

## Final Report

# Brilliant Marine Research Idea 2025

This report presents the results of research conducted under the Brilliant Marine Research Idea grant, supported by The Sea as a Good Cause (VLIZ philanthropy).

## 1. General information

Title of the idea	Exploring <i>Laminaria ochroleuca</i> and <i>Laminaria digitata</i> hybrid transcriptomes
Name PhD student	Sofie Peeters
Name supervisor	Olivier De Clerck, Sofie Vranken, Willem Stock
Flemish University or University College	Universiteit Gent

## 2. Brilliant Marine Research Idea – Report about the activities

### Abstract

Kelps, which are large brown seaweeds, are foundational organisms in cold and temperate marine ecosystems. They sustain an enormous amount of biodiversity, while also delivering numerous ecosystem services. Yet, kelps are under global decline due to warming oceans, eutrophication, and overgrazing. Understanding how these seaweeds function and interact with their environment is therefore crucial to anticipate future trends.

In Europe, the cold kelp species *Laminaria digitata* and the warm-temperate kelp species *L. ochroleuca* increasingly co-occur as *L. ochroleuca* loses habitat range in the south but expands northward due to climate change. Recent work demonstrated that *L. ochroleuca* and *L. digitata* can hybridize, raising the possibility that hybridization may alter thermal tolerance as a result of unique, hybrid gene expression profiles. This study investigates the performance and thermal response of reciprocal hybrids to assess their potential ecological significance under future warming.

*L. ochroleuca* and *L. digitata* inter and intra crossings were created for this experiment using the same strains recently proven to hybridise. Hybridisation was confirmed with microsatellite markers. Juvenile kelps (3 months old) were exposed to four different temperatures (control: 12°C, 18°C, 22°C and 24°C), simulating increasingly intense heatwaves. Growth of the kelps was assessed through surface area calculation. After 18 days, the individuals were harvested for RNA sequencing to characterize transcriptional responses (analysis ongoing).

The hybrid kelp outperformed the cold parental kelp species *L. digitata* in terms of growth rate across all temperatures tested. Additionally, hybrids survived above 22°C as opposed to the intra *L. digitata* crossings which showed extensive bleaching. As the growth of hybrids with *L. ochroleuca* mothers matched or exceeded the performance of the other crosses across the entire temperature range, we have shown that maternal effects outweigh paternal effects on the thermal response and that hybridization can generate phenotypes with enhanced thermal resilience.

This research provides a first insight into the dynamics of hybridization and adaptation of two of Europe's most important kelp species, improving our ability to predict their vulnerability and resilience to our continuously changing oceans.

## Intro

Kelps, which are large brown seaweeds, can be considered the trees of our oceans, forming vast underwater forests supporting most temperate marine ecosystems (1,2). They sustain an enormous amount of biodiversity, while also delivering numerous ecosystem services such as sequestering carbon, contributing to coastal defence, and providing a source for food, pharmaceuticals and textiles, just to name a few (1). Unfortunately, kelps are under global decline due to warming oceans, eutrophication, and overgrazing (3–5). Understanding how kelps function and interact with their environment is therefore crucial to anticipate future trends. In Europe, *Laminaria digitata* and *L. ochroleuca* are two of the most important habitat forming kelp species with overlapping habitats (1,6–9). *L. ochroleuca* ranges from the coastal waters of Morocco to the South of the UK (6,8), while *L. digitata* ranges from central France to Norway in European waters (7). *L. ochroleuca* is losing habitat in its most southern latitudes due to marine heatwaves but is expanding to the north (8), resulting in increased overlapping habitats and competition between these two kelps (10). Recent work demonstrated that *L. ochroleuca* and *L. digitata* can hybridize (11), raising the possibility that hybridization may alter thermal tolerance as a result of unique, hybrid gene expression profiles. This study investigates the performance and thermal response of reciprocal hybrids to assess their potential ecological significance under future warming.

## Material & Methods

Novel *L. ochroleuca* and *L. digitata* inter and intra crossings were created for this experiment using the same strains as specified in De Clercq K (2025) (11). The genomic kelp DNA was extracted using the OmniPrep protocol for Plant tissue, which was adapted for high molecular weight DNA extraction from brown algal tissue. Hybrid status was assessed and confirmed with microsatellite marker Ld2-167 (12) using the same PCR settings as specified in Mauger S. *et al.* (2021) (13). When the kelps were 3 months old, they were exposed to four different temperatures: 12°C (control), 18°C, 22°C and 24°C. The temperature was increased with 3°C every day from the 12°C baseline until the desired heatwave temperature was reached. Pictures were taken on day 0, day 11 and day 18. The relative growth rate of the kelps was determined based on surface area calculations which were done in ImageJ. On day 18, after the final picture was taken, the kelps were blotted dry and flash frozen in liquid nitrogen and stored at -80°C. RNA extractions were performed with an in-house extraction protocol optimized for brown algae. Samples were sent out to Novogene for Illumina sequencing. Transcriptomes were assembled *de novo* using SPAdes v4.1.0. Analyses of the RNA-seq data is still ongoing.

#### Results/Conclusions

The first results of this study revealed that each hybrid kelp crossing outperformed the cold parental kelp species *L. digitata* in terms of growth speed. Additionally, they did not die at heatwave 22°C and 24°C as opposed to the intra *L. digitata* crossings which showed extensive bleaching. This thermal tolerant pattern appeared to be partially sex dependent. The hybrid crossing with female *L. ochroleuca* and male *L. digitata* outperformed the female *L. digitata* and male *L. ochroleuca* hybrids. These effects are consistent with Martins N. *et al.* (2019) (14), where the female parents were more important in determining the thermal response phenotype than the male parents. The female *L. ochroleuca* and male *L. digitata* crossing performed on a similar level as the intra *L. ochroleuca* crossings at 22°C and 24°C, but did grow more rapid at 12°C and 18°C.

This research was delayed as initially it was anticipated that the first batch of hybrids established in the fall of 2024 could be used for the thermal tolerance experiment and RNA sequencing. However, in the end there was not enough healthy juvenile tissue left, leading to the fact that the hybrids had to be created and cultivated again prior to any experimental work. Because of this the raw RNA-seq data was only obtained in December 2025. This combined with the fact that I did not yet have a pipeline for *de novo* transcriptome assembly and analysis resulted in the fact that the RNA-seq data is not yet completely analysed. I do plan to finish these analyses this year and aim to publish these results in a peer reviewed paper.

This study provides a first insight into the dynamics of hybridization and adaptation of two of Europe's most important kelp species, improving our ability to predict their vulnerability and resilience to our continuously changing oceans. We demonstrated that hybrid vigour exists for thermal tolerance in hybrids between the foundational European kelp species *L. ochroleuca* and *L. digitata* with the maternal parent playing a stronger role in determining these effects.

#### References

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### 3. Overview of the expenditures

Describe in detail how the requested fund was spent within the implementation period (1 March 2025 and 28 February 2026). Be as specific as possible.

**The requested fund was used to fund the RNA sequencing done by Novogene. This cost was 4639,19 euro in total.**

### 4. Pictures

A set of five pictures (low resolution in this document). The five high resolution pictures should be delivered to VLIZ by email to karen.rappe@vliz.be.

