluated by multiple comparison Tukey's test. In animal fed with C diet, creatine value was higher confronted to other treatments. Results of Uric acid shown higher value in diet C confronted to 0FM0FO, 0FM0FO-50SP and 0FM0FO-0SP. Alkaline phosphatase and Total protein were both lower in diet 0FM100FO compared to 0FM0FO-0SP. Magnesium shown higher value in diet C compared to 0FM0FO-0SP. High density lipoprotein value was lower in 0FM0FO compared to 0FM0FO-0SP. Albumine/Globulin was higher in 0FM0FO compared to 0FM0FO-0SP. Values of Lactate were lower in OFM100FO, 0FM0FO-50SP and 0FM0FO-0SP compared to other treatments.

Discussion

This study highlighted the possibility to total replace wild FM and FO using by-product from fisheries and aquaculture with only a marginal reduction of the overall performance and considering the positive implication on the economic and environmental impact at industrial level. In particular, when only wild FM was totally replaced by fisheries by-product no differences were recorded, while the combine replacement of wild FM and FO resulted in a performance reduction. Interestingly, the further replacement of soy products by alternative plant proteins in the free wild fish diet did not result in a decline of performance. As the fish quality is a broad and complex concept embracing many components, the metabolomics study applied in this work will provide a comprehensive descriptor consisting of a pattern of molecular components undergoing metabolic changes related to the different diets.

Reference

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