**Annex S1: Detailed material and methods**

1. **qPCR analysis**

The various organs in each sample (i.e., spleen, kidney, gill, liver, and brain) were pooled and subjected to a one-minute treatment at 15 Hz using TissueLyser II (QIAGEN, Hilden, Germany). The RNeasy® Mini Kit (QIAGEN) was used to extract RNA from 30 mg of each sample in accordance with the manufacturer's instructions. ThermoFisher Scientific's NanoDrop Lite Spectrophotometer was used to quantify and evaluate the quality of all RNA extracts (A260/A280 ratio). All extracts were standardized in RNAase-free water to reach a 10 ng/μL final concentration.

Using Random Hexamers and SuperScriptTM II Reverse Transcriptase (Invitrogen) in accordance with the manufacturer's procedure, 10 ng of RNA was reverse transcribed into cDNA to produce first-strand cDNA. Using sequences deposited in GenBank (DQ524995.1 EU805481.1), the primer set for *HSP70* in seabream (Forward primer: 5'-ATCAGCGACAACAAGAGAGC -3' and Reverse primer: 5'-GGTGATGGAGGTGTAGAAGTC -3') was designed. In a 25 μL PCR reaction, one μL of cDNA and one μL of plasmid, in triplicate, were utilized along with 0.4 μM of forward and reverse primers and SYBR Green Master Mix (QIAGEN). The *HSP70* primers produced a 176 bp fragment. Since SYBR Green technology was used for all reactions, a dissociation step was added to the amplification cycle to determine the products' specificity. The plasmid was amplified three times at 10-fold dilutions in order to assess the assays' limit of detection.

1. **Swimming activity**

The tag was designed to measure acceleration over two axes (X and Z; tailbeat acceleration), excluding the backward/forward movement Y-axis. Energy expenditure was assessed by measuring acceleration (Alfonso et al. 2021). With a low-power frequency (40–80 seconds of transmitting delay) and a sampling rate of 12.5 Hz, the accelerometer tag implanted in the fish transmitted the tag ID and coded values corresponding to the acceleration of the tagged fish to an acoustic receiver Vemco VR2W (AMIRIX Systems Inc.) placed at the bottom of each tank. At T2, the receiver was taken out of the tank, and the VUE software (AMIRIX Systems Inc.) was used to extract the data from the receiver. The accelerometer tags yielded acceleration readings between 0 and 255, which were shown in arbitrary units (AU). The manufacturer's given equation was utilized to convert the received numbers into acceleration: acceleration (m/s2) = 0.01922(x), where the adimensional value that tags return is x.

1. **Statistical analyses**

Weight differences were evaluated using a linear mixed model with the sampling time (T0, T1, and T2), the diet group (control vs. innovative) and interaction between the two factors as fixed effects, while the fish ID was added as a random effect. A post-hoc test computing estimated marginal means (*emmeans* package; Lenth 2019) was performed to test differences between sampling times. Additionally, the SGR, FCR, and PER were compared between the two diet groups using Wilcoxon tests since conditions for application of linear models were not fulfilled.

For the analysis of physiological parameters related to stress, health, and welfare (i.e. hematocrit, glucose, lactate, cortisol, hemoglobin, RBCC, *Hsp70*), linear mixed models (packages *lme4* [Bates et al. 2014] and *lmerTest*;Kuznetsova et al. 2017) were applied to each parameter using the diet (control vs. innovative), the sampling time (T1 and T2) and the interaction between these two as fixed factors, with the tank included as a random factor. Cortisol was the only parameter analysed differently, using a generalized linear mixed model with a Gamma family and a log-link with the diet (control vs. innovative), the sampling time (T1 and T2), and the interaction between these two as fixed factors, and with the tank included as a random factor. When the interaction was non-significant, it was removed from the final model. A post-hoc test computing estimated marginal means was performed when the interaction between sampling time and diet was significant. Glucose, hemoglobin, lactate, and *Hsp70* values were log-transformed to meet the conditions of application. Regarding the analysis of immune parameters and protein content (i.e. total proteins, prealbumin, albumin, alpha 1, alpha 2, beta 1, beta 2, gamma, and immunoglobulin M levels), linear mixed models or linear models (i.e. when the tank effect was null) were used with the sampling time (T1 and T2) and the diet (control and innovative diets) as fixed factors and, if applicable, the tank as a random factor. Alpha 1 and beta 1 were log-transformed to meet the conditions of application. When the interaction was non-significant, it was removed from the final model.

We employed a generalized linear mixed model with Gamma family and log link (library *lme4*) to assess swimming activity. The fish individual was included as a random factor while the diet (control *vs* innovative), time of day (day *vs* night), and the interaction between diet and time of day were used as fixed factors. Furthermore, the entire dataset of swimming activity values collected by tags during the experiment was employed to analyse the frequency distribution between the two diets. This was done by combining the swimming activity values by slots of 10 (i.e., 0–10, 11–20, [...], 241–250, 251–255). A Chi-squared test was first performed, followed by row-wise z-tests (package *rstatix* [Kassambara 2023]) with p-values adjusted by Bonferroni correction in order to compare proportions of values between the two diets slot by slot.

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