

Single-cell proteins from *Candida utilis* as an alternative protein source in practical diets for gilthead seabream (*Sparus aurata*): a study on growth, immune response, and gut microbiota.

INTRODUCTION

The increasing global need to find alternative and sustainable protein sources has promoted research in the field for non-conventional feed ingredients, such as single-cell proteins (SCPs). SCPs production is based on the fermentation of microorganisms like yeast, bacteria, microalgae, and filamentous fungi. SCPs from yeast improve feed efficiency and can reduce inflammatory processes in fish. This study was undertaken to assess the effects of different inclusion levels of SCPs from yeast *Candida utilis* on growth, performance, immune response, and gut microbiota of gilthead seabream reared under normal and after suboptimal conditions.

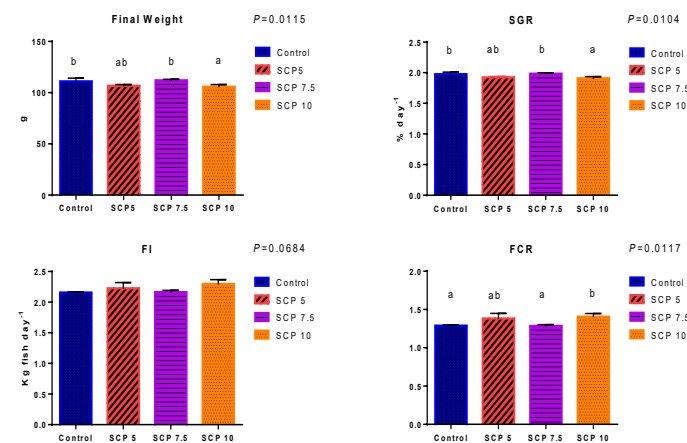
MATERIAL AND METHODS

Diets: Fish were fed over 76 days with four experimental diets containing different inclusion levels of SCPs meal (0% CTRL, 5% SCP5, 7.5% SCP7.5, and 10% SCP10) in substitution to FM.

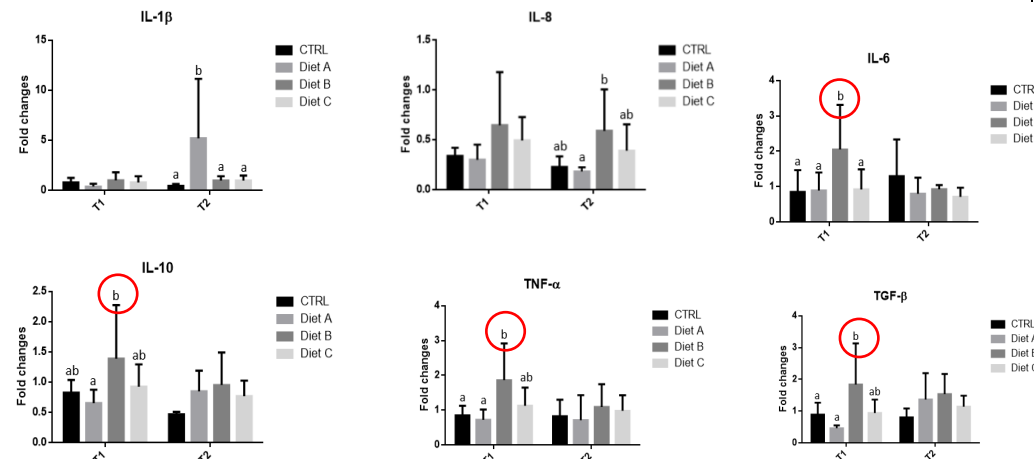
Stress challenge: After the end of the trial, fish were subjected to suboptimal rearing conditions (high water temperature, 30°C, and low oxygen, 70% saturation level) for 8 days.

Sampling: a piece of distal intestine and distal intestine content were collected to assess the expression of genes Interleukin 1 β , Interleukin 8, Interleukin 10, Interleukin 6, Transforming growth factor β , Tumor necrosis factor α , and gut microbiota at the end of the trial (T1) and after suboptimal rearing conditions (T2). Data were analyzed by a one-way ANOVA followed by Tukey's multiple comparison test.

Growth

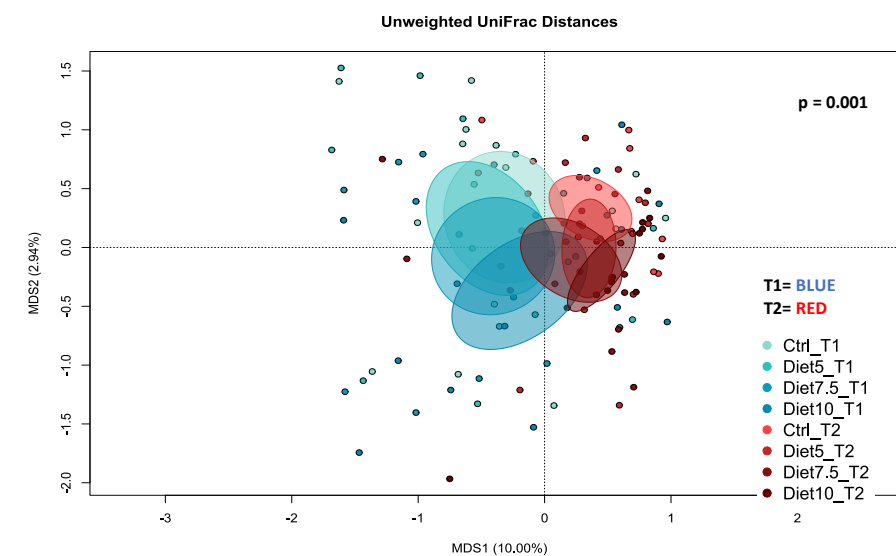


Immunological analysis



RESULTS

Gut Microbiota



CONCLUSIONS

- ✓ SCPs meal from *Candida utilis* can replace 5% of FM without compromising the growth and feed utilization.
- ✓ The 7.5 % inclusion level seems to show the best growth performance.
- ✓ 7.5% inclusion of SCP diet seems to enhance the local immune response.
- ✓ The environmental challenge of 1 week modified the gut microbiome in all groups