Ex Vivo Assessment of Macroalgae Extracts on Antioxidant and Immune Markers in European Seabass (*Dicentrarchus labrax*)

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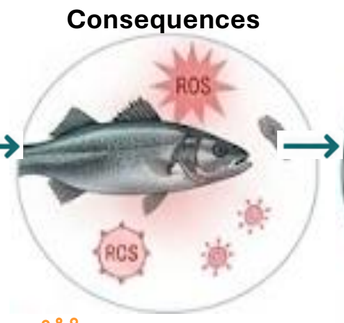
Introduction

Aquaculture Intensification



- High stock densities
- Poor water quality
- Environmental stressors

Consequences



- Oxidative stress
- Impaired growth
- Increased disease susceptibility
- Welfare decline

Current Approach



- Antibiotic resistance
- Environmental impact
- Consumers concerns

Macroalgae as Alternative



- Reach in bioactive compounds
- Immunostimulant potential
- Antioxidant capacity
- Circular economy

AIM

Evaluate the effect of different macroalgae extracts on the immune and antioxidant responses in European seabass intestine using an ex vivo model

Antioxidant defense + Immune response

Material and Methods



High-solid loading alkaline hydrolysis

Nades extraction 1/10 (W/V) ratio and incubated at 70°C 2h

Ex Vivo

1. Intestinal explants incubated with algal extracts for 2 h at 22°C, 100 rpm



2. Challenge with 0.04% H_2O_2 for 2 h at 22°C, 100 rpm

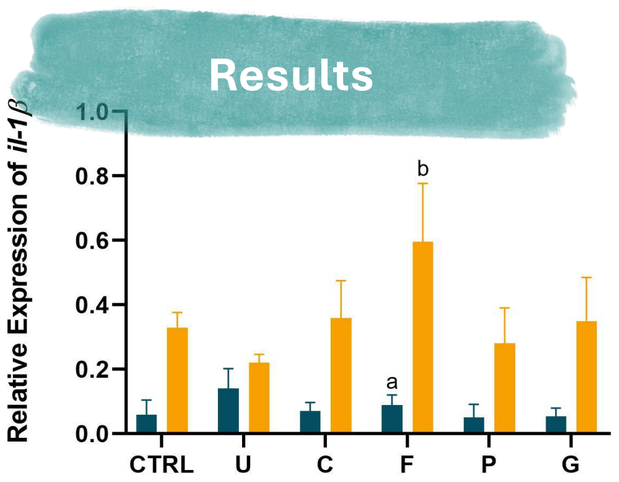


Gene expression analysis by Real-time PCR



- Immunity genes
- Oxidative stress genes

Results



CTRL- Control
U - *Ulva rigida*
C - *Codium tomentosum*
F - *Fucus vesiculosus*
P - *Palmaria palmata*
G - *Gracilaria gracilis*

Relative expression of *il-1β, tnf-α*, *cox2, casp9, cat, sod,* and *gpx*. Values are presented as means (n=6) and standard error (SE); Orthogonal contrasts were made to compare each macroalgae treatment with the control within the pre-challenge or challenge, and between pre-challenge and challenge values within each treatment: ★ denotes differences to the Control before the challenge; + denotes differences to the Control after the challenge; a and b denote differences between the pre-challenge and challenge within the same treatment.

Conclusion

The challenge induced a clear immune and oxidative stress response, with marked modulation depending on treatment.
Pro-inflammatory genes *il-1β* upregulated after the challenge in *F. vesiculosus* . In contrast, antioxidant-related genes (*sod and gpx*) generally showed higher expression prior to the challenge and were reduced post-challenge across most treatments, suggesting a downregulation of antioxidant defenses under stress conditions.

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