ULPGC

Toolkit for seaweed Hatchery operations

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Background, Current Practices, and Innovations

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LIST OF ABBREVIATIONS

AFLP	Amplified Fragment Length Polymorphism	
APT	Adenine Phosphoribosyl Transferase	
BSA	Bulk Segregant Analysis	
COI	Cytochrome Oxidase I	
CRISPR	Clustered Regularly Interspaced Short Palindromic	
CRISPR	Repeats	
DMSO	Dimethyl Sulfoxide	
DNA	Deoxyribonucleic Acid	
FEMS	Federation of European Microbiological Societies	
GBIF	Global Biodiversity Information Facility	
GBS	Genotyping By Sequencing	
GWAS	Genome-Wide Association Studies	
IMTA	Integrated Multi-Trophic Aquaculture	
ITS	Internal Transcribed Spacer	
LSU	Large Subunit	
MAS	Marker-Assisted Selection	
NGS	Next-Generation Sequencing	
PCR	Polymerase Chain Reaction	
PES	Provasoli Enrich Seawater	
PGR	Plant Growth Regulator	
PTFE	Polytetrafluoroethylene	
QTL	Quantitative Trait Loci	
RAD	Restriction Enzyme-Associated DNA Sequencing	
RAPD	Random Amplified Polymorphic DNA	
RFLP	Restriction Fragment Length Polymorphism	
RNA	Ribonucleic Acid	
SBMs	Seaweed Beneficial Microorganisms	
SLAF	Specific Locus Amplified Fragment	
SNP	Single Nucleotide Polymorphism	

SRAP	Sequence Related Amplified Polymorphism	
SSCP	Single Strand Conformational Polymorphism	
SSR	Simple Sequence Repeat	



1. SUMMARY

This toolkit provides a comprehensive introduction of the initial phase of seaweed cultivation, during which juvenile algae are obtained and propagated for subsequent production, the hatchery/nursery/seeding/planting or simply **hatchery phase**. It provides a comprehensive overview of the seaweed life cycle, detailing the process of algae propagation in controlled environments prior to their deployment in the production system.

To make this knowledge practical and ready for application, the toolkits will include a set of illustrations for selected seaweed species of economic importance in Europe. The illustrations will present the life cycles of each species and approaches to innovations. In addition, the publication contains fact sheets on hatchery techniques, along with distribution maps. This species-based approach is designed to guide farmers, researchers and entrepreneurs by offering concrete, visual examples they can replicate or adapt.

The document also highlights current tools and methods, as well as promising innovations to make seaweed farming more efficient and sustainable. While the industry is expanding in Europe, many hatchery practices are still underdeveloped. This toolkit supports improvement through six proposed innovations, including lab-based cultivation, the use of natural plant growth regulators, genetic identification, cryopreservation, microbiome enhancement, and biodegradable seeding materials.

A comprehensive European algae company database is available to assist users in exploring potential partnerships, market opportunities and research prospects across the seaweed sector. The establishment of a business in a particular sector is facilitated by the access to a database containing company contact information and activity details.

While the original text was intended for individuals unfamiliar with seaweeds, it also incorporates over 400 references and science mapping for those with more in-depth knowledge, including technicians and scientists.



2. INTRODUCTION AND BACKGROUND

Concept of the hatchery. The life cycle.

Plants and algae have the capacity for sexual reproduction and vegetative multiplication. The former consists in the mixing of the genetic endowment of a male and a female organism, which requires the production by both sexes of gametes, whose genetic endowment is quantitatively half and qualitatively modified by mixing processes during the formation of the gamete itself.

This process ensures the presence of the necessary subtle variations in the offspring from their parents. The process of gametogenesis involves the reduction and modification of the parental genetic material, which is achieved after a two-stage process of cell reproduction called meiosis (R!). Otherwise, organisms and their cells multiply by a non-reductive process of gene endowment called mitosis (R). Vegetative multiplication is based on this cellular capacity.

In land plants, meiosis for gamete production occurs in one type of individual if it is capable of producing both male and female flowers on the same plant stem (monoecious), or in two types of individuals if each individual produces only one type of gamete (dioecious). Gametogenesis is reduced to one reproductive structure, the flower, which is supported and nourished by the individual.

In the context of multicellular marine algae, the absence of flowers associated with individual organisms is notable. Instead, there are separate, often clearly visible stages (at least one of them) that alternate to complete the life cycle of the organism, producing spores. Overall, the differences between algae and plants can be outlined as shown in Figure 1 (Heesch et al., 2021).



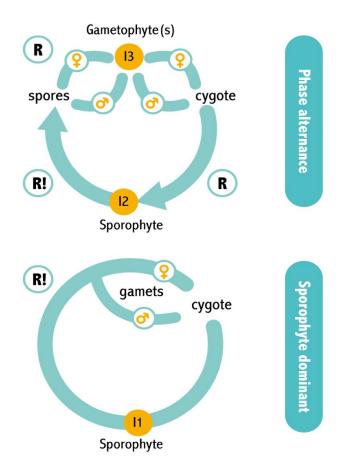


Figure 1. Phase alternation and dominance of the sporophyte. In terrestrial plants (below) an individual **I1** sporophyte (with one or both sexes) supports the reproductive organs (flowers) whose gametes fuse to give rise to new individuals. In algae (above) there is no flower-bearing individual, in fact there are no flowers at all, but structures in the **I2**-type individual whose spores form **I3** individuals, which in turn generate the gametes. The different stages are usually free-living and are known as sporophytes (I2) and gametophytes (I3). R! = meiosis; R = mitosis (Heesch et al., 2021).

The term "Hatchery" is very much a word associated with animal production and has been somewhat adopted by the seaweed/plant-based community. In the context of seaweed aquaculture, the early stages of production are critical for ensuring the efficiency and scalability of cultivation systems. These initial phases are often grouped under the general term "hatchery" (Table 1), although more precise terminology can help clarify the specific operations involved. Perhaps this community does not always make the association of a hatchery with the cultivation tasks they perform.





Table 1 Alternative terms exist for defining the first stages involved in seaweed cultivation that are usually summarised under the term 'hatchery'.

	Description	Examples
Hatchery (Nursery)	Controlled phase where	Cultivation of kelp (Laminaria spp.)
	stages (gametophytes or	gametophytes in tanks, producing sporophytes
	sporophytes) are obtained	for seeding.
	and cultured under optimized	
	conditions until they reach a	
	suitable stage for	
	transplantation.	
Seeding (Planting)	Process of transferring young	Inoculation of kelp (Laminaria spp.) juvenile
	algae (gametophytes or	sporophytes onto ropes for offshore cultivation.
	sporophytes, depending on	
	the species) to the final	
	cultivation environment (e.g.,	
	sea farms).	

Cultivation of algae consists of the mass production of one of the stages, the sporophyte or gametophyte, which can be obtained by vegetative multiplication or after total or partial completion of the life cycle. Hatchery operations therefore consist of obtaining, maintaining and propagating to juvenile stages the propagules that will then be cultivated, in-shore or off-shore, until algal biomass is obtained. Seeding operations consist of the implantation of these propagules in a substrate for transfer to the culture area.

Science Mapping seaweed aquaculture/ cultivation/ hatchery/ seeding.

Scientific mapping applied to the field of macroalgae cultivation ("macroalga AND cultivation") makes it possible to visualise the evolution of knowledge around key concepts such as "hatchery" and "seeding". A timely bibliometric analysis (years 1980 to 2025), based on 360 scientific publications indexed in Scopus and conducted following the methodology described in Chapter 8, identified 10 major thematic clusters. Among them, Seeding and Propagation emerge as subthemes directly related to macroalgal production and establishment, while Algal-Growth acts as the central node articulating the knowledge map.

The seeding category represents research focused on the seeding or inoculation of macroalgae in cultivation systems. It includes techniques such as spore attachment to ropes, nets or artificial





substrates, which are essential for the establishment of sustainable crops on a commercial scale. Although this topic has a lower density and centrality in the knowledge network - suggesting that it is still developing or seeking consolidation - its connection to areas such as genetics and physiology indicates its growing importance. References to the topic 'Hatchery' are scarce as specific papers on hatchery are barely found (interesting to note that the term 'seeding' is frequently employed as a keyword).

The mapping shows that themes such as Propagation and Genetics provide specialist knowledge, while Environmental impact and Nutrients provide the ecological context necessary to understand the dynamics of seeding and growth. Algal production is therefore a complex system involving both internal factors (reproductive biology) and external factors (environmental conditions). This analysis highlights the necessity to integrate molecular, physiological and culture techniques in the design of more efficient hatcheries, in line with sustainability and bioeconomy objectives (Figure 2).

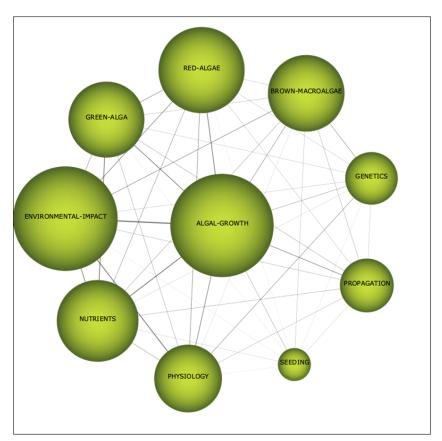


Figure 2. Science mapping hatchery/ seeding and conceptual network. Hatchery/seeding has a lower density and centrality in the knowledge network, suggesting that it is still developing or seeking consolidation, its connection to areas such as genetics and physiology indicates its growing importance.



3. MAPPING OF EUROPEAN ALGAE COMPANIES: A STRATEGIC RESOURCE FOR SECTORIAL INSIGHT AND COLLABORATION

We have developed a comprehensive and up-to-date mapping of European companies operating within the seaweed sector, covering the entire value chain—from seaweed production to applications in food, cosmetics, and biofertilizers. The dataset has been compiled using a rigorous methodology, combining information from existing databases with targeted manual searches. This approach has enabled both the validation and expansion of the available information.

The databases consulted for the development of this resource include:

- The European Business Register: https://e-justice.europa.eu/topics/registers-business-insolvency-land/business-registers- search-company-eu_en
- The European Commission's "Knowledge for Policy" platform, specifically the section "Bioeconomy in Different Countries" from which two datasets on the algae industry in Europe were extracted. These datasets cover macroalgae, microalgae, and spirulina; however, a filtering process was applied to retain only data related to the macroalgae industry (Vazquez-Calderon et al., 2022). https://knowledge4policy.ec.europa.eu/ visualisation/bioeconomy-different-countries_en
- Phyconomy Database: https://phyconomy.net/database/
- A review of companies participating in international conferences such as Seagriculture: https://seagriculture.eu/

The primary objective of this initiative is to provide a clear overview of the sector and to facilitate strategic connections between existing stakeholders and new entrants interested in engaging with the algae-based bioeconomy. By identifying active companies and the specific algae species they utilize, this tool aims to enhance visibility, foster connectivity, and strengthen investment opportunities within this rapidly evolving industry.



The resulting database PhyCo¹. is publicly accessible at www.phyco.ulpgc.es. It has been designed to be highly user-friendly (Figure 3). Users can retrieve information, either by company name or by algae species through dropdown menus, which helps to avoid typographical errors—a common issue given the complexity of accurately spelling scientific species names. This feature significantly improves accessibility for a broad audience, including investors, industry stakeholders, and users unfamiliar with scientific nomenclature or foreign company names. The database supports a wide range of applications, including market research, partnership development, technological scouting, and policy design.

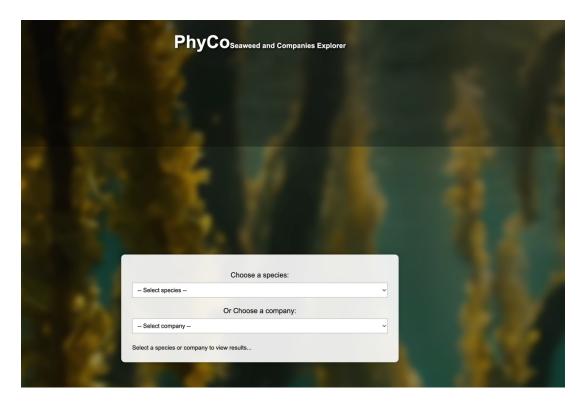


Figure 3. Frontpage of the European Companies in the Seaweed Sector Database. Publicly accessible at www.phyco.ulpgc.es

This DATABASE aims to be a valuable tool for stakeholders seeking to understand, invest in, or contribute to the sustainable growth of the European algae sector

¹ **Phyco-**" is a prefix used in scientific terms related to algae (like *phycology*, the study of algae), it comes from "*Phykos*" (φῦκος), the ancient Greek word that means "seaweed" or "alga. The name of the database combines phyco or seaweeds with Co., the abbreviation of company.





Functionality and Search Options

The type of output depends on the search criteria. When searching by species (Figure 4), the results include:

A brief general description containing: **Genus**; **Colour** (following the traditional classification of macroalgae, even if not taxonomically precise); **Common name**; **Number of Companies** operating with that species in Europe.

Following this summary, a detailed list of companies is displayed including **Company name**; **Country**; **Website**; **Value Chain**; **Production Process**; **Industry (Applications)**; **Subsector**.

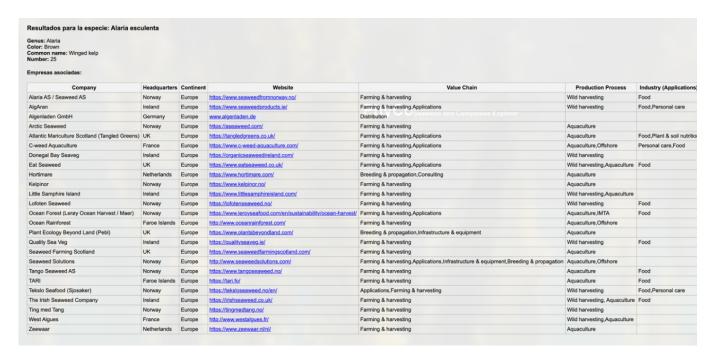


Figure 4. Example of a species-based search result for Alaria esculenta.

The database also features an interactive map (Figure 5), which displays the geographical distribution of companies by country. By clicking on each country, users can view the list of companies working with the selected species.



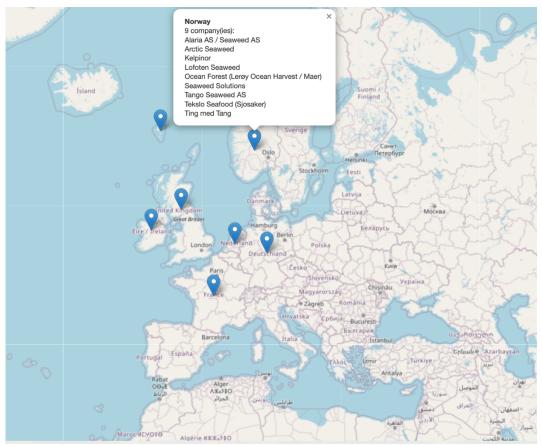


Figure 5. Interactive map showing the distribution of companies operating with Alaria esculenta across Europe. The figure highlights all countries with relevant companies and displays the list of nine companies based in Norway.

When performing a company-based search (Figure 6), the output is a table that includes: Company Name; Country (Headquarters); Value Chain; Website; Production Process; Industry Applications; Algae Species utilized by the company.



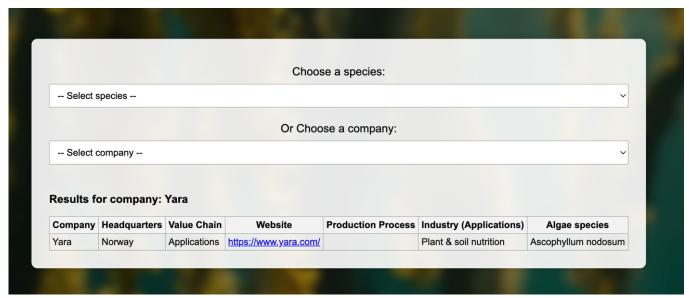


Figure 6. Example of a company-based search result for Yara.

Maintenance and Updates

If blank fields appear in the search results, it indicates that the information is currently unavailable at the time of publication. This database is conceived as a **living resource**, subject to continuous updates and improvements based on contributions from companies and institutions willing to share new or updated information.





4. ALGAE HATCHERY OPERATIONS. CASE STUDIES

Given the diversity of groups, morphologies and biological cycles that feed the culture, there is no single procedure, so we will cover this section by describing the existing procedures for each type of algae, expecting that the information provided may guide the use of other species in the future. The cases have been selected according to the relevance of the species in the European context (Araujo et al. 2021).

Pyropia/Porphyra spp.

Pyropia J.Agardh, 1899 and *Porphyra* C.Agardh, 1824 are closely related genera of red algae (Phylum Rhodophyta, class Bangiophyceae, order Bangiales) extensively cultivated for their nutritional value and bioactive compounds with antioxidant and anti-inflammatory properties. Additionally, they are rich in carotenoids –notably xanthophylls like lutein and zeaxanthin–, amino acids, and other nutrients, making them important for human consumption (Diehl et al., 2017; Xu et al., 2024). These genera are among the most commercially important macroalgae globally, used extensively in food products such as nori. Their cultivation is increasing due to demand and the need for sustainable marine resources (Piña et al., 2023; Knoop et al., 2019; Marin et al., 2023; Piña & Contreras-Porcia, 2021).

Both genera typically inhabit upper intertidal zones, with distribution influenced by temperature, humidity, light, and desiccation stress. Different morphotypes and species show preferences for specific microhabitats (e.g., rocky walls vs. flat platforms) (Meynard et al., 2019; Zapata et al., 2019; Contreras-Porcia et al., 2022).

These macroalgae have a broad cosmopolitan distribution, with high species diversity and complex evolutionary relationships revealed by molecular studies. Their presence spans multiple continents and diverse coastal environments, shaped by both natural and anthropogenic factors (Figure 7). *Porphyra* and *Pyropia* are found in both hemispheres, with confirmed presence in Asia (notably Korea, Japan, and China), Oceania (New Zealand), the Americas (North America, South America — including Brazil and Chile), and Europe (Diehl et al., 2017; Zapata et al., 2019; Contreras-Porcia et al., 2022; Guillemin et al., 2016; Yang et al., 2020; Meynard et al., 2019; Milstein et al., 2015; Sánchez et al., 2014; Piña & Contreras-Porcia, 2021; Lindstrom et al., 2015).





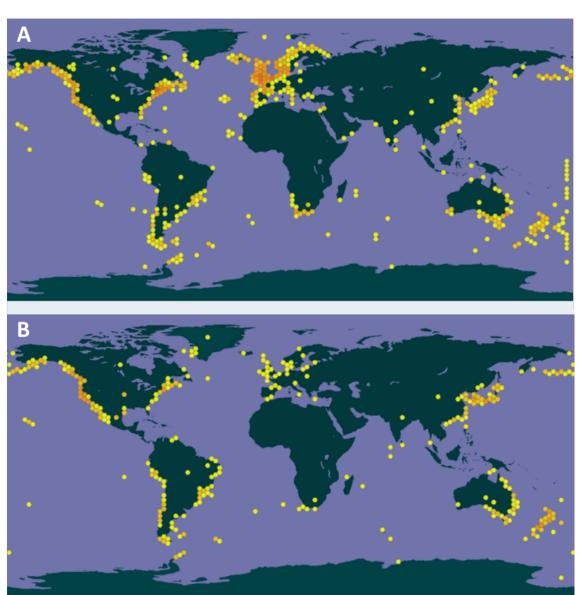


Figure 7. Worldwide distribution of **A.** Porphyra spp.; **B.** Pyropia spp. The points represent georeferenced occurrences of species: orange / reddish-orange: Data published as observations or specimen records (e.g., field observations, museum specimens); and, yellow: Literature-based records or other secondary sources; Light Green: Sensor-based data or camera trap records (GBIF Secretariat, 2023).

Life cycle

These red algae exhibit a heteromorphic haploid-diploid sexual life cycle in which the macroscopic leafy gametophyte (thallus) alternates with the microscopic filamentous sporophyte (conchocelis), with conchospores bridging the two. Understanding these stages is crucial for increasing the production in mariculture farming of this economically significant





marine resource (Knoop et al., 2019; Wang et al., 2019; Wang et al., 2020; Piña et al., 2023; Niu et al., 2024).

The simplified life history of *Pyropia* and *Porphyra* starts with male (spermatium) and female (carpogonium) gametes on the thalli fertilize to form diploid carpospores contained carposporangium (spore-producing structure) (Figure 8). The released carpospores penetrate a shell, where they undergo development into filamentous conchocelis (tetrasporophyte), residing within the shell. The conchocelis further matures into conchosporangia, eventually releasing conchospores. These spores undergo meiosis, ultimately leading to the development of gametophytic thalli. (Piña et al., 2023; Niu et al., 2024).

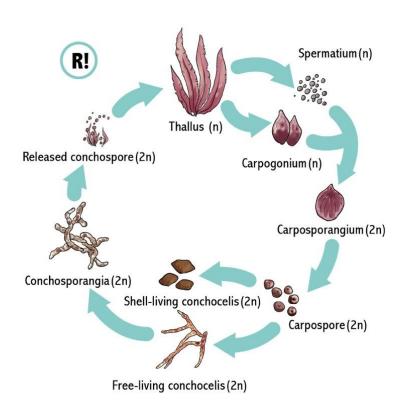


Figure 8. The simplified life cycle of Pyropia and Porphyra (Niu et al., 2024).



Hatchery techniques

Modern *Pyropia/Porphyra*, and all species, hatchery techniques depend on precise control of life cycle stages —particularly the conchocelis phase— optimization of abiotic factors like temperature, photoperiod and salinity. Environmental factors, particularly temperature and photoperiod, play a crucial role in regulating transitions between reproductive stages, including conchospore release and blade development (Knoop et al., 2019; Wang et al., 2019; Wang et al., 2023).

Overall, the conchocelis phase grows on shells under controlled conditions and, in autumn, releases conchospores that adhere to nets for cultivation in the sea. These conchospores subsequently grow into thalli, which are later harvested (Polne-Fuller et al., 1984; Pattiasina et al., 2023; Piña et al., 2023).

The following fact sheets present hatchery techniques for *Pyropia/Porphyra*, with further details available in the cited bibliography.





Pyropia / Porphyra hatchery

Start material

Spore released and seeding

Sporeling growth and yield

Out-growth

Conchospores

Produced by mature **Conchocelis** (filamentous sporophyte). Cultured on substrates (e.g., oyster shells Hannach & Waaland, 1989) or in suspension. (Stekoll & Lin, 1999; Piña *et al.*, 2023). Conchospore release: 9–15°C (Piña et al., 2023). Conchospore germination: 9°C (Knoop et al., 2019). Light intensity: low light intensity increases

Conchocelis culture conditions
Light intensity: 40–80 µmol photons m⁻² s⁻¹ (Hannach & Waaland, 1989).

conchospore germination.

Photoperiod: 8:16 h (light:dark) (Piña et al.,

2023). **Temperat**

Temperature: 11–20°C, varies by species (NamilGil, 1999; Stekoll & Lin, 1999; Knoop et al., 2019; Piña et al., 2023).

Optimal spore stocking densities for cultivation are generally between 5,000-10,000 spores mL⁻¹ (Flavin *et al.*, 2013).

Gametophyte

Blade growth: 5–20°C, young blades (gametophytes) prefer lower temperatures; consistent blade development at higher temperatures (20°C) (NamiGil, 1999; Knoop et al., 2019; Piña et al., 2023). Light intensity: lower light intensity increases conchospore germination.

Gametophyte fronds can be cultivated in land-based tanks (inshore) or natural upper intertidal zones, where they naturally grow. Substrate for blades: Nylon or cotton traditional ropes; synthetic seedstrings such as Gore C type which improve efficiency (Xing et al., 2025).

Conchospores: the germination of conchospores into young blades is a major bottleneck. Even with optimized conditions, germination rates remain very low, indicating this is the stage where propagation is least successful (Knoop *et al.*, 2019).







Alaria esculenta

Alaria esculenta (Linnaeus.) Greville, 1830 (Phylum Ochrophyta, class Phaeophyceae, order Laminariales), also known as dabber locks or winged kelp, is a brown seaweed valued for its high productivity and rich content of carbohydrates, proteins, vitamins, minerals, and bioactive compounds. It is cultivated for food and biomass, especially in Europe, and is recognized for its rapid growth and potential as a source of phlorotannins and other beneficial compounds (Duarte, 2017; Kerrison et al., 2020).

This macroalga primarily colonizes wave-exposed, subtidal rocky shores in cold, clear waters, where light is abundant and sedimentation is low (Kraan & Guiry, 2000; Kraan, 2020). Its distribution is limited in sheltered, turbid, or sediment-rich environments, and it is sensitive to changes in temperature and salinity, especially during early development.

Alaria esculenta is predominantly found in temperate to cold waters of the Northern Hemisphere, inhabiting the Atlantic and Pacific coasts of Canada and the USA, as well as northern Europe — specifically the United Kingdom, Greenland, the Faroe Islands, and the Nordic countries— (Figure 9). Its distribution is largely restricted to areas where the water temperature does not exceed 16°C, explaining its absence from warmer southern regions such as the southern North Sea and beyond the English Channel (Murúa et al., 2018; Inaba et al., 2022; Kraan & Guiry, 2000; Kraan, 2020; Kraan et al., 2001).



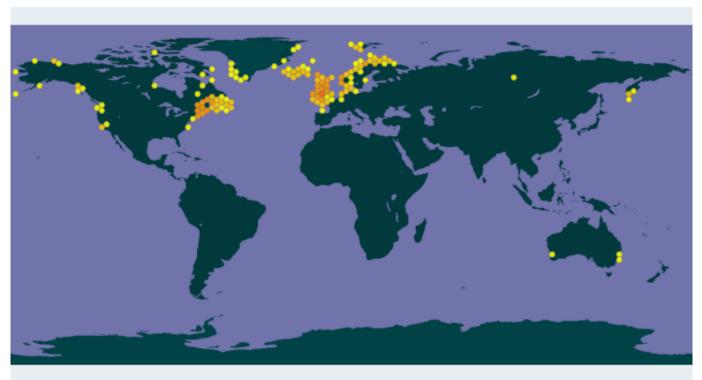


Figure 9. Worldwide distribution of Alaria esculenta. The points represent georeferenced occurrences of species: orange / reddish-orange: Data published as observations or specimen records (e.g., field observations, museum specimens); and, yellow: Literature-based records or other secondary sources; Light Green: Sensor-based data or camera trap records (GBIF Secretariat, 2023).

Life cycle

Alaria esculenta has a heteromorphic life cycle, alternating between a microscopic gametophyte stage and a macroscopic sporophyte stage (Fredersdorf et al., 2009; Silva et al., 2022; Zacher et al., 2019; Ebbing et al., 2021) (Figure 10).

The large visible kelp (sporophyte) produces zoospores through meiosis (meiospores). These zoospores settle and develop into microscopic male and female gametophytes (Fredersdorf et al., 2009; Zacher et al., 2019; Silva et al., 2022). Gametophytes produce gametes (eggs and sperm). The fertilization of the gametes results in a zygote, which develops into a sporophyte, completing the cycle (Zacher et al., 2019; Ebbing et al., 2021; Silva et al., 2022).



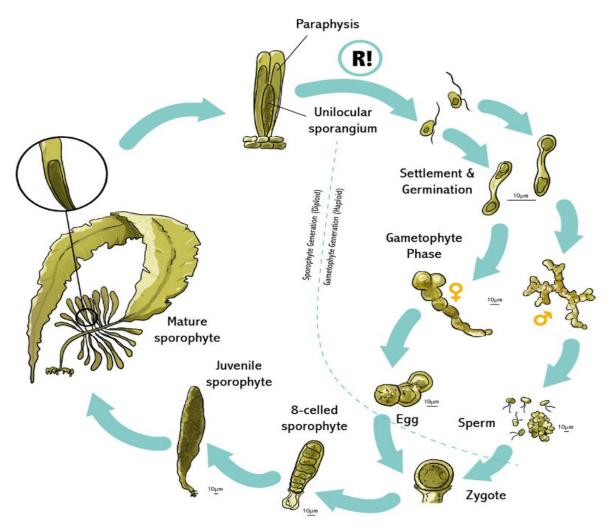


Figure 10. The life cycle of Alaria esculenta (adapted from Redmond et al., 2014).

Related to seasonal timing, in Arctic conditions, gametophyte growth and reproduction are halted during winter darkness and resume in spring and summer. In *A. esculenta*, sexual reproduction and sporophyte recruitment mainly occur in summer and autumn (Silva et al., 2022).

Hatchery techniques

Hatchery and seeding techniques for *Alaria esculenta* are central to its cultivation for food and biomass. Research has focused on optimizing seedling production, comparing traditional and innovative seeding methods, and understanding how these affect yield and morphology.



Alaria esculenta hatchery

Start material

Spore released and seeding

Sporeling growth and yield

Out-growth

Zoospores

main dispersal and reproductive propagules.

They are produced in the sporangia of the adult sporophyte through meiosis, making them haploid cells. These zoospores or meiospores are motile and can germinate to form gametophytes (Duarte, 2017).

Photoperiod: A 16:8 h light:dark Temperature: 7–13 °C are optimal for zoospore photosynthesis, germination, and early development (Roleda, 2009).

Optimal spore stocking densities for cultivation are generally between 5,000-10,000 spores mL⁻¹ (Flavin *et al.*, 2013).

Gametophytes

This method allows for a constant, year-round supply of propagules, unlike the seasonal limitation of zoospore release (Duarte, 2017). Photoperiod: 16:8 h (light:dark) photoperiods yield higher sporophyte production and growth (Martins et al., 2021).

Binder-Seeding: Binder-seeding onto specialized textiles (AlgaeRope, AlgaeRibbon) can reduce costs. Biomass yield is similar across natural and artificial materials, but higher sporophyte density on AlgaeRibbon lead to shorter, thinner fronds. (Kerrison et al., 2020).

Juveniles are grown on twine in hatcheries and then deployed at sea. Alaria esculenta can grow and be cultivated in both inshore and natural environments (Kerrison et al., 2020).

Vegetative gametophyte stage: Gametophytes can remain in a vegetative (non-reproductive) state and cannot be used for reproduction in hatcheries until fertility is induced by specific conditions, such as changes in light or temperature (Duarte, 2017; Martins *et al.*, 2021).



Sporeling production



Ulva spp.

Ulva spp., commonly known as sea lettuce, are green seaweeds (Phylum Chlorophyta, class Ulvophyceae, order Ulvales) valued for their high productivity, environmental tolerance, and nutritional properties. They are increasingly cultivated for food, feed, and biofuel applications, with commercial interest growing globally due to their versatile uses and ease of cultivation in various systems, including photobioreactors and open sea farms (Steinhagen et al., 2022; Balar & Mantri, 2019).

These green macroalgae have a broad global distribution inhabiting a wide range of marine habitats from intertidal to subtidal zones, and even some freshwater environments, due to their tolerance to light, temperature, and salinity variations (Kirkendale et al., 2013; Mantri et al., 2020; Yohannan et al., 2024) (Figure 11). Studies report high species diversity in specific regions:

Jeju Island, Korea: Nine *Ulva* species identified, with *U. australis, U. ohnoi,* and *U. procera* being predominant (Kang et al., 2019).

Australia: Overwhelmingly cosmopolitan flora with both native and nonindigenous species, and several new records and range extensions (Kirkendale et al., 2013).

New Caledonia: Fifteen species found, including ten newly described species, highlighting significant undiscovered diversity in tropical regions (Lagourgue et al., 2022).

India: 28 taxa recorded, with seven endemic taxa and highest diversity in Gujarat (Yohannan et al., 2024).

China: Six new records, with both temperate and subtropical species expanding their ranges, especially *U. meridionalis* (Xie et al., 2020).

Brazil: Ten taxa identified, including new occurrences and cryptogenic species, with evidence of misapplied traditional names (Carneiro et al., 2023).

Northeast Atlantic and North America: Multiple species present, but with significant misidentification issues in public databases (Fort et al., 2021; Lamb et al., 2019).

In Europe, *Ulva* spp. are broadly distributed across marine, brackish, and freshwater environments, with species composition and distribution patterns shaped by local ecological conditions. Among these, *Ulva flexuosa* is the predominant freshwater species, exhibiting distinct





ecological preferences across its subspecies: *U. flexuosa subsp. pilifera* is commonly found in inland freshwater systems, while subsp. *flexuosa* and subsp. paradoxa are more frequently associated with marine and coastal habitats. *U. flexuosa* is considered indigenous and can form blooms under certain conditions (Mareš et al., 2011; Czerwik-Marcinkowska et al., 2020). Another prominent species, *Ulva rigida*, is among the most frequently encountered *Ulva* taxa in European coastal seawaters. Due to its abundance and resilience, *U. rigida* is often included in studies focused on macroalgae applications in food production, aquaculture, and environmental management, underscoring its ecological prevalence and growing commercial relevance across the continent (Neto et al., 2018; Research et al., 2020; Da Costa et al., 2020; Califano et al., 2020; Moreira et al., 2021; Gao et al., 2018; Karray et al., 2017; Naldi & Viaroli, 2002).

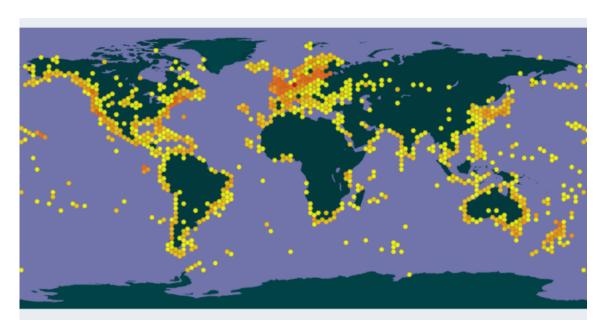


Figure 11. Worldwide distribution of Ulva spp. The points represent georeferenced occurrences of species: orange / reddish-orange: Data published as observations or specimen records (e.g., field observations, museum specimens); and, yellow: Literature-based records or other secondary sources; Light Green: Sensor-based data or camera trap records (GBIF Secretariat, 2023).

Life cycle

Reproduction in these macroalgae occurs both sexually and asexually (Figure 12). The life cycle is biphasic, consisting of two distinct phases: the gametophyte and the sporophyte. It is also isomorphic, meaning that the gametophyte and sporophyte generations are morphologically similar yet genetically distinct. (Graham & Wilcox, 2000; Mantri et al., 2020).





Sexual reproduction involves the production of haploid biflagellate gametes that fuse during fertilization, resulting in the formation of a diploid zygote. This zygote then develops into a diploid multicellular adult sporophyte thallus. As these typical vegetative cells mature, they transition into spore or zoospore mother cells, which undergo meiosis to produce haploid quadriflagellate zoospores (Figure 12). These zoospores germinate and give rise to haploid male and female isomorphic adult gametophytic thalli (Costa, Cotas & Pereira, 2024). At maturity, these thalli once again produce their respective gametes through mitosis. This reproductive process is termed a "haplodiplontic" life cycle (Figure 12). Both zoospores and gametes have no cell walls and are described as naked and are produced mainly in cells at the end of the thallus (Graham et al., 2000; Mantri, et al., 2020).



Figure 12. Typical life cycle of Ulva spp. (Fusco & Minelli, 2019).





Some *Ulva* species, such as *Ulva rigida*, are capable of parthenogenetic reproduction, whereby their gametophytes can produce clonal gametes even in the absence of a mating partner (Steinhagen et al., 2022; Balar & Mantri, 2019). Notably, parthenogenesis—where offspring develop from unfertilized gametes—is a widespread and ecologically significant reproductive strategy among several *Ulva* species. This mode of reproduction contributes substantially to their life cycle flexibility, population resilience, and ecological success. It is particularly relevant in the context of species that drive large-scale green tide events and those utilized in aquaculture, as it enables rapid population expansion and persistence under varying environmental conditions.

The seasonal timing of *Ulva* spp. reproduction is influenced by environmental factors such as temperature, light, and photoperiod, as well as endogenous biological rhythms. *Ulva* species display distinct seasonal reproductive patterns, with peaks in reproduction and biomass often linked to specific times of year and environmental cues.

Hatchery techniques

Effective hatchery and seeding practices for *Ulva* spp. rely on high seeding densities, optimal nursery periods, and efficient in vitro seeding methods. Environmental factors like salinity and phosphorus play supporting roles, while life cycle selection can further enhance productivity. These insights support the development of reliable, large-scale *Ulva* aquaculture.



Ulva spp. hatchery

Spore released and seeding

growth and yield

Out-growth

Germ cells

Thallus is directly used by segmenting or chopping, which can induce the formation of germ cells (zoospores or gametes) or allow for vegetative regrowth (Vesty et al., 2015; Tao et al., 2021).

Light intensity: 100-400

µmol m⁻² s⁻¹.

Photoperiod: 8:16 h and 12:12 h (light:dark), depending on the species.

Temperature: 15-22°C.

Stocking thallus fragments at 5-20 g fresh weight L-1 results in a doubling of growth each week (Pettett, 2009).

Sporophyte or gametophyte blades

Germ cells can germinate and develop into new thalli, with high germination rates observed under optimal nutrient and salinity conditions.

Induction protocols allow reproducible and standardized inoculum production (Vesty et al., 2015; Bastos et al., 2019). Nutrients and Water: Nitrogen (N) and phosphorus (P) are essential; growth increases with higher DIN (Dissolved Inorganic Nitrogen); excess phosphate can be toxic; high nitrate is well tolerated. Continuous water flow enhances seedling coverage and nutrient removal efficiency (Teichberg et al., 2009 Salvi et al., 2021; Nederlof et al., 2022).

Temperature: Some species are more cold-tolerant, but warmer conditions generally boost biomass (Yoshida et al., 2015).

Seeding: 621,000 swarmers/m rope, 5-day nursery (optimal growth) (Castelar et al., 2014).

Ulva spp. are highly adaptable and grow well in both natural and landbased (inshore) environments. Controlled seeding of juvenile sporophytes on nylon nets or ropes enhances biomass yield, with nvlon outperforming natural fibers such as jute or bamboo in terms of coverage and growth, especially under continuous water flow (Castelar et al., 2014; Li et al., 2014; Geng et al., 2015; Salvi et al., 2021).

Thalli used for cultivation may be either sporophytes (2n) or gametophytes (n) as they are morphologically identical. Gametophyte-origin fragments generally lead to faster blade development, however Late-stage or senescent thalli as well as clonal gametophytes, are generally not used for hatchery starts, as they do not support optimal growth or biochemical quality in *Ulva* crops (Van Der Loos et al., 2024; Steinhagen et al., 2022). Optimizing the choice and management of life-history phases could significantly benefit *Ulva* aquaculture in the future.



Sporeling production



Saccharina latissima

Saccharina latissima (Linnaeus.) C.E. Lane, C. Mayes, Druehl & G.W. Saunders, 2006 commonly referred to as sugar kelp, is a perennial brown macroalga belonging to the phylum Ochrophyta, class Phaeophyceae, and order Laminariales. This species plays a critical ecological and economic role in temperate marine environments. Renowned for its physiological adaptability, high nutritional value, and contributions to coastal ecosystem services, *S. latissima* is increasingly recognized as a keystone species in marine habitats and a promising candidate for sustainable aquaculture and bioproduct development (Diehl et al., 2023; Rey et al., 2019; Burgunter-Delamare et al., 2023). Beyond its resilience, *S. latissima* is highly regarded for its rich nutritional profile, comprising a high amount of carbohydrates, proteins, and health-promoting lipids, particularly polyunsaturated fatty acids known for their beneficial effects on human health (Rey et al., 2019; Vasconcelos et al., 2024).

This kelp dominates many temperate coastal ecosystems as a canopy-forming species — growing tall and extending its fronds outward to form an overhead canopy— thereby playing a pivotal ecological role as an ecosystem engineer. By modifying its environment and creating complex habitats, it supports biodiversity and enhances ecosystem structure and function (Diehl et al., 2023; Tourneroche et al., 2020; Burgunter-Delamare et al., 2023).

Saccharina latissima is widely distributed across the cold and temperate coastal waters of the Northern Hemisphere, from the Pacific to the Atlantic, including Arctic and sub-Arctic regions (Figure 13). The species shows high adaptability to local environmental conditions, supporting its broad distribution.



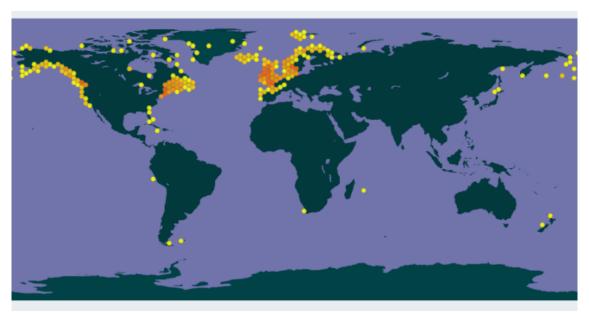


Figure 13. Worldwide distribution of Saccharina latissima spp. The points represent georeferenced occurrences of species: orange / reddish-orange: Data published as observations or specimen records (e.g., field observations, museum specimens); and, yellow: Literature-based records or other secondary sources; Light Green: Sensor-based data or camera trap records (GBIF Secretariat, 2023).

Life cycle

Saccharina latissima has a complex biphasic life cycle that alternates between a large diploid sporophyte and a microscopic haploid gametophyte stage (Figure 14). The sporangia located in sporophytes, during meiosis, form zoospores (n) by a large multicellular sporophyte (2n). The spores settle onto the seafloor and develop into male and female gametophytes (n). Sterile gametophytes can be clonally propagated and used as seed stock for further breeding and cultivation. Male and female gametophyte form antheridia that produce sperm and oogonia that produce eggs, respectively. The sperm fertilizes the egg, and a zygote is formed that develops into a sporophyte (2n) (Visch et al., 2019).



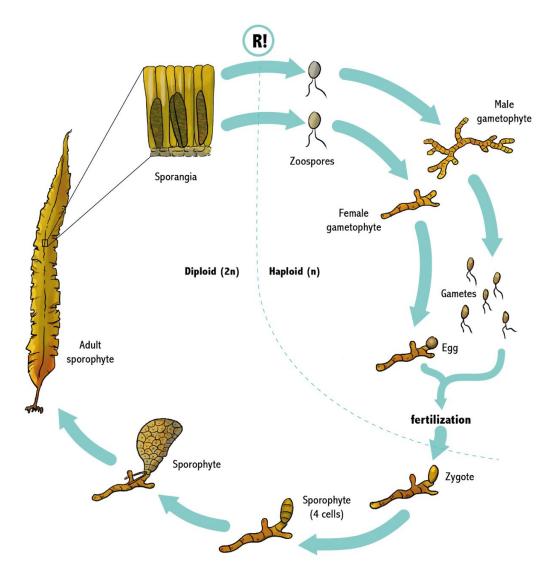


Figure 14. Life cycle of Saccharina latissima (from Visch et al., 2019).

Understanding its life cycle is crucial for aquaculture, breeding, and environmental management, as various environmental factors and cellular processes influence its development and reproduction. The life cycle of *S. latissima* involves several stages, including hatchery (spore production and early growth), cultivation (growth on longlines in the sea), and harvesting. The process also includes preservation methods such as drying, ensiling, or freezing to maintain product quality after harvest (Thomas et al., 2020).

Hatchery techniques

Optimizing Saccharina latissima hatchery methods involves careful management of nutrient concentrations, sterilization, and seeding techniques. Twine seeding remains the most reliable





method, while binder-seeding offers cost advantages in some contexts (i.e. may be lower than traditional twine seeding in more dynamic environments, (Umanzor et al., 2020)). The choice of nutrient source and twine material significantly affects early growth and yield. Sustainable practices and efficient hatchery operations are key to supporting the expanding kelp aquaculture industry. Kuralon twine is a standard, effective substrate for seeding *S. latissima*, supporting robust nursery growth and high yields, especially in sheltered sites. It remains a key material in traditional kelp farming practices (Boderskov et al. 2021).





Saccharina latissima hatchery

Start material

Spore released and seeding

Sporeling growth and yield

Out-growth

Meiospores

or zoospores, from mature sporophytes.

Sorus induction achieved year-round by short-day treatments and removing the basal blade meristem (Forbord *et al.*, 2012).

Settlement Conditions for meispores:

- Dark.
- Nutrient enriched media.
- Pre-treatment of surfaces with commercial yeast extract.

Sporophyte

Seeding juvenile sporophytes onto textiles (Kuralon twine/textile) using a binder is highly effective and may reduce hatchery space requirements (Kerrison et al., 2018).

Nutrient: Continued nutrient enrichment in hatchery crucial for sporophyte growth and survival (Kerrison et al., 2016; 2015; 2019; Jevne et al., 2020). Temperature: Optimal temperature is 10°C Some southern populations of *S. latissima* can tolerate higher temperatures (up to 20°C) in land-based systems. (Jung et al., 2024; Azevedo et al., 2016; Krasnow et al., 2024).

Juvenile sporophytes are used for outplanting, as they show better growth and survival compared to gametophytes or meiospores when seeded onto cultivation substrates (Kerrison et al., 2018).

Gametophytes can be kept free in liquid culture for propagation and storage, and then attached to a substrate to induce sporophyte formation and facilitate seeding. Both approaches are complementary and are used depending on the stage and purpose of cultivation (François et al., 2023; Forbord *et al.*, 2018).





Palmaria palmata

Palmaria palmata (Linnaeus) F. Weber & D. Mohr, 1805 commonly known as dulse, is a red seaweed (Phylum Rhodophyta, class Florideophyceae, order Palmariales) valued for its nutritional content and commercial applications and has long been used as a food source. Due to increasing demand and limited availability in the wild, cultivation methods are being developed to support sustainable production.

This red macroalga thrives on rocky shores in cold-temperate regions and is easily recognized by its soft, edible, reddish fronds. It has traditionally been harvested for human consumption and as animal feed (Grote, 2019; Pang & Lüning, 2006; Stévant et al., 2023). Dulse is notable for its high content of proteins, minerals, and bioactive compounds, making it a sought-after ingredient in the food industry, dietary supplements, and livestock nutrition (Grote, 2019; Stévant et al., 2023; Liboureau & Pampanin, 2024). Although it was historically hand-harvested, it is now the focus of aquaculture initiatives aimed at meeting growing market demand while ensuring sustainable use (Grote, 2019; Stévant et al., 2023).

Palmaria palmata is primarily distributed along the North Atlantic coasts (Figure 15), within latitudes of approximately 40° to 80°N. It is found on the shores of Western Europe, Canada (notably New Brunswick and Nova Scotia), and the USA (Maine) (Stévant et al., 2023; Grote, 2019; Xu et al., 2024).



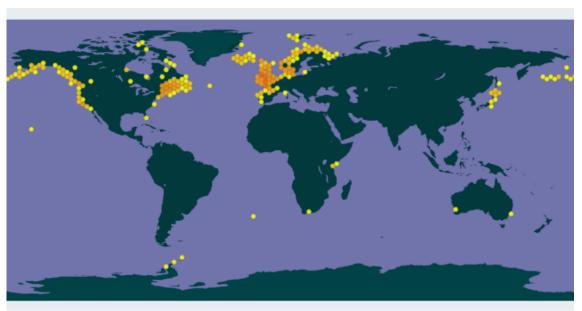


Figure 15. Worldwide distribution of Palmaria palmata. The points represent georeferenced occurrences of species: orange / reddish-orange: Data published as observations or specimen records (e.g., field observations, museum specimens); and, yellow: Literature-based records or other secondary sources; Light Green: Sensor-based data or camera trap records (GBIF Secretariat, 2023). Notice that morphologically similar species previously grouped under this species in the North Pacific are now recognised as genetically distinct, including Palmaria moniliformis and several species of the genus Devaleraea (Skriptsova & Kalita, 2020; Skriptsova et al., 2023).

Life cycle

Palmaria palmata is considered pseudo-perennial since the fronds grow, reproduce and senesce from a holdfast that survives multiple years. It has a distinct life cycle among red seaweeds, involving both sexual and asexual stages (Figure 16). Haploid tetraspores develop within the sori (or sorus in plural, are reproductive structures) of the frond of diploid tetrasporophytes through meiosis. The haploid tetraspores germinate into either microscopic female or blade-like male gametophytes of a similar morphology to diploid tetrasporophytes. The female gametophyte develops oogonia with trichogynes (i.e. hair-like structures) to catch spermatia (i.e. non-motile male gametes) released from a mature male gametophyte (at least one-year-old). The zygote resulting from the fertilization of a female gamete by a spermatium grows into a diploid tetrasporophyte from the encrusting female gametophyte, which is overgrown at an early stage as the tetrasporophyte develops its own discoid holdfast.



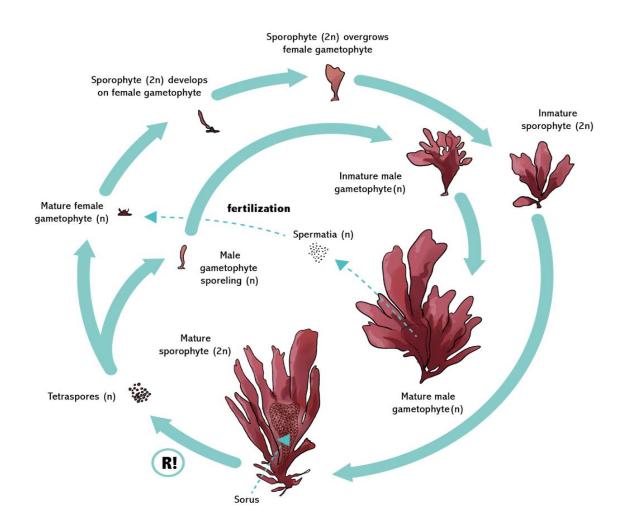


Figure 16. Life cycle of Palmaria palmata (Based on Visch et al., 2019).

The species can reproduce from spores or vegetative fragments, and both approaches are currently being explored to support reliable and scalable cultivation (Grote, 2019; Pang & Lüning, 2006; Stévant et al., 2023; Liboureau & Pampanin, 2024).

Hatchery techniques

Hatchery and seeding methods to propagate *Palmaria palmata* have historically faced challenges such as low spore-to-seedling efficiency and high mortality. Recent research has led to significant advancements in hatchery techniques by optimizing the amount of sori tissue, boosting spore yield, promoting even spore settlement on substrates, enhancing seedling survival, and unlocking





the potential for large-scale cultivation. Lately innovations in hatchery and seeding methods—especially those involving water agitation, propagule mixes, and vegetative propagation—have significantly improved the efficiency and scalability of *P. palmata* cultivation (Schmedes et al., 2019; Stévant et al., 2023; Titlyanov et al., 2006). The tetraspores constitute the initial propagules and it is the male gametophyte that is propagated and grown to tanks or in nature.







Palmaria palmata hatchery

Spore released and seeding

Sporeling growth and yield

Out-growth

Tetraspores

Fertile fronds (sori) are placed in sporulation tanks with strong water agitation to induce spore release.

Light intensity: < 20 µmol photons m2 s-1 is suggested for best results.

Photoperiod: A 16:8 h light:dark.

Temperature: The range of

8-12 °C. Salinity: 34–35 ppt Nutrients and Water: not

critic.

In-shore propagation

Spore yield (spores/g FW):5,000-67,906 (higher with agitation).

Spore density (cm²): ~500 (mean), up to 10 seedlings/

Sori tissue for seeding 5-15 g FW per 3 nets over 9

Seedling survival (3 months) ~35% (Schmedes et al., 2019; Gall et al., 2004).

Male gametophyte

Tetraspores are first released, within a few days, both male and female gametophytes germinate from these tetraspores, the mixture of germinated male and female gametophytes can be collected and used as a new inoculum for settlement on other substrates (GMA method (Grote, 2019; Pang & Lüning, 2006; Stévant et al., 2023; Liboureau & Pampanin, 2024).

The conditions must be adjusted after tetraspore setlement, particularly Higher light intensity (>20 µmol photons m² s⁻¹)and **Nutrients and Water:** Frequent seawater exchange and adequate nutrients (F/2 medium or urea (0.05-0.10 g/L) (Pang & Lüning, 2006; Grote, 2019; Schmedes & Nielsen, 2020; Liboureau & Pampanin, 2024).

After hatchery seeding, male gametophyte fronds can be further cultivated either in land-based tanks (inshore) or transferred to natural environments for continued growth.

Female gametophytes remain microscopic and are essential for sexual reproduction, but do not contribute to the visible crop.

Tetrasporophytes do not propagate or contribute to the main crop unless sexual reproduction is specifically induced, which is not typical in standard cultivation for biomass.





5. INNOVATIONS AND FUTURE TRENDS

For the sector to be considered feasible and strong, several EU standards must be adopted, such as nutritional control, health issues, and sustainability, environmental of course, but also economical, all along the value chain. Concerning aquaculture, the industry has to overcome the rather scarce and sometimes random availability of raw material and substitute for a strong basement of farmer supplier, aquaculture is in the base of the EU seaweed industry.

As revealed by Ebbing et al. (2021) in the culture of *Saccharina latissima* there are two ways to feed field cultures, the more pragmatic but uncontrolled way of hatchery conditions and the more efficient but costly way of controlled culture. Being the first one the predominant one, we understand however, that European standards force us to ensure the provision of culture material from fully controlled hatchery conditions. We propose in this document six innovations aimed precisely at increasing our possibilities to control the quantity and quality of the material that finally ends up in the culture sites.

The expected intensive cultivation work requires a support of quality material to nurture the cultivars. European industry standards require control and sustainability of operations throughout the entire life cycle of the product. For many European species of interest these methods are very poor developed or non-existent.

The following six innovations are recommended for exploration within the context of a hatchery concept executed under controlled conditions:

- In vitro culture for micropropagation and germplasm conservation.
- Spore induction and culture with plant growth regulators.
- Genetic characterization of species. The first step to breeding
- Cryopreservation for germplasm conservation
- Seaweed microbiome and aquaculture
- Seedling materials to increase seeding efficiency and sustainability.





In vitro culture for micropropagation and germplasm conservation.

Plant tissue culture includes a set of biotechnological tools that allow for the controlled growth and multiplication of plant material outside the natural environment, supporting both basic research and a wide range of practical applications in agriculture, industry, and conservation. It refers to the methods used to grow and maintain plant cells, tissues, or organs under sterile (in vitro) conditions on a nutrient culture medium. These techniques enable the propagation, regeneration, and genetic manipulation of plants by culturing isolated plant parts such as cells, tissues, or organs in a controlled environment. Applications include plant propagation, production of disease-free plants, genetic improvement, conservation of rare species, and the production of valuable bioactive compounds (Compost & Compost, 2018; Loyola-Vargas & Ochoa-Alejo, 2018; Shinde et al., 2020).

Plant tissue culture has been an area that has always held high expectations for incorporation into the field of algal biotechnology. This can be seen in the periodic reviews that have been published on the subject, among the most recent ones: Chandimali et al., (2023) provides an upto-date and thorough overview of seaweed callus culture, a key tissue culture technique. The review explains the principles of callus culture, its advantages for rapid and efficient metabolite production, and the current limitations compared to terrestrial plant tissue culture. For example, cell suspension cultures from protoplast-derived cells are rare in seaweeds, limiting the ability to produce homogeneous cell lines for research and industrial applications. In summary, there is a lack of comprehensive understanding of the physiological and developmental processes in seaweed tissue culture, which hinders the optimization and scaling of these techniques.

Science mapping seaweed tissue culture

Certainly, scientific mapping offers us a rather disjointed panorama of scientific production, which is impossible to constitute into concepts. Different groups of algae (red, brown and green) have been worked on for very different purposes, which makes it impossible to generate a common body of doctrine (Table 2.).





Table 2. Essentials on Science mapping of the field seaweed tissue culture.

Data	Description	Comments	
Period	1984-2025		
Documents	71	(see references in Annex II)	
Keywords	401		
Groups	10	(See groups and associated key	
		words in Annex II)	

Minimal Growth as a Viable Strategy for In Vitro Seaweed Germplasm

Preservation

Admittedly, it may not yet be useful for the production of secondary metabolites from free cells, however cultivation of seaweeds in vitro has been suggested as useful for seaweed aquaculture in its present status because it enables clonal propagation of seed material for mariculture, allowing for the selection and cultivation of desirable seaweed strains. The technique allows explants to be cultivated axenically in enriched or artificial seawater culture media, achieving regeneration and even callus formation, which can be exploited for marine agronomy and the propagation of seaweed strains for mariculture (Baweja et al. 2009). In other words, it is an innovative method for the necessary control of operations and plant material needed in the hatchery phase.

In the context of cells fully differentiated into mature thallus, it is not surprising that on some occasions no response has been found when testing the effect of plant hormones, whose action, as we know, is based on cellular competence for growth and differentiation (Pulianmackal et al., 2014).

The preservation of seaweed germplasm in vitro does not necessarily require active proliferation; minimal growth may be sufficient, provided that the primary objective is long-term conservation rather than rapid biomass production. A growing body of research demonstrates that seaweed explants can survive for extended periods under basic or suboptimal culture conditions, even in the absence of plant growth regulators (PGRs), thereby supporting the viability of minimal-growth protocols for germplasm maintenance.

Xu et al. (2024) reported that *Sargassum fusiforme* holdfasts remained viable in vitro for up to 120 days when cultured under controlled temperature (8°C) and salinity (19‰), without the application of PGRs. During this period, explants maintained photosynthetic activity, exhibited low





levels of stress biomarkers, and retained morphological integrity, indicating that basal metabolic activity is sufficient to sustain viability and structural stability over time. Similarly, Liboureau and Pampanin (2024) observed that explants of *Palmaria palmata* demonstrated sustained but modest growth (~5% daily) under laboratory conditions. Although not aimed at propagation, such slow proliferation was adequate to preserve and gradually increase germplasm biomass, highlighting its relevance for long-term storage with minimal input.

Investigations into species such as *Kappaphycus alvarezii* further emphasize the importance of physical factors—particularly salinity and temperature—in maintaining explant viability under PGR-free conditions. Studies by Luhan and Mateo (2017) and Aris et al. (2021) confirmed that even in the absence of chemical stimulants, precise environmental control can promote low yet stable growth sufficient for conservation purposes.

In contrast to micropropagation techniques, germplasm conservation prioritizes genetic integrity and viability over time. Minimal or slow growth is often preferred, as it reduces the likelihood of somaclonal variation and lowers nutrient and energy demands. Fine-tuning parameters such as temperature, salinity, and photoperiod is thus critical for maintaining explant stability and function without inducing excessive metabolic activity. This approach offers a cost-effective, biologically sound, and scalable strategy for the long-term in vitro conservation of seaweed germplasm.



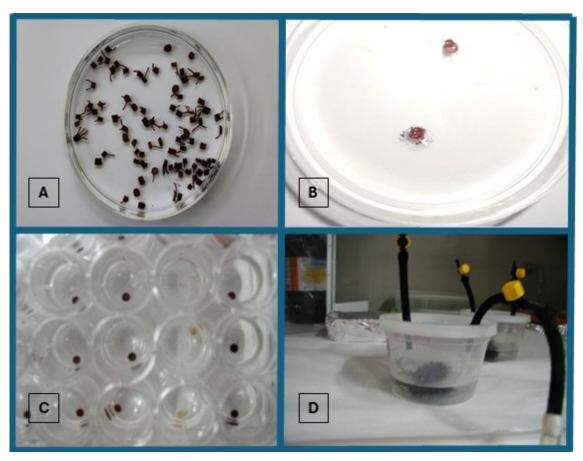


Figure 17. In vitro culture of explants and spores of the red seaweeds Grateloupia imbricata. The cultures lasted for months in Provasoli Enriched Seawater media (PES, Provasoli 1968), particularly the cultures of carpospores (**A**, **B**). Multiwells for antibiotic treatments to establish aseptic cultures (**C**), Bottelgario for ethylene treatments to induce sporulation (**D**). Source: Physiology and Biotechnology Research Group own records



In Vitro Propagation of Gelidium canariensis





Objective

Establish axenic cultures of *Gelidium canariensis* sporelings for controlled in vitro propagation and biotechnological research



Source Material

Thalli Colection: Epiphyte-free *G. canariensis* from the north coast of Gran Canaria Explants used: Sporangial branchlets



Sterilization & Sporulation Protocol

- Disinfection
 - · Rise in distilled water (2x)
 - · Treat with 1% sodium hypochlorite for 2 minutes
- 2 Induce sporulation
 - · Incubate overnight in 0.3 mL autoclaved seawater in multiwell plates
 - Allow 30-50% water evaporation to induce hydric stress
 - Result: 90% of branchlets sporulated under stress (vs. only 40-50% in not-stressed controls)
- 3 Antibiotic treatment
 - PES medium+ antibiotic cocktail:
 - Ampicillin: 0.2 mg/mL
 - Penicillin: 0.2 mg/mL
 - Rifampicin: 0.2 mg/mL
 - Nystatin: 0.2 mg/mL
 - GeO: 0.1 g/mL (anti-diatom agent)



Development timeline

Days 3-4: spore germination begins (germ tube forms)
Days 50-45: axenic spore clusters
(85-100 spores) appear on branchlet surface



Outcomes

- Axenic sporelings succesfully established
- No bacterial, fungal or algal contamination detected
- Morphogenesis matches other Goliolales species

Figure 18. Factsheet outlining the in vitro propagation of red seaweeds without plant hormones (the case of Gelidium canariensis) under sustained growth conditions.





Spore induction and culture with plant growth regulators.

Plant growth regulators (PGRs) are natural or synthetic compounds that play a critical role in modulating the growth, development, and physiological responses of plants, including marine macroalgae. Various studies have confirmed the natural occurrence of PGRs in numerous seaweed species, often at concentrations comparable to those found in terrestrial plants. The major classes of PGRs identified in seaweeds include auxins, cytokinins, gibberellins, abscisic acid, polyamines, and ethylene, along with more recently characterized groups such as jasmonates and brassinosteroids (Spagnuolo et al., 2022; Stirk & Staden, 2014; Prasad et al., 2010; Panda et al., 2012).

The application of auxins and cytokinins, either individually or in combination, has been shown to enhance cell division and tissue growth in seaweed cultures, although excessively high concentrations can inhibit regeneration (Bradley & Cheney, 1990). Gibberellins promote cell elongation and biomass accumulation, while abscisic acid and ethylene are involved in stress responses and developmental regulation (Spagnuolo et al., 2022).

In agricultural applications, the effectiveness of seaweed-based biostimulants is largely attributed to their PGR content rather than merely their mineral composition (Crouch & Staden, 1993; Panda et al., 2012).

Consequently, the study and utilization of PGRs in seaweeds represent a key area for advancing both ecological understanding and the development of commercial biotechnological applications.

PGRs have been shown to be particularly effective when tested on competent tissues, i.e. cells in a hormone-receptive state due to their high multiplicative activity, e.g. spores. PGRs have been shown to be particularly effective when tested on competent tissues, i.e. cells in a hormone-receptive state due to their high multiplicative activity, e.g. spores or sporangium.

Research shows that polyamines, especially spermine, can induce and promote sporulation in seaweeds, thus Polyamines, particularly spermine, induce the maturation of the cystocarp in several species of this group (Guzmán-Urióstegui et al., 2002; Sacramento et al., 2004, 2007, Kumar et al. 2015).





There is a wide variety of volatile organic compounds in marine macroalgae (Garcia-Jimenez et al., 2013; Garcia-Jimenez & Robaina 2017, 2019) and among them, two especially active also described in higher plants: ethylene and methyljasmonate (Garcia-Jimenez et al., 2012, 2016; 2017, 2018, Garcia-Jimenez & Robaina 2017, 2019).

Both methyljasmonate (MeJa) and ethylene cause drastic changes in the reproductive status of red algae species, such as *Pterocladiella capillacea* and *Grateloupia imbricata* in the short term, seven days for ethylene and only 2 days for MeJa. Ethylene induced the maturation of tetrasporangia of the sporophytic phase (2n) of *P. capillacea* (Garcia-Jimenez et al., 2012); in the case of MeJa, its action with effects as sudden as the reduction of the maturation period and the dehiscence of the cystocarp, makes us suspect a parthenogenetic induction of the formation of carpoespores in *G. imbricata* (Garcia-Jimenez et al., 2016; Garcia-Jimenez & Robaina 2017, 2019). The effects of these two volatile hormones are translated at the molecular level into a symphony of activation, deactivation and / or gene coordination according to the reproductive events and / or synthesis of these regulators (Garcia-Jimenez et al., 2016, 2017, 2018).

Although their action on differentiated tissues remains controversial, there is evidence of the usefulness of growth regulators in inducing the development of reproductive structures and the growth of the propagules, which may prove to be an innovation for the future development of efficient hatcheries. Inducing sporulation/reproductive structure with PGRs in hatchery work is to overcome reliance on seasonal collections of wild material.

Science-mapping PGR's and seaweeds sporulation

The scientific mapping of the field seaweed or alga and spore and hormone or plant regulator returns 85 papers between 1989 and 2025, of which the keyword analysis (n =613) with a preponderance of studies on red algae (Figure 19).



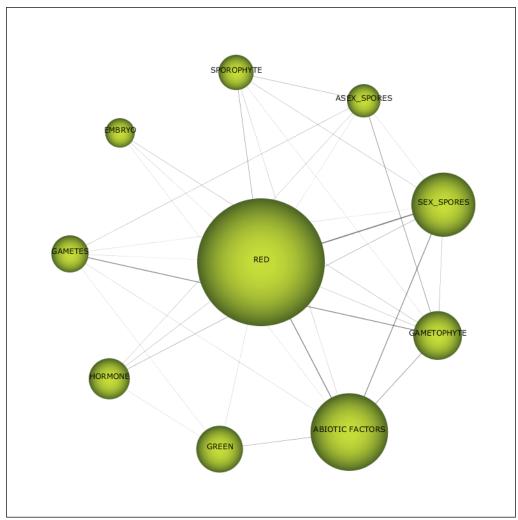


Figure 19. Concept network as a result of science mapping of seaweed or alga and spore and hormone or plant regulator field







100 µm MeJa in 0.01% ethanol in sterile seawater



Spray on 100 mg thallus in Petri dish (3x)



Initial exposure: 1 hour at 50 µmol photons m⁻²s⁻¹



Subsequent culture: Aerated seawater (200 mL)



Photoperiod: 18 h light / 6 h dark

Figure 20. The effects of the plant growth regulator Methyljasmonate (MeJa) on the induction of sporulation in red seaweeds. A simple procedure to induce sporulation is outlined



Genetic characterization of species. The first step to breeding, disease combat and genome editing.

Seaweed aquaculture under European standards requires precise control over the species being cultivated, even at the strain level. This is particularly important if breeding programs are to be implemented, given the high phenotypic plasticity of these organisms (Figure 21).



Figure 21. Specimens of the genus Enteromorpha (filamentous, left) and Ulva (blade, right), formerly separated into two genera and to date reassigned as Ulva genus after Hayden et al. 2012

Various genetic approaches have been employed to investigate the diversity, population structure, and adaptive potential of marine macroalgae. Population genetics studies have utilized tools such as microsatellites, RAPDs, SSCPs, RFLPs, isoenzymes, and DNA sequencing, particularly in red and brown algal species, to assess genetic structure and variability among populations; genetic barcoding using the COI (cytochrome oxidase I) marker has proven effective in distinguishing closely related species due to its higher interspecific divergence compared to other markers like rbcL; while Genome-Wide Association Studies (GWAS) have become a powerful tool in the genetic characterization of cultivars and the selection of high-performing varieties, particularly in major agricultural crops such as rice, maize, wheat, and soybean.



Science mapping genetic characterization of cultivated seaweed species

Improvements in our methods for sequencing genetic material have recently allowed us to access the fine structure of the genome of complex organisms such as seaweeds, so that more and more data are accumulating from areas of the genome with sufficient variability to characterise at the cultivar level, or to associate that variability with traits of interest. The novelty and innovation of the field means that the data are concentrated on one type of seaweed or marker, but we estimate that it will soon be possible to find markers of variability useful for the selection and genetic improvement of all interesting seaweeds. In this sense, the most progress has been made in brown seaweed (Figure 22) and among the markers found, the bibliography found points to those described in Table 3.

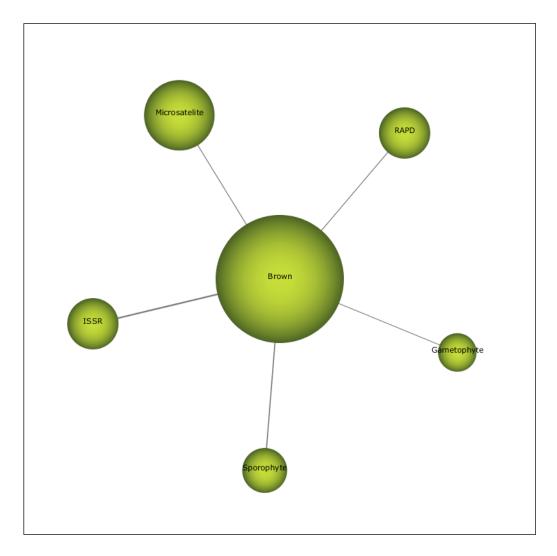


Figure 22. Concept network as a result of science mapping field **genetic markers and seaweed and cultivated** (32 papers since 2004, 246 keywords analysis)





Table 3. Genetic markers found when mapping the field **genetic markers and seaweed and cultivated**

Full Name	Acronym	Description	Examples / Notes
Inter-Simple Sequence	ISSR	A marker technique that amplifies	Used in genetic
Repeat		regions between microsatellites using	diversity studies in
		primers designed for SSRs. It detects	plants (e.g., Oryza
		polymorphisms in multiple loci.	sativa, Zea mays).
Single Nucleotide	SNP	A variation at a single base pair in the	
Polymorphism		DNA sequence among individuals.	
		Highly abundant and stable.	
Microsatellite Repeats	SSR	Short tandem repeats of 1–6 base pairs.	Forensic DNA profiling,
		Highly polymorphic and codominant.	parentage testing.
		Also known as SSRs (Simple Sequence	Example: (CA)n
		Repeats).	repeats.
Random Amplified	RAPD	PCR-based method that amplifies	Used in genetic
Polymorphic DNA		random DNA segments with single	fingerprinting and
		primers of arbitrary sequence.	biodiversity analysis.
Gene Sequence Marker	_	Specific gene or sequence known to be	rbcL, Cox genes
		associated with a trait or phenotype.	
Genome-Wide	GWAS	A method to associate specific genetic	GWAS identifying loci
Association Study		variants (mainly SNPs) with traits	linked to Type 2
		across the genome in large populations.	Diabetes, height, or
			Alzheimer's.

It follows an overview of all these techniques, highlighting how to approach them experimentally and key application in seaweed aquaculture.





DNA barcoding for molecular species of species

DNA barcoding is a taxonomic technique that uses a short, standardised genetic fragments to identify species by comparison with a database of known sequences. For example, universal markers such as mitochondrial or chloroplastic genes (COI, rbcL) and ribosomal regions (ITS) are used depending on the algal group. In green macroalgae of the genus *Ulva*, the ITS (internal transcribed spacer) region of ribosomal DNA has been successfully used to distinguish species, given its high variability between closely related taxa (Favot et al., 2019). This methodology is based on PCR amplification and sequencing of the genetic marker, followed by comparison with references to determine the identity of the sample.

Key Applications of DNA Barcoding in Seaweed Aquaculture

Species verification: Confirms the identity of cultivated species and detects unwanted or wild-growing species (e.g., *Ulva flexuosa* in Portugal) (Favot et al., 2019).

Quality control & traceability: Prevents fraud and ensures the processed product matches the declared species (e.g., *Porphyra/Pyropia, Kappaphycus, Eucheuma*) (Tan et al., 2012).

Hidden diversity revealed: Detects cryptic species or lineages, aiding in selecting high-performance strains for cultivation.

Environmental monitoring: Early detection of invasive or contaminant species via eDNA and metabarcoding enhances biosecurity.

Business and production impact: Reduces risk of misidentification, improves yield and product consistency, and ensures market confidence.

Support for innovation: Facilitates the creation of genetic databases, discovery of bioactive compounds, and protection of commercial strains.



Microsatellites, SNPs and molecular fingerprinting to distinguish genotypes

Molecular tools make it possible to **distinguish genotypes within species** and to quantify genetic variability. Polymorphic DNA markers are used for this purpose, including microsatellites (SSRs) and **SNPs** (single nucleotide polymorphisms). *Microsatellites* are highly variable short repetitive sequences that act as genetic "fingerprints" of each individual, while SNPs are point changes in the genomic sequence that can be detected in large numbers by sequencing. Historically, techniques such as RAPD, AFLP or RFLP were also used, but in the last decade, SSRs and especially SNPs have gained prominence thanks to massive sequencing. In macroalgae, developing these markers used to be a challenge, but today there are efficient methods such as **RAD-seq** (restriction enzyme-associated DNA sequencing) or **GBS** (genotyping-by-sequencing) to discover thousands of SNPs and microsatellites quickly. A recent study (Mauger et al. 2023) showed that ddRAD-seq could identify thousands of novel microsatellite loci in several macroalgae quickly and affordably, yielding 105 useful polymorphic markers in 6 different species. In contrast to traditional marker development methods, which were slow and expensive - next-generation sequencing has greatly accelerated the availability of genetic tools for macroalgae.such as RAD-seq (restriction enzyme-associated DNA sequencing) or GBS (genotyping-by-sequencing) to discover thousands of SNPs and microsatellites guickly. A recent study (Mauger et al. 2023) showed that ddRAD-seg could identify thousands of novel microsatellite loci in several macroalgae quickly and affordably, yielding 105 useful polymorphic markers in 6 different species. In contrast to traditional marker development methods, which were slow and expensive - next-generation sequencing has greatly accelerated the availability of genetic tools for macroalgae.



Key Applications of Seaweed Microsatellites, SNPs and molecular fingerprinting in seaweed Aquaculture

Assessment of genetic diversity: SSRs and SNPs reveal narrow genetic bases in cultivated lines (e.g., few clonal genotypes in *Kappaphycus* and *Eucheuma*; Teasdale et al., 2021). In Malaysia, limited mitochondrial haplotype variation has been observed (Satriani et al., 2023; Lim et al., 2021; Zuccarello et al., 2006).

Strain identification and traceability: Molecular markers verify clonal identity and differentiate elite lines, as shown in *Kappaphycus alvarezii* through genetic fingerprinting tools (e.g., MARINER Sugar Kelp Selective breeding project, Seamark project, BlueBioBoost project)

Parent stock selection: In breeding systems like kelp (*Saccharina*), markers confirm parentality and identify superior hybrid crosses (Bråtelund et al., 2024).

Monitoring genetic changes: Markers track genetic erosion in vegetatively propagated crops and detect gene flow between wild and cultivated populations.

Identifying genes of interest: Neutral markers (e.g., SSRs, SNPs) support the discovery of genes linked to desirable traits (see QTL/GWAS studies).

Business impact: Marker use accelerates cultivar development (e.g., elite *Saccharina* lines in China) and enhances product traceability, resilience, and competitiveness.

Bioprospecting and innovation: Genetically profiled collections help identify strains with valuable biochemical properties, supporting targeted product development and R&D.



Next-generation sequencing and genomic resources in macroalgae

The last decade has seen a significant increase in the availability of macroalgal genomic data, largely due to the development and application of high-throughput next-generation sequencing (NGS) technologies. Advances in mass sequencing (Illumina, PacBio, Oxford Nanopore, etc.) have led to significant developments in this field, as it made possible to decipher the **complete genomes** of numerous macroalgae and to construct **transcriptomic libraries** to understand gene expression. Since the first nuclear genome of a macroalga, *Ectocarpus* sp., a model brown alga, was published in 2010 (Cock et al., 2010), **genomes of representatives of all major groups** (red, brown and green algae) have been **sequenced**.

Some milestones include the genome of the Laminariales *Saccharina japonica*, nori (*Pyropia yezoensis/Neopyropia*), the red alga *Chondrus crispus*, the green alga *Ulva mutabilis*, and more recently that of macroalgae of commercial interest such as *Sargassum fusiforme* or *Macrocystis pyrifera*. In parallel, transcriptomes (with RNA-seq) have been generated for dozens of species under different conditions, providing catalogues of active genes and metabolic pathways. These initiatives have given rise to **genomic resources** (sequences, gene annotations, genome-scale SNP-type markers, etc.) that are the basis for advanced association studies and genetic manipulation. However, it is important to note that many macroalgal genomes remain partially uninterpreted: assessments indicate that more than 50% of predicted genes in algae still lack known function, reflecting how much remains to be investigated in the molecular biology of these organisms (Liang et al., 2014; Xu et al., 2016; Li et al., 2021; Liu et al., 2023, Root, 2022; Poo et al., 2018).



Key applications of whole genomics in seaweed aquaculture

Gene and metabolic pathway discovery: Genomes and transcriptomes help identify genes linked to growth, stress tolerance, and biosynthesis of key compounds (e.g., agar, carrageenan).

Genome-wide SNP databases: Genomic references enable SNP mapping for GWAS and genomic selection, e.g., SNP chips in Saccharina (Zhang et al., 2015).

Reproductive cycle insights: Genomics clarifies life cycle regulation (e.g., sex markers, phase transition), supporting breeding of improved sporophytes.

Transcriptomics for stress resilience: Comparative expression studies reveal resistance pathways (e.g., in *Saccharina japonica*; Zhuang et al., 2024), guiding selection and treatments.

Metagenomics of algal microbiomes: Microbiome analysis identifies beneficial or harmful microbes, enabling probiotic applications in seaweed culture.

Business impact: Accelerates elite variety development, reduces losses, and allows trait-specific breeding (e.g., agar yield, color, texture).

Bioproduct development: Genomic data enable biotechnological innovations in biofuels, pharmaceuticals, and materials; supporting biotech diversification and R&D partnerships.





Marker-assisted selection, QTL mapping and GWAS studies

Once abundant genetic markers and genomic data are available, advanced breeding strategies such as marker-assisted selection (MAS) and genome-wide association studies (GWAS) can be undertaken. These techniques seek to correlate molecular variants with important quantitative phenotypic traits (growth, metabolite content, disease resistance, etc.). There are two main approaches:

- QTL (Quantitative Trait Loci) mapping: this consists of obtaining a mapping population (e.g. offspring from a cross between contrasting parents, or haploid/diploid lines in species with alternating cycles) and genotyping it with markers and then associating regions of the genome with variations in the trait of interest. The result is QTL loci at certain markers that explain part of the phenotypic variation. In macroalgae, this approach has been applied to algae with manageable sexual reproduction. A pioneering example is *Pyropia yezoensis*, where a genetic linkage map was constructed using SRAP markers and QTL were identified for several economic traits of the algae such as stem width and length (Huang & Yan, 2019). Similarly, in *Saccharina japonica* mapping studies have detected QTL for yield traits such as frond length and frond width (Wang et al., 2023).
- GWAS (Genome-Wide Association Studies): This approach exploits genetic variation in broad populations (whether wild, crop collections or varieties) to find statistical associations between SNPs distributed across the genome and the trait of interest. It requires genotyping many closely unrelated individuals with sufficient historical recombination events. Although more common in terrestrial plants, it is recently spreading to macroalgae as genomically characterised populations become available. For example, in 2024 Wang et al. published a GWAS in *Neopyropia yezoensis* (nori seaweed) that analysed 124 genomes from cultivated and wild populations, identifying specific SNPs associated with **thallus length traits** and detecting traces of domestication selection in certain candidate genes (e.g., growth-related). This study combined GWAS with *selective sweep* analysis, marking a milestone in the application of association methods in cultivable red algae.



Key applications of Marker-Assisted Selection and QTL/GWAS in Seaweed Breeding

Development of improved varieties: SNP markers linked to traits like growth or disease resistance enable early selection (e.g., *Saccharina japonica, Pyropia haitanensis*; Wang et al., 2018; Liu et al., 2024).

Improvement of quality traits: GWAS can identify SNPs for traits like carrageenan yield or protein content, aiding selection of superior *Kappaphycus* or *Ulva* strains.

Disease and stress resistance: MAS facilitates the introgression of resistance QTL (e.g., ice-ice resistance in Kappaphycus; Azizi et al., 2018) into cultivated stocks.

Optimised breeding programmes: Knowing favourable alleles enables strategic crosses and gene stacking to create multi-trait elite varieties.

Foundation for genomic selection (GS): Although not yet widely applied in macroalgae, GS promises even more accurate selection using thousands of SNPs.

Business impact: Elite strains with improved growth, resistance, or quality traits increase profitability, reduce losses, and open new product markets.

Innovation and competitiveness: MAS/GWAS support proprietary cultivar development, IP protection, and targeted bioproduct research (e.g., high-ulvan *Ulva*, pharmaceutical-grade Sargassum).





Molecular diagnosis of diseases in seaweeds

Seaweed diseases (caused by fungi, oomycete-like protists, bacteria or viruses) represent a significant risk to intensive farming, and molecular tools are transforming their diagnosis and control. Traditionally, pathogen detection in algae was late (when symptoms were already evident, e.g. spots, rots) and relied on microscopic observation or microbiological culture, slow and sometimes inconclusive methods.

Rapid techniques such as pathogen-specific **PCR**, **real-time quantitative PCR (qPCR)** to estimate infectious loads, and even metagenomic approaches to discover unknown aetiological agents are now available. The basic principle is to amplify DNA/RNA sequences characteristic of the pathogen (e.g. fungal ITS, bacterial 16S genes, viral genes) from samples of algal tissue or culture water, and to detect their presence even at early stages of infection.

These techniques offer **very high sensitivity** - they can detect minute amounts of pathogenic material before it spreads widely. For example, researchers in China developed a qPCR assay capable of detecting in seawater concentrations as low as **10 zoospores per mL** of the oomycete *Pythium porphyrae* (the pathogen causing the "stripe rust" disease of *nori*), and 100 zoospores/mL of *P. chondricola* (another similar oomycete) (Liu et al., 2024). Furthermore, molecular biology allows differentiation between very similar pathogens: using specific markers or enzymatic digests (PCR-RFLP), the same study was able to unequivocally distinguish between *P. porphyrae* and *P. chondricola*, which is crucial given that both species cause similar symptoms but may have different epidemiology (Lee et al., 2021).



Key application of molecular techniques to early disease detection and combat

Accurate identification of causative agents: DNA tools reveal pathogens behind syndromes like ice-ice in Kappaphycus (e.g., *Vibrio, Cytophaga* spp.).

Strain-specific diagnostics: PCR can distinguish virulent strains (e.g., green spot virus in *Pyropia*), guiding targeted responses.

Quantification of infection: qPCR measures pathogen load, helping define action thresholds (e.g., Pythium abundance correlates with red disease risk).

Resistance breeding support: Identifying specific pathogens (e.g., *Pythium porphyrae* in *Pyropia*) enables selection of resistant lines using molecular markers.

Business impact: Early detection prevents harvest losses, enables better planning, reduces treatment costs, and allows certified pathogen-free seed production.

Innovation and product quality: Disease-free cultures ensure reliable bioproduct yields; understanding pathogen-host interaction supports new health strategies (e.g., probiotics, immunity markers).



Genome editing and advanced biotechnology in macroalgae

The latest frontier of molecular tools in macroalgae is **genome editing and genetic engineering**, which allows direct modification of the DNA of algae to give them desired characteristics.

For a long time, genetic manipulation in macroalgae lagged behind due to the difficulty of transforming their cells (resistant cell walls, complex life cycles, etc.). However, recent advances show that CRISPR/Cas9 and other editing technologies can work in some macroalgae, at least under laboratory conditions. In fact, proof-of-concept CRISPR editing has already been achieved in two brown algae (including Saccharina japonica itself) and in a green alga (Ulva prolifera), marking the first cases of gene editing in macroalgae (De Saeger et al., 2024). In these initial studies, to circumvent the low editing efficiency, researchers co-introduced constructs targeting the adenine phosphoribosyl transferase (APT) gene, so that they could select edited cells (mutating APT confers resistance to certain adenine analogues, making it easier to isolate mutants).

Even with these advances, the percentages of edited cells obtained have been low, and **the field faces challenges** such as the need to improve stable transformation of macroalgae and to better understand how these organisms repair DNA (repair is key to increasing CRISPR's efficacy). In addition to CRISPR, classical random mutagenesis techniques (radiation, chemicals) combined with molecular selection are being explored to generate improved varieties.



It should be recalled that even before CRISPR, **spontaneous or induced mutant breeding had already produced** in macroalgae: for example, strains of red algae with faster growth, different pigmentation (pale green vs. deep red) or high spore production were isolated, which then served as the basis for commercial strains (De Saeger et al., 2024). Genome editing takes this to the next level by allowing precise alterations in specific genes.

Key applications of gene editing in seaweed aquaculture

Trait enhancement: Editing can deactivate growth-limiting genes or overexpress biosynthetic genes to boost production (e.g., Tic20 for leaf size in *S. japonica*).

Disease/stress resistance: Introducing resistance genes or removing pathogen entry points can enhance algal resilience (e.g., antifungal pathways in Porphyra).

Reproductive cycle control: Editing may block sexual phases, induce sterile lines for biosafety, or synchronize spore production.

Bioproduct synthesis: Macroalgae could become biofactories for pharmaceuticals, enzymes, or bioplastics via engineered biosynthetic pathways.

Functional gene studies: Knockout mutants help understand gene roles, improving target identification for future breeding.

Business impact: Edited strains may dominate high-value markets (e.g., faster-growing *Kappaphycus* or carrageenan-enhanced lines); increases yield and adaptability. The use of these techniques will position companies at the biotech frontier, attracting R&D collaborations in pharma, materials, and marine bioenergy.

Future outlook: CRISPR editing in *Saccharina japonica* (Shen et al., 2023) and *Ulva prolifera* (Ichihara et al., 2021) mark early successes. First edited commercial strains could emerge within 5–10 years; transformative R&D potential supports sustained industry investment (De Saeger et al., 2024).



Cryopreservation for germplasm conservation

Cryopreservation is the process of cooling and storing biological materials—such as cells, tissues, or organelles—at very low (subzero) temperatures to halt all biological activity and preserve their viability and physiological functions for future use. This technique is essential for long-term preservation, as it prevents cellular damage and death that would occur with simple freezing due to ice crystal formation, osmotic shock, and membrane damage (lussig et al., 2019; Jang et al., 2017; Parihar et al., 2023; Elliott et al., 2017; Rajan & Matsumura, 2018).

The origins of cryopreservation can be traced back to early observations of freezing tolerance, but the field began to advance significantly with the accidental discovery of glycerol's protective effects on cells in the mid-20th century. The first major successes in cryopreservation, particularly for reproductive cells, were achieved in the 1980s. Since then, the development of new cryoprotectants and techniques, such as vitrification, has greatly improved outcomes and expanded applications in medicine, biotechnology, and conservation (lussig et al., 2019; Carr et al., 2002; Vaishnav et al., 2022; Elliott et al., 2017; Marcantonini et al., 2022; Murray & Gibson, 2022).

Key Elements of cryopreservation are cryoprotectants, cooling and thawing rates and storage conditions

Cryoprotectants are chemical compounds added to biological samples before freezing to prevent damage from ice formation and osmotic stress. Common cryoprotectants include glycerol, dimethyl sulfoxide (DMSO), and sugars. They work by reducing ice formation, stabilizing cell membranes, and sometimes enabling vitrification (the formation of a glass-like state without ice crystals). However, their use must be carefully balanced, as high concentrations can be toxic to cells (Carr et al., 2002; Parihar et al., 2023; Vaishnav et al., 2022; Elliott et al., 2017; Rajan & Matsumura, 2018; Marcantonini et al., 2022; Murray & Gibson, 2022).

The rate at which samples are cooled and thawed is critical. Slow cooling can help prevent intracellular ice formation, while rapid cooling (vitrification) can avoid ice altogether but requires higher concentrations of cryoprotectants. Both approaches have their own advantages and challenges, and the optimal method depends on the type of biological material being preserved (lussig et al., 2019; Jang et al., 2017; Carr et al., 2002; Bai et al., 2023; Parihar et al., 2023).





Maintaining ultra-low temperatures (typically in liquid nitrogen at -196°C) is essential for long-term storage, as it ensures that all metabolic and biological processes are effectively stopped (Jang et al., 2017; Parihar et al., 2023; Rajan & Matsumura, 2018).

Science-mapping cryopreservation of seaweeds

Scientific mapping offers us a panorama of scientific production since 1990, discrete in terms of productivity, but important in terms of the consideration of the phycology community for having these techniques. Work has been carried out with the different groups of algae (red, brown and green), particularly with brown algae, focusing on obtaining a good cryoprotectant (Figure 23).

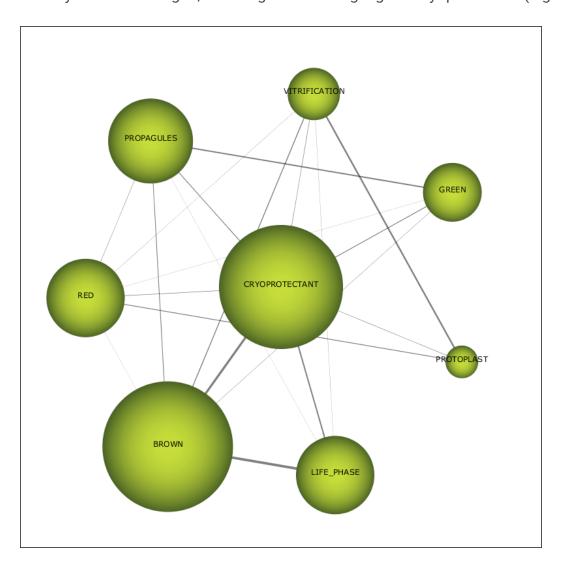


Figure 23. Concept network as a result of science mapping of seaweed/alga cryopreservation scientific field.





Effectiveness of Seaweed Cryopreservation

Cryopreservation has been shown to maintain high viability in various seaweed species, including both model and economically important algae. Post-thaw viability rates can reach 64–87% depending on the species and protocol used, indicating that cryopreservation is a reliable preservation method for seaweeds (Avila-Peltroche et al., 2023; Visch et al., 2019; Taylor & Fletcher, 1998).

Concerning cryoprotectant substances, glycerol and proline (10% :10%) proline has been particularly effective, yielding the highest post-thaw viability in *Ectocarpus siliculosus* and *Acinetospora asiatica* (Avila-Peltroche et al., 2023). For *Saccharina latissima* gametophytes, 10% DMSO used with controlled-rate cooling produced the best results for both male and female gametophytes (Visch et al., 2019).

The following tables summarize the protocols used for different authors in different seaweeds *Ectocarpus* sp. and *Laminaria digitata*, and in the marine plant *Posidonia oceanica* by two authors of this report (**PGJ, MCA**).

The conventional colligative **cryopreservation protocol** developed by Heesch et al. 2012 for the filamentous brown alga *Ectocarpus* sp. involves the following materials and steps:

Material

- A programmable, controlled rate cooler, or alternatively a passive cooling unit and a -80°C freezer.
- Cryoprotectant solutions: 10% (v/v) DMSO and 9% (v/v) d-sorbitol in an appropriate culture medium.
- Plasticware: membrane filters (0.5 μm pore size).
- Petri dishes (5 cm diameter).
- Universal tubes (20 mL).
- Modified Provasoli (MP) medium (West JA & McBride DL, 1999).





Experimental procedures

Cryopreservation of cultures

- 1. One to two weeks before cryopreservation separate thalli into explants (approximately 1–2 mm in length). Then transfer to Erlenmeyer flasks containing 100 mL of culture medium under the same culture conditions.
- 2. Prepare 10 mL aliquots of cryoprotectant solution (10% [v/v] DMSO and 9% [v/v] d-sorbitol in the appropriate culture medium) and filter-sterilize into a sterile universal tube.
- 3. Aseptically transfer 1 mL aliquots of sterilized cryoprotectant solution into 2 mL cryovials.
- 4. Aseptically transfer intact sections of thalli to each cryovial, seal the cryovials, and incubate for 15–30 min at room temperature.
- 5. Program the controlled cooler:
 - Start temperature 20°C;
 - ramp, cool at -1°C min to -40°C;
 - dwell, hold at -40°C for 10 min.
- 6. Start the program to purge the system with nitrogen vapor and to allow the system to stabilize at the start temperature.
- 7. On reaching the start temperature (most systems have an audible alarm), transfer the cryovials to the cooling chamber of the programmable cooler and initiate the cooling ramp.
- 8. After the end of the program, an alarm will sound; rapidly transfer the cryovials to a small dewar containing liquid nitrogen using long forceps.
- 9. Samples for storage should be transferred to the cryostat (ultra-cold freezer) in the liquid nitrogen containing dewar. Transfer of cryovials to the storage system should be performed rapidly using long forceps.

Recovery of cultures

10. To recover cultures, vials are thawed by placing in a preheated water bath (40°C) and agitated until the last ice crystal has just melted.





- 11. On thawing, rapidly transfer to a laminar flow/biological safety cabinet and wipe the outside of the vial with 70% (v/v) ethanol.
- 12. By using a disposable plastic pipette (Pastette), the cryoprotectant solution is aseptically removed, discarded, and replaced by 1 mL of fresh sterile medium. The thallus is then aseptically transferred to a labeled Petri dish containing 10 mL of an appropriate medium. Then cover in aluminum foil and relabel with the strain designation and date.
- 13. Incubate at the standard culturing temperature for the cryopreserved organism; after 24 h, partially remove the foil and after a further 24–96 h, remove all the foil covering.
- 14. After one week, by using standard aseptic techniques, replace the medium.





The **vitrification-based protocol** developed is based on Harding et al. 2008 and successfully employed for *Laminaria digitata* gametophytes, involves the following materials and steps:

Material

- Alginate (5% w/v) encapsulation solution is made from low viscosity (3%) sodium salt. The alginate solution is prepared in preheated (60°C) culture medium in a 250 mL Schott bottle; 5 g of sodium alginate is directly added to the bottle containing deionized water (which should contain a magnetic stirring rod). The bottle contents are vigorously shaken (not stirred) until the alginate is wet (it will not completely dissolve) and thoroughly dispersed in the solution. Sterilize by autoclave the alginate at 121°C for 15 min. Remove the bottle between 80°C and 100°C and place it on a magnetic stirrer until the alginate dissolves (this can be overnight).
- Calcium chloride (100 mM) solution is prepared in deionized water.
- Sucrose (0.5 and 0.75 M) dehydration medium is made in the appropriate culture medium.
- Sterile 9 cm filter papers.
- Sterile 9 cm Petri dishes.
- Multiwell recovery plates (Biddy Sterilin Ltd., 100 mm square Petri dish, or equivalent).
- Sterile forceps.
- Heated magnetic stirrer.
- Thermometer and humidity meter (optional).
- ESP culture medium.

Experimental procedures

Preparation of encapsulated beads

- 1. One to two weeks before cryopreservation, separate thalli into explants (approximately 1 mm in length). Then transfer to Erlenmeyer flasks containing 100 mL of ESP culture medium, under the same culture conditions.
- 2. Remove the supernatant and add \sim 10 mL of 5% (w/v) alginate.
- 3. Gently swirl the mixture of algae and alginate to evenly distribute the sections of thalli, but ensure that air bubbles are not formed.
- 4. By using a disposable sterile plastic Pastette and holding it in a vertical position, slowly dispense the alginate/algal solution dropwise into a 150 mL of 100 mM CaCl₂ and allow the encapsulated beads (henceforth beads) to equilibrate for 60 min.





- 5. Carefully, decant off the calcium solution and transfer the beads to 0.5 M sucrose in culture medium to osmotically dehydrate the cells for 24 h (under standard light and temperature conditions).
- 6. Decant this medium and replace with 0.75 M sucrose in culture medium for another 24 h (under standard light and temperature conditions).
- 7. Remove the beads from the pre-culture sucrose solution and remove excess liquid sucrose medium by blotting the surface of the beads on sterile filter (7–8 cm) papers placed on Petri dishes.
- 8. Transfer the beads to sterile Petri dishes (9 cm) ensuring that they are not touching each other and that they are evenly distributed throughout the dish.
- 9. Place the open Petri dishes with the beads in a horizontal flow laminar airflow cabinet. Note and monitor the temperature (~25°C optimum) and laboratory relative humidity.
- 10. Air-dry the beads in the airflow (\sim 1 m s⁻¹) for 3 to 4 h. This normally results in beads with a residual moisture content of \sim 25%–30% (w/w).

Cryopreservation of cultures

11. Transfer the desiccated beads into cryovials (10 beads per cryovials) and plunge directly into liquid nitrogen in a 1 L dewar.





The conventional colligative cryopreservation protocol developed by Carrasco-Acosta and Garcia-Jimenez (2021) for free cells of the seagrass *Posidonia oceanica* consists of the following materials and steps:

Material

- Liquid Murashige and Skoog (MS) medium (pH 5.7) + 30 g/L sucrose
- Rotary shaker
- Solution of 1.3 M DMSO
- Solution of 60% glycerol
- Sterile filter paper
- Laminar air flow hood (work entirely under laminar air flow using autoclave-sterilized equipment).

Experimental procedures

Cryopreservation of cells

- 1. Cells were suspended at a concentration of 10⁶ cells/mL in a cryoprotectant mixture of 1.3 M DMSO with 60% glycerol.
- 2. The cell suspension was transferred into sterile cryovials.
- 3. Cryovials were first placed at −20°C for 5 minutes to initiate freezing.
- 4. Subsequently, the cryovials were stored at -80°C for 24 hours for long-term freezing.



Seaweed microbiome and aquaculture

Seaweeds host complex communities of microorganisms—known as the seaweed microbiome or holobiont—that play essential roles in their health, development, and ecological function. The seaweed microbiome is highly dynamic, shaped by both the host and environmental factors, and includes bacteria, fungi, viruses, and other microbes that can be beneficial, neutral, or harmful.

Ongoing research is expanding understanding of these complex relationships, with promising applications in aquaculture, biotechnology, and ecosystem management (Ren et al., 2022; Marzinelli et al., 2024; Saha & Weinberger, 2019; Li et al., 2022).

Science-mapping seaweed/algae microbiome and aquaculture

The scientific mapping provides an overview of scientific production since 2015. Work has been carried out with the different groups of algae (red, brown and green algae), particularly with brown algae, focusing on the bacterial characterisation of the microbiome using state-of-the-art genetic techniques. This is confirmed to be an emerging field of research of great interest, as described below (Figure 24).





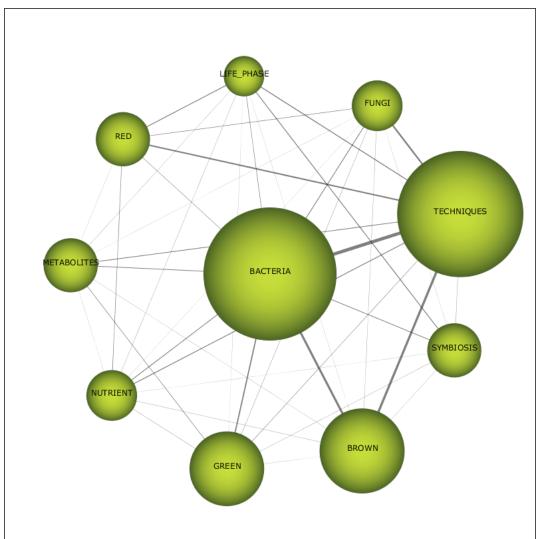


Figure 24. Scientific-mapping Seaweed and Microbiome. The works have focus in the characterization of microorganism, particularly bacteria, using modern techniques in red, green and brown seaweeds.

Microbiomes enhance algal growth and disease resistance

The microbiome facilitates seaweed adaptation to conditions of environmental stress as the release of bacterial promoting factors for algal growth and morphogenesis is crucial for the healthy development of macroalgae. Seaweed beneficial microorganisms (SBMs) can promote seaweed growth and improve disease resistance, offering a pathway to enhance commercial seaweed cultivation (Zhang et al., 2022). Also, biosynthesis of secondary metabolites and degradation of complex polysaccharides by microbial communities enhance nutrient availability for host (Mohapatra 2023). Examples of synergy between seaweed and microbiome are reported for green seaweeds such as *Ulva* species, and for brown seaweeds, such as *Saccharina japonica*





and *Macrocystis pyrifera*, because their microbiomes are linked to rapid growth rates, stress tolerance, disease resistance and bioremediation potential.

Enhancing algal development has been reported for the green seaweed *Ulva rigida* in presence of phyla Cyanobacteria, Planctomycetes, Verrucomicrobia, and Proteobacteria and genus *Glaciecola* (Califano et al., 2020). Specific bacteria can restore normal morphogenesis in *Ulva mutabilis*, which otherwise develops abnormally in their absence (Wichard 2022; Alsufyani et al., 2020). These bacteria release morphogenetic compounds that are crucial for the development of seaweed structures (Alsufyani et al., 2020). Moreover, key bacterial genera such as *Sulfitobacter* and *Roseobacter*, are also associated with growth promotion in cultivated *Ulva* (van der Loos et al., 2021, 2024).

Additionally green seaweeds are used in integrated multitrophic aquaculture as *Ulva* species can reduce the bacteria load through decreasing the abundance of *Vibrio* (de Jager et al., 2024). Otherwise, *Ulva lactuca* (sea lettuce) and *Rhizobia* are associated for fixing nitrogen by bacteria and making it available to *Ulva*, which in turn provides carbohydrates to the bacteria (Kong et al., 2023).

In the brown seaweed *Saccharina latissima*, the core microbiome which includes taxa *Blastopirellula* and *Pseudoalteromonas*, is essential for nutrient cycling and immune regulation (Park et al., 2023; Zhuang et al., 2024). Also, it has been reported that the microbiome of the giant kelp *Macrocystis pyrifera* affected to blade development. Thus, mature blades mainly show Bacteroidia and Gammaproteobacteria (Esaian et al., 2024) that is associated with an increase of exudation of dissolved organic carbon and, in turn, supported microbial growth.

Likewise, the red seaweeds such as *Porphyridium purpureum* get benefits from nitrogen-fixing bacteria, such as *Rosembaum*, which produce vitamins and secondary metabolites that enhance algal growth and reduce oxidative stress (Kim et al., 2024). Furthermore, other red seaweeds such as *Neoporphyra haitanensis* have been reported as recruitment of beneficial bacteria which contribute to nutrient (C, N and S) cycling during early stages of culture and reduce environmental pollutants (Liu et al., 2024).

Regarding disease resistance, it has been reported that microbiome enhances disease resistance as microorganisms can mitigate disease and deter pathogens as well as produce antimicrobial compounds. In this sense, beneficial microorganisms associated with seaweeds play crucial roles in enhancing the health and defence of their host. For example, certain bacteria exhibit





antiviral, antimicrobial, and antioxidant properties, which can protect seaweeds from pathogens. It has been reported that, early successional bacterial strains can protect seaweeds from pathogenic strains, highlighting the importance of microbiome composition in disease prevention (Longford et al., 2019).

Moreover, introduction of bacteria endophytes into *Ulva* sp. reveals bioactivity against the aquaculture pathogen *Streptococcis iniae* (Deutsch et al., 2023). Likewise beneficial bacteria such as *Vibrio alginolyticus* X-2 can protect seaweeds like *Saccharina japonica* from diseases such as bleaching disease by maintaining healthy microbial communities and enhancing the host's immune responses (Zhuang et al., 2023; Wang et al., 2014). Also, *Vibrio* produce biofilms that help red seaweed *Gracilaria vermiculophylla* to attach to surfaces and resist environmental stressors (Düsedau et al., 2023).

Otherwise *Proteobacteria* and *Firmicutes* produce bioactive compounds that help protect seaweed from harmful microorganisms (Ravindra & Reddy 2014). Seaweeds can chemically attract beneficial microbes while deterring pathogens, a process observed in *Agarophyton vermiculophyllum*. This selective recruitment helps in forming protective microbial communities that prevent diseases (Saha & Weinberger, 2019).

Also, Laminaria digitata and Pseudoalteromonas work in synergy in a manner such as Pseudoalteromonas produce antibiotics and other secondary metabolites that help protect Laminaria from pathogens (Handayani et al., 2024). On the other side, Roseobacter spp. produce secondary metabolites that help protect Fucus vesiculosus (bladder wrack) from oxidative stress (Martens et al., 2007).

Ultimately, such beneficial microorganisms can be used in aquaculture to improve the health and resilience of seaweed crops, thereby ensuring a reliable supply of healthy sporelings. Therefore, manipulation of the microbiome can work in favour of seaweed aquaculture practices, as the use of antibiotics in cultures could be reduced.





Table 4. Summarised information on seaweeds and main features of their microbiome with implications for aquaculture

Seaweed type	Seaweed name	Key Microbiome Features	Implications for Aquaculture
BROWN	Ascophyllum, Fucus,	Host Roseobacter, Vibrio, Aeromonas, etc.	Source of biotechnological compounds
	Laminaria saccharina		like antibiotics, antioxidants
	Fucus vesiculosus	Associated with Roseobacter producing antioxidants	Enhances disease resistance; reduces
		and secondary metabolites	oxidative stress
	Laminaria digitata	Synergy with Pseudoalteromonas producing	Disease control through natural microbial
		antibiotics	defense
	Saccharina japonica	Vibrio alginolyticus protects from bleaching; core microbiome includes <i>Blastopirellula</i>	Improves immune response and resilience
	Macrocystis pyrifera	Mature blades host Bacteroidia,	Supports microbial growth, enhances
		Gammaproteobacteria	nutrient cycling
	Saccharina latissima	Core microbiome includes Pseudoalteromonas,	Supports immune regulation and nutrient
		Blastopirellula	exchange





GREEN	Ulva spp	Hosts Sulfitobacter, Roseobacter, Glaciecola, and	Promotes morphogenesis, growth, and
		phyla Proteobacteria, Verrucomicrobia,	pathogen resistance; key in IMTA system
		Cyanobacteria	
	Ulva rigida / Ulva	Dependent on bacteria for proper morphogenesis	Essential bacterial interaction for
	mutabilis		cultivation success
	Ulva lactuca	Associated with <i>Rhizobia</i> (N-fixation)	Enhances nutrient availability, supports
			bacteria-alga mutualism
RED	Porphyridium	Associated with Rosembaum (produces vitamins,	Enhances growth, stress resistance
	purpureum	secondary metabolites)	
	Neoporphyra	Recruits bacteria for C, N, S cycling	Nutrient cycling and early-stage pollution
	haitanensis		mitigation
	Gracilaria	Vibrio helps with surface attachment, biofilm	Increased environmental resilience and
	vermiculophylla	formation	anchorage





Implications of microbiome studies for hatchery management

The integration of microbiomes into algal hatchery systems is a growing field of interest due to its potential to enhance production efficiency and sustainability. However, practical implementation remains limited due to an incomplete understanding of how microbial communities function in artificial systems, ranging from laboratory setups to industrial-scale ponds (Lian et al., 2018).

The success of algal cultivation depends not only on physical and chemical conditions but also on the complex interactions between algae and their associated microorganisms. These interactions can be mutualistic or antagonistic and change throughout the algal life cycle. Understanding the influence of environmental factors on these microbial communities, and their functions, is key to designing strategies that manipulate the microbiome to improve algal health and productivity (Bossier et al., 2016; van der Loos et al., 2024).

In green algae such as *Ulva* spp., bacterial symbionts play an essential role in morphological development. *Ulva mutabilis*, for instance, depends on *Roseovarius* sp. and *Maribacter* sp. to produce morphogenetic compounds such as thallusin, which is critical for rhizoid and cell wall formation (Alsufyani et al., 2020). Additionally, Gram-negative bacteria can regulate zoospore settlement via quorum sensing (Joint et al., 2007), and cross-domain signalling mechanisms have been reported to trigger carpospore release in red algae such as *Acrochaetium* and *Gracilaria* (Weinberger et al., 2007; Singh, 2013).

Bacterial consortia are also fundamental for maintaining healthy algal cultures. In *Saccharina latissima*, the brown endophyte *Laminarionema elsbetiae* interacts with bacterial communities that help protect against disease (Bernard et al., 2018). In coculture, *Ulva mutabilis* shows dramatic improvements in growth, increasing from 0.04 to 3.79 mm/day, and accumulates significantly more glucose and glycerol (Polikovsky et al., 2020).

Effective microbiome management in hatcheries involves several strategies. First, maintaining high microbial diversity ensures ecosystem stability and resilience (Bush, 2015). This can be encouraged by providing a variety of environmental conditions (temperature, pH, nutrient levels) to create diverse ecological niches.





Second, microbial interactions can be manipulated by introducing beneficial strains, such as nitrogen-fixing or antimicrobial-producing bacteria, to displace harmful microbes and enhance the functional capacity of the holobiont.

Third, optimizing nutrient cycling involves monitoring and controlling the availability of key nutrients such as nitrogen, carbon, and sulfur. Ensuring proper nutrient balance supports both microbial functionality and algal productivity.

To implement these strategies, the isolation and selection of functional bacteria is essential. This requires the collection and cultivation of epiphytic and endophytic bacteria from either wild or cultivated algae. Selected bacterial strains are then identified using 16S rRNA sequencing and biochemical characterization.

For endophytic bacteria, small seaweed fragments are incubated in seawater with an antibiotic solution (penicillin, ampicillin, nystatin, GeO₂). After one week, the fragments are transferred to nutrient agar plates, incubated, and colonies are isolated and purified.

For epiphytic bacteria, algae fragments are sonicated in sterilized seawater. The resulting suspension is plated on nutrient agar and incubated. Bacterial colonies are then isolated and purified through successive subcultures.

Tailoring the microbiome to specific algal species remains challenging due to species-specific associations and environmental variability. The ratio of bacteria to algal biomass must be carefully adjusted depending on the desired outcomes.

Case studies demonstrate the impact of microbiome manipulation. *Enteromorpha* and *Hypnea* host diverse bacterial communities that enhance algal morphology and disease resistance (Lakshmanaperumalsamy & Purushothaman, 1982; Egan et al., 2013). Cocultures of *Maribacter* sp., *Roseovarius* sp., and *Ulva mutabilis* improve not only growth but also carbohydrate and amino acid profiles (Polikovsky et al., 2020). Furthermore, bacteria such as *Vibrio parahaemolyticus* and *Bacillus amyloliquefaciens* have shown carbon conversion efficiencies of 22–25% from algal biomass (Kooren et al., 2023).





Table 5. Basic procedures for the integration of the microbiome in the hatchery operations

Procedure	Description	Purpose	
Endophyte Isolation	Incubation of seaweed fragments in antibiotic solution, followed	Access internal microbes and remove surface	
Litaophyte isolation	by culturing	contaminants	
Epiphyte Isolation	Sonication in sterile seawater and plating of supernatant	Isolate bacteria from algal surfaces	
Antibiotic Treatment	Penicillin, Ampicillin, Nystatin, GeO ₂	Selectively eliminate unwanted microbes	
Culture on Nutrient	Growth and isolation of colonies	Obtain pure bacterial strains	
Agar	Growth and isolation of colonies	Obtain pure bacterial strains	
Molecular	16S rRNA sequencing and biochemical testing	Identify functional strains	
Identification	103 Triva sequencing and biochemical testing	identity functional strains	
Screening for	Test for growth promotion, morphogenesis, nutrient cycling,	Select strains for hatchery application	
Functions	pathogen resistance	Select strains for natchery application	
Reintroduction to	Inoculation into algal hatchery systems	Enhance algal development and resilience	
Culture	modulation into digarnatenery systems	Emiliance argan development and resilience	





Seedling materials to increase seeding efficiency and sustainability

Seaweed seedling operations require specific materials to ensure successful cultivation, attachment, and growth of young seaweed plants. The most commonly used materials are ropes (often synthetic or biodegradable), frames, and various culture media for laboratory propagation. Concerns about plastic pollution have led to the development of biodegradable ropes made from seaweed extracts, which offer similar or better durability and strength compared to synthetic options and are environmentally friendly. New materials, such as ropes made from polysaccharides extracted from seaweed species (e.g., *Gracilaria dura, Gelidiella acerosa, Kappaphycus alvarezi*), are being developed to replace synthetic ropes, offering both durability and eco-friendliness (Herlekar, 2015).

Scientific mapping seaweed/algae seeding materials

The concern to replace current seeding materials with materials that increase efficiency while ensuring that their chemical constitution ensures degradation is a relatively recent concern, hence only 6 articles appear in a search for SEAWEED OR ALGA AND SEEDING AND MATERIALS + AQUACULTURE. It is therefore not possible to construct a network of concepts, but it is possible to describe what materials are being proposed and what their properties are.

New biodegradable materials for seaweed seeding. Banana fiber.

Biodegradable ropes made from polysaccharides extracted from seaweeds such as *Gracilaria dura*, *Gelidiella acerosa*, and *Kappaphycus alvarezii* have demonstrated excellent mechanical properties and seawater durability. These ropes remained intact for over 45 days in field conditions and over six months in laboratory-controlled seawater. With a tensile strength of 65 MPa—higher than that of many synthetic counterparts—they present a viable replacement for conventional plastic ropes in marine environments (Herlekar, 2015).

Seaweed waste, particularly from *Eucheuma cottonii*, can be transformed into biodegradable films with tensile strengths ranging from 23 to 39 MPa. These values are comparable to those of common plastics such as PTFE and polypropylene. Notably, these films decompose completely within 14 days, emphasizing their potential for rapid biodegradability (Hidayati et al., 2021).





Incorporating microcrystalline cellulose from bamboo or calcium carbonate fillers into seaweed-based films significantly enhances their tensile strength, water resistance, and overall durability. These composites are even more suitable for demanding marine applications, such as packaging and structural support in aquaculture (Hasan et al., 2019; Khalil et al., 2018).

Several findings suggest that banana fiber is a promising biodegradable material with properties that could make it suitable for aquatic plant cultivation, including seaweed seeding.

Banana fiber, derived from the banana plant's pseudostem, is highly biodegradable, renewable, and possesses good mechanical strength. It has been successfully used in eco-friendly applications such as biodegradable pots, bioplastics, and composite materials for horticulture, demonstrating its ability to support healthy seedling growth and degrade naturally in the environment (Balda et al., 2021; Bordon et al. 2021; Anirudh et al., 2024; Pongsuwan et al., 2022; Akatwijuka et al., 2023).

Banana fibers can be extracted using seawater-based processes, which enhances their environmental compatibility for marine applications and reduces the freshwater footprint (Akatwijuka et al., 2023).





6. INNOVATIONS ALREADY TESTED ON THE MOST WIDELY CULTIVATED SPECIES IN THE EU

Some of the innovations described in the previous section have already been tested on the most cultivated species, and although they cannot be considered fully established methods given the occasional, non-systematic nature of the studies, they do show that their application is possible, so that expectations of their contribution to the European seaweed industry increase with the results obtained. In table 6, main results obtained with the different species are summarized.





Table 6. Innovations introduced so far in hatchery/seeding operations for the most popular species in Europe.

Innovation	In vitro tissue culture	PGR induction of spores or
Species		Sporulation
Porphyra/Pyropia	Axenic Tissue Culture Established: Porphyra	Ethylene (via ACC)
	yezoensis was successfully cultured aseptically	Promotes sexual spore
	in defined synthetic media, enabling controlled	formation <i>Pyropia</i>
	studies of its development.	yezoensis
	Sporophyte (Conchocelis) Phase: Filamentous	Methyl jasmonic acid
	thalli retained their normal, densely tufted,	Enhances
	uniseriate filament structure under axenic	conchosporangia maturation
	conditions, showing no major differences from	Pyropia haitanensis
	standard cultures.	
	Gametophyte (Foliose) Phase: Under axenic	
	conditions, conchospores that would typically	
	form foliose blades instead developed into	
	callus-like masses. Most gametophytes lost their	
	typical morphology after the first cell division.	
	Callus and Rhizoid Formation: Some callus-like	
	masses formed rhizoid-like structures, either in	
	specific areas or along the entire mass.	
	Research Applications: The axenic tissue culture	
	system is highlighted as a promising tool for	
	identifying growth and morphogenetic factors in	
	Porphyra yezoensis	
Alaria	No evidences to date No evidences to date	
Saccharina	No evidences to date	No evidences to date
Palmaria	Plantlets and tetraspores were produced from No evidences to date	
	meristematic tissue within 6 weeks using a	
	freezing-thawing method.	
Ulva	U. mutabilis Axenic culture, full life cycle in vitro No evidences to date	
	U. linza Axenic culture, induced sporulation	
	U. lactuca Morphology controlled by	
	bacteria in vitro	
	U. rigida Reproduction induced by	
	fragmentation	





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Table 6 (cont.)

Innovations	Genetics	Cryopreservation
Species		
Porphyra/Pyropia	SSR/microsatellites Identification and genetic	Gametophytic thalli
	diversity (Wi et al., 2021; Varela-Álvarez et al.,	in DMSO +
	2016)	polymers, Liquid N ₂
	Genomic sequencing cultivar differentiation	storage >95%
	(Hwang et al., 2014; Ge et al., 2019)	survival, clonal
	Trait-specific genes Marker-assisted selection	maintenance
	(Xie et al., 2024; Chen et al., 2021)	Conchocelis by
		Prefreezing,
		encapsulation
		65-90%
		survival, colony
		formation
		Protoplasts
		Vitrification 66.5%
		survival, plant
		regeneration
		Spores/gametes
		Controlled
		cooling/vitrification
		successful
		cryopreservation
Alaria esculenta	SNPs Identification of origin, traceability,	No evidences to
	selection (Ghriofa et al., 2022)	date
	Microsatellites (SSRs) Genetic diversity,	
	population structure, breeding (Creis et al.,	
	2023)	
Saccharina latissima	Genomic selection (GS) Prediction and selection	Male gametophyte
	of superior cultivars (Yarish et al., 2023; Huang	Controlled-
	et al., 2022)	rate cooling + 10%





	Reference genomes Gene identification, marker	DMS0 High
	development (Plott et al., 2025; Serrão et al.,	viability, normal
	2016)	development
	Microsatellites and SNPs Diversity, structure,	Female
	traceability, selection (Cock et al., 2025; Goecke	gametophyte
	et al., 2024; Zhan et al., 2022; Serrão et al., 2016;	Controlled-
	Riddell et al., 2018)	rate cooling + 10%
		DMS0 High
		viability, normal
		development
Palmaria palmata	Reference genome Gene analysis, assisted	No evidences to
	selection (Schmid et al., 2024)	date
	Diversity analysis Identification of groups and	
	crosses (Schmid et al., 2024)	
Ulva spp.	Comparative genomics Species and strain	Gametophytic thalli
	differentiation (Cascella et al., 2020; Lebrault et	Two-step
	al., 2019; Lopez et al., 2019)	cooling, 20%
	High-throughput phenotyping Selection of	glycerol 91%
	strains with better traits (Lebrault et al., 2019;	viability, normal
	Sawicki et al., 2023)	development
	Gene editing (CRISPR) Targeted breeding (Ribera	Vegetative thalli
	et al., 2025; Yamazaki et al., 2024)	Liquid
	Selection of asexual variants Stable and	nitrogen storage
	productive cultivars (Sato et al., 2021)	(up to 120 days)
		82% average
		survival, regrowth

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7. CONCLUSIONS

This toolkit outlines the essential knowledge and innovations required for advancing seaweed hatchery operations in Europe. As seaweed aquaculture expands, the development of efficient and sustainable hatchery practices becomes critical for supporting the industry's growth. Traditional methods, while foundational, often lack the control and scalability needed to meet modern demands.

This report has highlighted six key innovations—ranging from in vitro culture and spore induction with plant growth regulators, to genetic characterization, cryopreservation, microbiome integration, and biodegradable seedling materials—that together create a pathway toward fully controlled hatchery systems.

The integration of these innovations enhances the quality, traceability, and resilience of seedstock, contributing to a more robust value chain and aligning with EU standards for bioeconomy and environmental sustainability. Furthermore, the compilation of species-specific case studies and practical hatchery techniques offers valuable guidance for farmers, researchers, and entrepreneurs aiming to scale operations effectively. The cases studied can be expanded following the same structure as new species are consolidated.

Investing in hatchery innovation is not just a technical upgrade—it is a strategic necessity to ensure long-term productivity, environmental compatibility, and competitiveness of the European seaweed sector in the global blue economy. However, a lot of research is still needed to consolidate controlled methods of hatchery, in view of the difficulty for SME's to address major R&D activities, the alternative approach is to define European reference laboratories that work for the sector.





8. SCIENCE MAPPING METHODS

The scientific mapping of an area of knowledge is a methodology recently imported into the experimental sciences from the social sciences, where it has been widely used (Small, 1973). It is about giving an overview of the dimensions of knowledge in an area of science, but with an objective treatment of the bibliographic records because the records are not chosen on the basis of a previously conceived idea, but it is the processing that gives us the dimensions that the area objectively contains. These dimensions are translated into circles of a network of interactions (Figure 2), in which the relative size of the circle expresses its relative importance and the connection expresses the degree of interaction, the thicker the connection. Behind all this is a mathematical operationalisation that is solved with analysis models, for which various software possibilities are available (Table 7).

Scientific mapping (SM) is an ideal tool when an overview of a particular topic is required, but a standard scientific thematic review cannot be undertaken for reasons of time or efficiency and operationality. SM is more objective and automated, based on large volumes of data extracted from databases such as Web of Science or Scopus, the more interpretative and critical review can include the author's view of the state of the art.

Table 7. Tools available to perform science mapping analysis

Tool	Description
VOSviewer	Software for constructing and visualizing bibliometric
	networks, such as co-citation or co-authorship.
CiteSpace	Tool for detecting emerging trends and transient patterns
	in scientific literature.
CitNetExplorer	Tool for visualizing and analyzing citation networks of
	scientific publications.
Bibliometrix / Biblioshiny	R package for comprehensive bibliometric analysis, with a
	web interface for ease of use.
BibExcel	Tool to assist in bibliometric data analysis and prepare
	data for external visualization.





HistCite	Software for generating historiographs and identifying key
	papers in a research area.
Science of Science (Sci2) Tool	Modular tool for scientific study supporting geospatial,
	temporal, and network analyses.
pyBibX	Python library for bibliometric and scientometric analysis
	with Al-powered topic modeling.
Connected Papers	Visual tool for exploring papers related to a seed article via
	similarity maps.
Inciteful	Generates literature maps from multiple seed articles to
	find connected research.
ResearchRabbit	Al-based tool for exploring and visualizing academic paper
	networks.
Open Knowledge Maps	Web platform for creating visual maps of research fields
	from academic databases.
Citation Gecko	Discover relevant academic literature based on known
	papers and visualize their links.
ScholarGPS	Al-powered platform that analyzes and ranks researchers
	and institutions globally.
scanR	French government-developed platform for large-scale
	mapping of scientific communities.

SCIMAT (Cobos et al. 2012) is an open-source software designed for scientific mapping and bibliometric analysis, enabling the identification and visualization of the intellectual, social, and conceptual structures of a research field based on bibliographic data. It allows researchers to analyze scientific production, detect emerging trends, and evaluate research performance over time. SCIMAT performs co-word analysis by clustering keyword co-occurrences, helping to reveal the conceptual structure of a research area. It also tracks the evolution of research themes across different time periods, showing how topics develop or disappear. Additionally, the software provides performance analysis by offering statistical insights into the productivity and impact of authors, institutions, and countries. Its graphical visualization capabilities generate easy-to-interpret maps, graphs, and networks to represent bibliometric relationships. SCIMAT supports the analysis of data from major bibliographic databases such as Web of Science (WoS) and Scopus.





METHODOLOGY FOR SCIENCE MAPPING WITH SCIMAT 1.1.06 (as used in this study)

All the analyses carried out to complete this report have followed the same methodology.

- 1.- Bibliographic search in Scopus (www.scopus.com) limited to a maximum of approximately 300 records, but relevant in terms of subject matter and chronology (from the 80's to the present).
- 2.- Grouping in group set/words group by distances mode in Scimat v1.1.06.
- 3.- Selection of groups with elimination if they induced tautology or were not representative.
- 4.- Exporting groups and group statistics
- 5.- Analysis following the following protocol and parameter values (selection based on Cobos thesis).
- 1. Define Time Periods:_Split the dataset into relevant time periods for your analysis (e.g., 2010–2014, 2015–2019, etc.).

Configure the Analysis

- Select defined time periods.
- Choose 'Words' as the unit of analysis.
- Set the minimum repetition threshold (e.g., 2).
- Select 'Co-occurrence matrix'.
- Define edge thresholds (e.g., minimum value: 2).
- Choose normalization method: recommend the Equivalence Index.

Clustering Algorithm

Select the clustering method. Recommended: Simple Centers Algorithm.

Define minimum and maximum number of clusters (e.g., 2 to 10).

Map Generation

Generate maps using Core Mapper and Secondary Mapper.

Add quality metrics, such as total citations per cluster.





If using the h-index, make sure to extract it from Scopus.

Longitudinal Maps

To analyze topic evolution, use Evolution Equivalence Index and Longitudinal Equivalence Index.

Save and Document

Save the analysis to your desktop for later transfer.

Export maps via File > Save HTML. This allows recovery of visualizations later.

6.- Generation of reference tables.





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	Phaeophyceae) through tissue culture		Journal of Plant	
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	combined with tissue-cultured method		Science	
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	alvarezii (Gigartinales, Rhodophyta)		Environmental	
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Cryopreservation for germplasm conservation

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Kass, R.	of the food alga <i>Undaria pinnatifida</i>		Resources	207-215
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Renard, P., Arbault, S., Kaas, R.,	A method for the cryopreservation of the	1992	Comptes Rendus de	Vol. 315, pp.
Perez, R.	gametophytes of the food alga <i>Undaria</i>		l'Academie des	445-451
	pinnatifida (Laminariales)		Sciences - Series III	
Kuwano, K., Aruga, Y., Saga, N.	Cryopreservation of the conchocelis of the	1993	Plant Science	Vol. 94, pp.
	marine alga <i>Porphyra yezoensi</i> s Ueda			215-225
	(Rhodophyta) in liquid nitrogen			
Vigneron, T., Arbault, S., Kaas, R.	Cryopreservation of gametophytes of	1997	Cryo-Letters	Vol. 18, pp.
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	encapsulation dehydration			
Kono, S., Kuwano, K., Saga, N.	Cryopreservation of Eisenia bicyclis	1998	Journal of Marine	Vol. 6, pp.
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Liu, H., Yu, W., Dai, J., Gong, Q.,	Cryopreservation of protoplasts of the alga	2004	Plant Science	Vol. 166, pp.
Yang, K., Lu, X.	Porphyra yezoensis by vitrification			97-102





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K., Shin, H.W.	Ulva spp. in cold storage with ampicillin			399-404	
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improve cryopreservation of volvocine green			202-213
algae			
Toxicity of cryoprotectants to gametophytic	2012	Fisheries and	Vol. 15, pp.
thalli of red algae Porphyra yezoensis		Aquatic Sciences	77-81
Cryopreservation of the model alga	2012	Cryo-Letters	Vol. 33, pp.
Ectocarpus (phaeophyceae)			327-336
Cryopreservation of the model alga	2012	Cryo-Letters	Vol. 33, pp.
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Rhodophyta) blade viability		Biology and Ecology	
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	Aquaculture and Conservation		Commercial Seaweed	
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Seaweed microbiome and aquaculture

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Portetelle, D., Michel, G., Vandenbol, M.	brown alga Ascophyllum nodosum is		Microbiology	
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	degrading bacteria			
Zozaya-Valdés, E., Roth-Schulze, A.J.,	Effects of temperature stress and	2016	Frontiers in	Vol. 7
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	macroalga <i>Delisea pulchra</i> and its			
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	microbiomes as a source of		of Phycology	452-465
	antimicrobial chemical diversity			
Lian, J., Wijffels, R.H., Smidt, H., Sipkema,	The effect of the algal microbiome on	2018	Microbial	Vol. 11, pp.
D.	industrial production of microalgae		Biotechnology	806-818





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Mayali, X., Lane, T.W.	the rotifer Brachionus plicatilis			
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Costa, R., Wichard, T.	Effects of Integrated Multi-Trophic		Marine Science	
	Aquaculture on the Microbiome of <i>Ulva</i>			
	rigida (Chlorophyta)			
Polikovsky, M., Califano, G., Dunger, N.,	Engineering bacteria-seaweed	2020	Algal Research	Vol. 49
Wichard, T., Golberg, A.	symbioses for modulating the			
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Badis, Y., Klochkova, T.A., Brakel, J., Arce,	Hidden diversity in the oomycete genus	2020	European Journal	Vol. 55, pp.
P., Ostrowski, M., Tringe, S.G., Kim, G.H.,	Olpidiopsis is a potential hazard to red		of Phycology	162-171
Gachon, C.M.M.	algal cultivation and conservation			
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Wichard, T.	Seaweeds Under Environmental		Marine Science	
	Stresses: A Perspective			
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	(Phaeophyceae) Species			
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Background, Current Practices, and Innovations

