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Large-Scale Environmental Drivers of Kelp Biofouling Based on Literature Data

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ABSTRACT

Macroalgae are increasingly studied for their critical contributions to coastal ecosystems, their potential to mitigate climate change, and their promise as a sustainable food source. While wild macroalgae host diverse epiphytic and invertebrate epibiont communities that enhance biodiversity and ecosystem functioning, biofouling epibionts on farmed macroalgae can negatively impact growth, physiology, and product quality. Although an increasing number of longitudinal studies are trying to establish the drivers of macroalgae biofouling, localized approaches lack sufficient contrasts in environmental conditions to reveal macro-ecological patterns in epibiont occurrence. To gain these contrasts, we analyze data on macroalgae and epibiont taxonomy, study location, and environmental conditions that we have compiled from a systematic literature review and from Marine Copernicus and NASA-OBPG databases of marine data. Our results show that 58.18% of macroalgae epibiont studies focus on the North-East Atlantic coast, which is particularly useful in understanding the potential for the expansion of seaweed aquaculture in this region. Bryozoan fouling depends on sea surface temperature (SST) and an increased biofouling risk was predicted for latitudes greater than 58° in the NE Atlantic coast and around coastal areas in Scotland with cold freshwater inflows. Hydrozoans and gastropods showed a higher probability of occurring on farmed or planted as opposed to wild kelp, whereas gastropods tended to be absent at salinities lower than 30 psu. Our findings provide a first basis for understanding seaweed biofouling risks in the North-East Atlantic and can serve for the spatial planning of the positioning of new seaweed farms.

1 | Introduction

Macroalgae aquaculture is rapidly gaining popularity due to the benefits of derived products for human health [1], its positive effects on biodiversity and ecosystem services [2], and its potential key role in reducing worldwide hunger [3, 4] and mitigating climate change [5, 6]. If properly exploited, seaweed

farming represents a €9B opportunity for Europe and could create 115,000 jobs over 10 years [7]. Despite the recognized suitability of North-East Atlantic coasts for the expansion of seaweed aquaculture [8], the seaweed farming industry in the UK and Europe is mostly characterized by small farms operating with limited use of technology [9]. Although the UK seaweed industry is on the cusp of scaling to commercial

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profitability, a major limitation in the mesotrophic waters of the North-East Atlantic is the proliferation of biofouling organisms on cultivated seaweed [10] which can have unpredictable and devastating impacts on product yield and quality [10, 11]. Despite the clear benefits of macroalgae aquaculture for ecosystem health and human societies and the damages incurred by biofouling to the industry, there is very limited knowledge on how the conditions in the marine environment are driving the presence of epibionts on macroalgae. Shedding more light on this topic is key to predicting the well-being of coastal seaweed under future temperatures and seascapes as well as empowering more sustainable and profitable seaweed aquaculture practices.

In macroalgae, and specifically kelp aquaculture, hydrozoans are among the most problematic epibionts as they are particularly resistant to physical removal and chemical treatment, whereas their spread cannot be controlled due to their ability to rapidly reproduce and regenerate [12]. Bryozoans are equally problematic due to their capacity to encrust the seaweed in dense lace-like mats [13]. Although bryozoans and hydrozoans contribute disproportionately to the biofouling biomass [10], gastropods and amphipods can also be particularly damaging due to direct grazing effects on seaweed [14, 15] and increased allergen risks for humans [16]. When biofouling invertebrates attach and colonize the macroalgae surface, they interfere with photosynthesis, respiration, and gas exchange by physically blocking and shading the surface area of the blade. The build-up of epibionts alters the pH and oxygen concentration of the surrounding water while it increases the weight and drag of the macroalgae, impacting their ability to take up nutrients via passive movement [11]. For instance, hydrozoan colonies are associated with a decrease of several key nutrients in the kelp, such as copper, cadmium, nickel and chromium [17]. Due to these effects, biofouling highly impacts the health of farmed seaweed and leads to reduced crop yield, product quality, market value, increased waste, and human health risks [11, 18].

Latitudinal studies of epibiont monitoring over an annual cycle are important for understanding the succession of biofouling species on wild or farmed macroalgae, thus assisting in regulating the timing of optimal macroalgae harvesting times [19]. Site-specific studies can also be useful for fine-scale adjustments within existing farms, such as orientation and depth positioning of seeded lines [20]. However, latitudinal studies, being geographically constrained, often lack sufficient information and contrast in environmental conditions to empower causal modeling of biofouling drivers. To overcome this limitation, data on macroalgae epibionts from multiple published studies can be compiled with environmental data from open-source databases such as Copernicus and NASA-Ocean Biology Processing Group (NASA-OBPG).

The aim of the present study was thus to investigate the environmental drivers of macroalgal biofouling taxa and their large-scale distribution patterns. To achieve this goal, we compiled data from a systematic literature review of papers on macroalgae epibionts as well as from E.U. Copernicus Marine Service Information (CMEMS), Marine Data Store (MDS) and NASA-OBPG. Specifically, we first aimed to identify which areas globally have received higher sampling effort on the topic

of macroalgae biofouling communities and second, which specific macroalgae groups have received the highest attention. Focusing on the area and taxon of highest coverage, we then identified the environmental variables driving the presence of specific biofouling taxa and modeled the distribution of biofouling taxa spatially. Our findings represent the first milestone toward quantifying seaweed biofouling risk at a broad scale and thus enabling spatial planning of new farm locations as well as predictions of biofouling risk under climate change scenarios.

2 | Methods

2.1 | Overview of Methodological Approach

The study aims were addressed by the following steps. First, we compiled data on macroalgae epibionts from a systematic literature review, and we supplemented this with environmental data from the CMEMS, the MDS and the NASA-OBPG. Second, we identified geographical regions that have received increased research focus and thus a higher sampling effort on macroalgae epibiont communities. Third, using all compiled data, we modeled the relationship between the probability of occurrence of seaweed biofouling taxa as a function of environmental covariates. Finally, we further supplemented environmental data from the North-East Atlantic region, which was identified in step 2, and, using the model developed in step 3, we modeled and graphed the spatial distribution of prevalent biofouling taxa.

2.2 | Systematic Literature Review

A systematic literature review of published papers on communities of epibionts on macroalgae was conducted on Google Scholar, using the following keywords: “seaweed” OR “kelp” OR “macrofauna” + “epibionts” OR “epifauna” OR “biofouling.” The search was initiated from the year 1976, when the oldest relevant publication was recorded, until April 15th, 2023. This initial search resulted in 364 papers on macroalgae epibionts. A further selection process took place whereby a set of criteria was applied based on the abstract, materials, and methods of each publication (Figure S1). An important criterion applied at this stage was the selection of papers which focused on invertebrate communities of epibionts rather than a single epibiont species or epiphytic algae. This approach was essential for addressing our objectives whereby the absence of an epibiont implied that the species was either absent or sufficiently rare instead of non-investigated. This secondary selection process resulted in 54 publications, which corresponded to 234 sampling events: 112 samplings on Kelp (Laminariales), 102 on other brown algae (other Ochrophyta), 16 on green algae (Chlorophyta), and 24 on red algae (Rhodophyta). “Sampling event” does not entirely overlap with “sampling site”, “algae species”, and “sampling period”; for example, multiple “sampling events” of the same “algae species” might take place within a “sampling site.” After the full selection process, the earliest “sampling event” recorded in our dataset was in 1978, and the latest was in 2019. Finally, we supplemented the resulting dataset with our own monitoring of a seaweed farm from the Island of Skye, NW Scotland that was

sampled between September 2021 and July 2022 (described in the Supporting Information).

2.3 | Data Compilation

For each of the 54 publications we extracted the seaweed species, epibiont taxa (at species level whenever possible), season and year of sampling, and condition (wild vs. not wild). We collected the GPS position of the sampling site provided by each article. In some cases, GPS position had to be deduced from the map provided in the paper with a precision of <3 km. This level of precision was possible because all the studies were conducted on a small geographical scale (<50 km). For each epibiont taxon, complementary information on higher taxonomic levels was extracted from the World Register of Marine Species (WoRMS) using the “Taxon match tool” function of the website. Only 3 out of 5794 epibiont observations were not recognized by WoRMS and were thus deleted from the dataset. In situ environmental data were not represented in our dataset across multiple studies, either because they were not measured, they were not provided or they were measured with non-comparable protocols. To ensure the availability of consistent environmental data for our analysis, we thus used satellite data to obtain sea surface temperature (SST), salinity, wave height and chlorophyll-a concentration for each sampling site. All data were obtained from Copernicus Marine Data Store or the NASA Earthdata website and represented the value at sea surface level (Table 1). Each sampling location was associated with a mean value of environmental data weighted by area at a 5 km radius buffer circle.

For each environmental covariate, a mean was calculated for each sampling location across time. Due to data availability, the local averages of SST and chlorophyll-a were calculated from January 2003 to December 2019, and the local averages of salinity and wave height were calculated from 1993 to 2019 (2019 corresponding to the last epibiont sampling event in our dataset). Data averaging was essential to minimize the effect of seasonal and interannual variation, to obtain a more representative value of the general environmental conditions at each sampling

location, and finally to ensure consistency, as publications were often not defining the sampling season.

2.4 | Data Analysis

To test which of the algal groups in our study (Laminariales, other Ochrophyta, Rhodophyta, Chlorophyta) are richer in epibiont phyla, we used two indicators of diversity and namely the phyla richness per sampling event as well as the Whittaker index [25], WI:

$$WI = \frac{S}{a} - 1$$

where S is the total number of epibiont phyla recorded for a given algal group and a is the average number of distinct epibiont phyla per sampling event for the given algal group. The WI index is based on presence-absence data thus making it more robust against sampling biases that affect abundance measures. The WI is reflecting community turnover and thus offers complementary insights to phyla richness. Specifically, higher WI values are expected for algal groups in which sampling events were more different to each other in terms of their epibiont phyla composition. Essentially, WI values are reflecting the epibiont phyla turnover observed via phyla accumulation curves which we calculated with the “specaccum function” of the “vegan” package [26], using a randomization method of 1000 permutations.

We fitted a binomial generalized mixed effects model to estimate the probability of biofouling presence of specific epibiont taxa on macroalgae fronds as a function of macroalgae group (kelp vs. other Ochrophyta), kelp condition (wild vs. not wild), SST, salinity, chlorophyll-a, and wave height. The publication identifier was included as a random effect to account for differences in sampling protocol and effort as well as the fact that each publication might have repeated measures across different algae species and sites. Each epibiont taxon was treated as a binomial response (presence/absence) because abundance was often not recorded, or was expressed in non-comparable units, and because studies often sampled different seasons which were pooled together, inducing bias on measures of epibiont biomass. Models were

TABLE 1 | Publicly available data sources from where environmental variables were compiled from and were used in the seaweed biofouling distribution models.

Variable (unit)	Resolution	Years	Identifier	Reference
SST (°C)	0.042° (~4 km)	01–2003 12–2019	MODIS_AQUA_L3_SST_ MID-IR_DAILY_4KM_ NIGHTTIME_V2019.0 [21]	NASA-OBPG, 2020; DOI: 10.5067/MODAM-1D4N9
Salinity (psu)	0.083° (~8 km)	01–1993 12–2019	GLOBAL_MULTIYEAR_ PHY_001_030 [22]	Global Ocean Physics Reanalysis; DOI: 10.48670/MOI-00021
Chl-a (mg m ⁻³)	0.042° (~4 km)	01–2003 12–2019	AQUA MODIS Level-3 Binned Chlorophyll, Version 2022 [23]	NASA-OBPG, 2022; DOI: 10.5067/AQUA/MODIS/L3M/CHL/2022
Wave height (m)	0.2° (~22 km)	01–1993 12–2019	GLOBAL_MULTIYEAR_ WAV_001_032 [24]	Global Ocean Waves Reanalysis; DOI: 10.48670/MOI-00022

fitted with the “glmer” function of the lme4 package version 1.1–32 in R [27]. We performed backward selection of important variables using the Likelihood Ratio Test. Using the model formula predicting the probability of specific epibiont presence as a function of environmental variables and using spatial environmental layers, we were able to spatially predict the probability of presence of Bryozoa and Cnidaria (phylum), Hydrozoa (Class), Gastropoda and Gymnolaemata (Class), Littorinimorpha and Cheilostomatida (Order), and Ischyroceridae (Amphipod family) (Table 2). This analysis was done using the “predict” and “st_rasterize” functions from the “stats” and “stars” packages respectively [28, 29].

3 | Results

3.1 | Geographical Distribution of Studies on Seaweed Biofouling

From a total of 55 studies (54 from the literature review + our own dataset), over half (58.18%) took place in the North Atlantic, whereas much less took place in the South Atlantic Ocean (5.45%). From the remaining studies, 18.18% took place in the Pacific Ocean, 7.27% in the Arctic Ocean, 5.45% in the Mediterranean Sea, 3.64% in the Indian Ocean, and 1.82% in the Antarctic Ocean. Sampling effort varied across algae groups: a total of 11 species of Laminariales (kelp), 38 species of other

Ochrophyta, 12 species of Rhodophyta, and only four species of Chlorophyta were the focal species of studied macroalgae (Figure 1).

The systematic review gathered 5791 observations of epibionts, with 62.64% reported at the species level and 92.01% at least at the genus level. In total, 23 different phyla, 45 classes, 122 orders, 675 genera, and 844 species were catalogued. Higher total phyla richness of epibionts was observed on Laminariales (total phyla richness = 21; mean = 4.17 ± 2.57) and on the other Ochrophyta (total phyla richness = 17; mean = 5.19 ± 2.91) than on Rhodophyta (total phyla richness = 12; mean = 4.17 ± 2.63) or Chlorophyta (total phyla richness = 11; mean = 4.08 ± 2.61).

3.2 | Comparison of Epibiont Phyla Richness and Turnover Between Algal Groups

The mean phyla richness of epibionts was calculated from all sampling events within each algae group, and no significant difference was found between the four examined algae groups (ANOVA, $p=0.121$) (Figure 2A x-axis). However, epibiont phyla found on kelp were the most variable between sampling events compared to the other three algal groups ($WI_{kelp} = 3.73$; $WI_{\text{Other Ochrophyta}} = 2.47$; $WI_{\text{Rhodophyta}} = 2.07$; $WI_{\text{Chlorophyta}} = 1.65$) (Figure 2A y-axis). This was also reflected by the cumulative epibiont phyla by increasing sampling

TABLE 2 | Effects of environmental variables chl-a, salinity, SST, wave height and kelp condition (wild vs. not wild) on the probability of different epibiont taxa being present or absent on kelp fronds.

Response variable	Chl-a	Salinity	Temperature	Wave height	Condition	Sample size (n)			
						Taxon present		Taxon absent	
	LRT (p)	LRT (p)	LRT (p)	LRT (p)	LRT (p)	Wild	Not wild	Wild	Not wild
All Bryozoa	0.727 (0.394)	0.236 (0.627)	15.328 (<0.001)	0.001 (1.00)	1.301 (0.254)	30	30	26	13
Gymnolaemata	0.266 (0.606)	0.042 (0.838)	11.202 (<0.001)	0.419 (0.517)	0.499 (0.480)	28	21	28	22
Cheilostomatida (Membranipora)	0.266 (0.606)	0.042 (0.838)	11.202 (<0.001)	0.419 (0.517)	0.499 (0.480)	28	21	28	22
All Cnidaria	2.477 (0.116)	1.501 (0.221)	0.037 (0.847)	0.813 (0.367)	5.839 (0.016)	16	32	40	11
Hydrozoa	1.242 (0.265)	1.160 (0.281)	0.056 (0.813)	0.138 (0.710)	7.800 (0.005)	14	32	42	11
All Gastropoda	0.095 (0.758)	5.968 (0.015)	2.375 (0.123)	0.049 (0.825)	1.133 (0.287)	51	14	5	29
Littorinimorpha	3.017 (0.082)	1.202 (0.273)	0.180 (0.671)	0.469 (0.493)	4.811 (0.028)	29	12	27	31
Ischyroceridae (mostly Jassa)	-0.058 (1.000)	4.682 (0.030)	0.285 (0.593)	0.732 (0.392)	1.143 (0.285)	34	9	22	34

Note: Results are presented for different taxonomic levels as effects were not always consistent within specific phyla (e.g. see Gastropoda) and also because for some taxa (e.g. Amphipoda) information might be available only for one family (e.g. Ischyroceridae). Sample size available for the comparison between kelp condition (wild vs. not wild) is also provided. (p-values corresponding to significant effects are in bold).

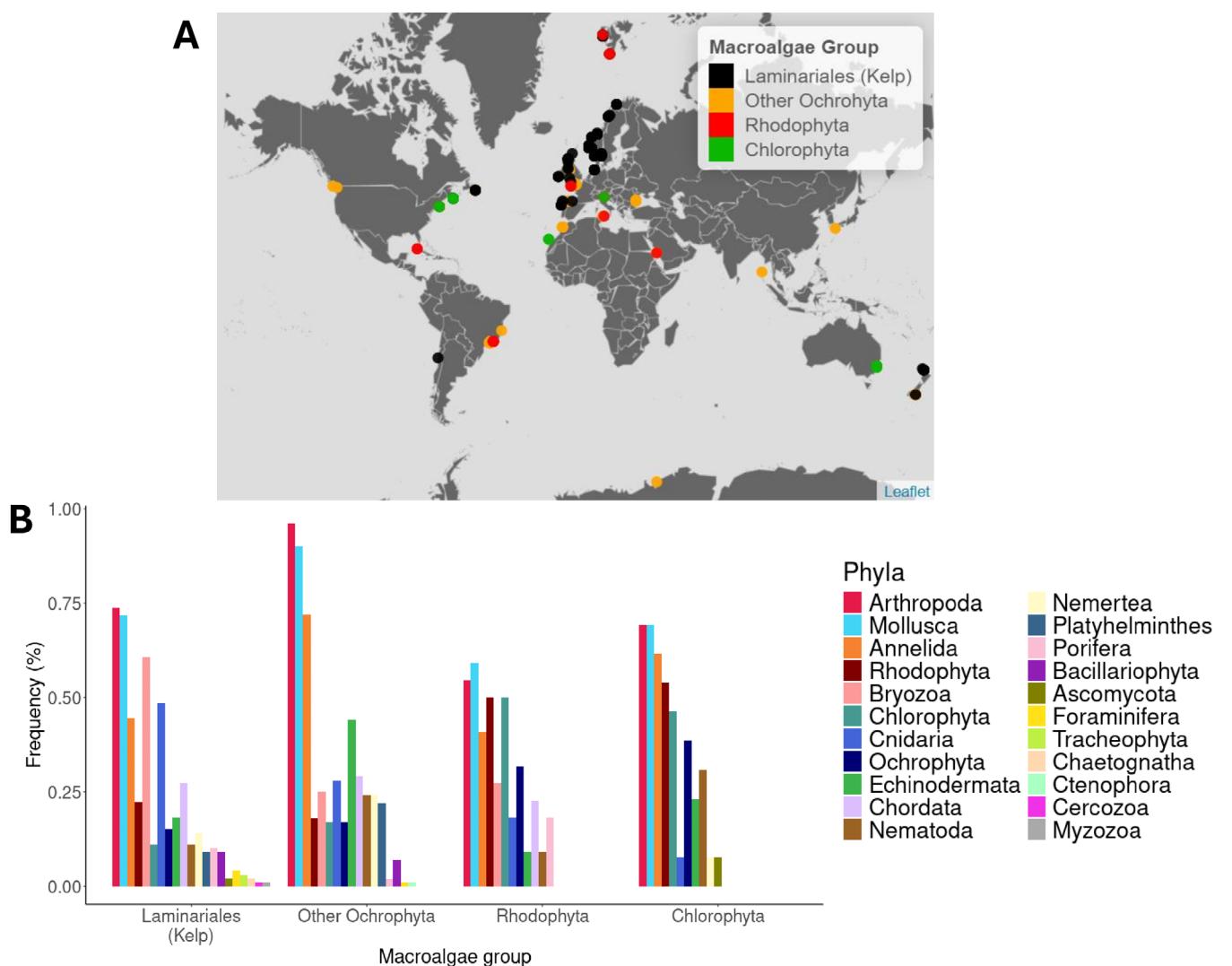


FIGURE 1 | (A) Geographical distribution of 55 studies on macroalga epibiont communities (note that some points overlap). (B) Frequency of all epibiont phyla observed on each of the four algae groups.

events (Figure 2B). In addition, the leveling-off curves of kelp, other Ochrophyta, and Rhodophyta might be indicative that sampling effort within these groups has been more exhaustive than Chlorophyta.

3.3 | Environmental Drivers of Kelp Epibiont Taxa

Irrespective of taxonomic level (phylum, class, order), there was a significantly higher probability of bryozoan presence on kelp for temperatures below 11°C (Table 2; Figure 3A). Bryozoan presence did not depend on whether kelp was wild or not wild (i.e., farmed/planted) (Table 2). On the other hand, Cnidaria, and more particularly hydrozoan presence, was only dependent on whether kelp was wild or not wild (Table 2). Specifically, a significantly higher probability of hydrozoan biofouling was found on kelp that was not wild (farmed/planted) compared to wild populations (Figure 4). Finally, the probability of the presence of Gastropoda and Ischyroceridae amphipods significantly increased with increasing salinity (Table 2; Figure 4B).

Using the data from the NASA and Copernicus databases, the mapped probability of bryozoan presence in the North-East Atlantic shows a low risk of biofouling at the south of the English Channel, an intermediate area between 53°N and 60°N where presence is likely to be determined by coastal factors such as cold freshwater inflows lowering the local SST, and finally an area with a high risk of biofouling, northern than 58°N (Figure 5). We only present the map for bryozoans as this was the only taxon that was consistently affected by temperature across all three epibiont taxonomic levels examined, and its distribution based on temperature can be clearly visualized according to the large-scale SST patterns. On the other hand, gastropods and amphipods, which are more influenced by inshore patterns in salinity, cannot be visualized in this map.

4 | Discussion

The results of our study provide critical insights into the environmental drivers of macroalgal biofouling, particularly in the North-East Atlantic, where the expansion of seaweed

aquaculture is rapidly increasing. Our findings highlight significant variations in epibiont communities, with bryozoans showing a strong dependency on lower SST, while hydrozoans preferentially colonize farmed kelp over wild kelp populations. This differentiation underscores the complex interactions between environmental conditions and biofouling dynamics, suggesting that site-specific factors, such as local salinity and temperature fluctuations, play crucial roles in shaping epibiont assemblages. By compiling data from multiple sources, we identified geographic hotspots of research and established a foundation for predictive modeling of biofouling risks to investigate responses to future global warming scenarios. These insights are essential for informing sustainable aquaculture practices

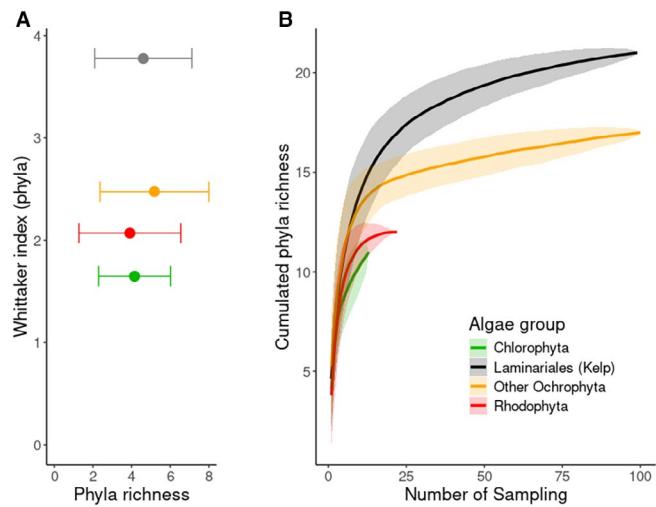


FIGURE 2 | Comparison of the mean phyla richness (x-axis) and Whittaker index (y-axis) among the four algae groups (A). Whiskers around the mean represent the 95% confidence interval. Comparison among algae groups of cumulative epibiont phyla richness by increasing number of sampling events after 1000 simulations (B). Shaded areas represent 95% standard error intervals.

and enhancing the resilience of macroalgal farms against the challenges posed by biofouling organisms.

Hydrozoan presence on kelp fronds was not associated with any of the studied environmental covariates. However, hydrozoans had a significantly higher probability to be present on non-wild kelp (i.e., farmed/planted) than on wild kelp populations. One hypothesis is that the higher density of farmed kelp reduces hydrodynamic forces, creating a more favorable environment for the settlement and growth of hydrozoan larvae [30, 31]. This hydrozoan prevalence might also be associated with an absence of benthic predators (e.g. snails, worms, anemones, crabs) in farmed kelp as they are not in contact with the benthic communities. Another possibility is that as farmed kelp is hanging vertically from the lines, this orientation is favoring more heterotrophic epibionts [32] compared with the fronds of wild kelp which are more exposed to light. Finally, another explanation might be related to density-dependent effects of larvae transmission and settlement between the fronds in the more densely packed cultivated kelp; however, these hypotheses remain to be tested in future studies on the topic.

Bryozoan presence in our study was linked to temperatures below 11°C. The relationship between temperature and bryozoan biofouling remains uncertain in the literature. For example, a previous model based on 29 sites predicted an increase in bryozoan biofouling with rising temperatures [33], while in situ observations indicate a higher percentage of bryozoan coverage in northern Norway (where water is colder) compared to southern Norway [13]. Literature specifically addressing bryozoan biofouling on kelp is more prevalent in Norway and diminishes further south, suggesting that bryozoans may be less problematic in more temperate latitudes. Although our analysis incorporated samples from various seasons, bryozoans typically exhibit a strong peak in abundance and coverage around late June, indicating that we may have underestimated their distribution range.

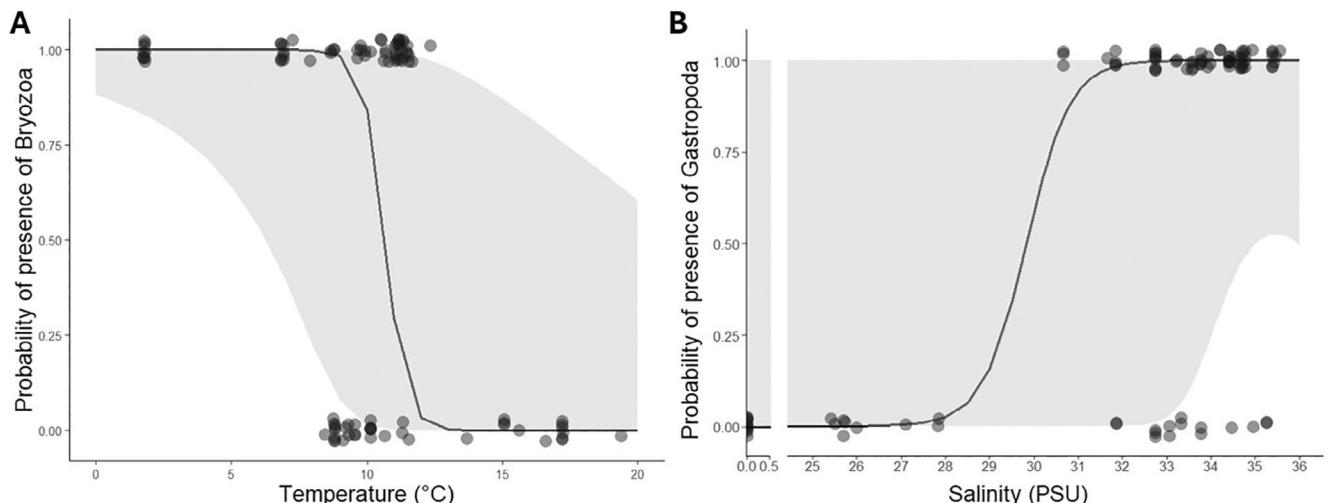


FIGURE 3 | Probability of kelp biofouling by Bryozoa with increasing temperature (A) and gastropods with salinity (B) in the North-East Atlantic. Points represent the presence or absence of the biofouling taxon from the kelp fronts (1-present, 0-absent) using the data collected from our systematic literature review (note that points may overlap). Black lines represent the fitted probability values from the binomial model (see also Table 2) and gray funnels represent 95% confidence intervals.

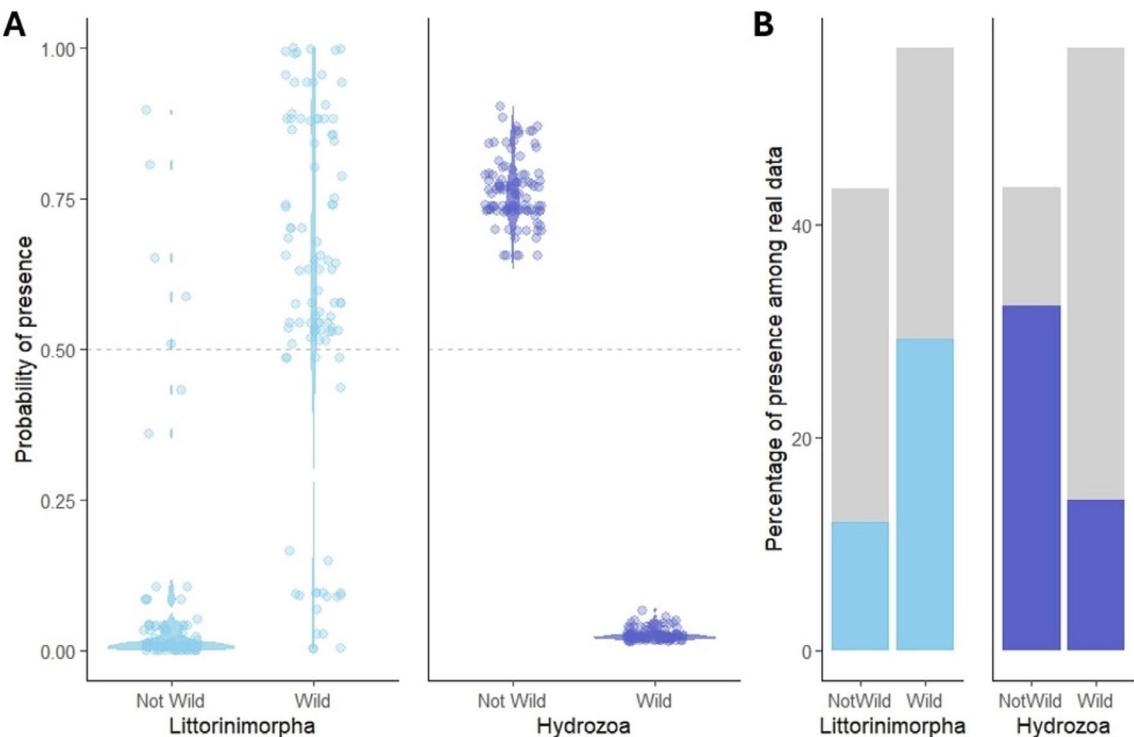


FIGURE 4 | Probability of presence estimated using a binomial Generalized Mixed Effects Model (A) and real data (B) for Littorinimorpha and Hydrozoa, according to the condition (wild/non-wild) of kelp (Laminariales). Both analyses are based on 99 samplings across 26 publications. In panel B, the colored area represents presence, while the gray area indicates absence of the taxon.

The sensitivity of Gastropoda to low salinity seen in our study aligns with industry mediation measures where kelp fronds are washed with freshwater to remove gastropods [34]. Our results also align with previous studies, albeit the salinity threshold we identified is more stringent. For example, it has been demonstrated that the activity of *Littorina littorea*, a species present in circa one third of our samples, is altered for at least a week following just 12 h in 15% salinity [35]. Similarly, *Rissoa parva*, the third most abundant species in our study, has been reported to perish after 1 week of exposure to salinity levels below 14% [36]. However, many studies have focused primarily on the adult stage, typically at a single temperature, for short durations, and without repeated stress, which may result in an inflated tolerance to low salinity compared to field conditions. In contrast, our threshold represents a yearly mean tolerance, reflecting the overall environmental conditions that a population can sustain.

Since bryozoans and hydrozoans primarily feed by suspension, we aimed to use chlorophyll-a concentration as a proxy for food availability [37]. However, kelp is known to grow in highly productive coastal areas where mean chlorophyll concentrations are likely to exceed limiting levels. Measurements of growth rates for *Electra pilosa*, a common bryozoan, indicated a homogeneous range for chlorophyll concentrations between 1.26 and 6.3 µg/L [38]. In our dataset, comprising 55 macroalgae studies, 85 out of 99 samples collected from kelp sites had chlorophyll-a concentrations above 1.26 µg/L, with the minimum concentration being 0.86 µg/L. Therefore, it is probable that chlorophyll concentrations in the North-East Atlantic are frequently above limiting levels, thus minimizing the impact of this variable on

the growth of most epibionts. However, it should be noted that due to metadata availability limitations, our analysis did not account for seasonal variations, which might have masked the importance of seasonal variations of chlorophyll-a on epibiont occurrence. This is particularly true given that recent studies have highlighted that fouling intensity is higher in late spring and summer [19]. This limitation in the current dataset highlights the importance of obtaining primary large-scale data on biofouling epibionts over a full annual cycle.

Wave exposure can have pervasive impacts on both macroalgae species composition [39] and epibiont composition [11]. Specifically, higher biomass of biofouling and especially hydrozoans has been linked to weak hydrodynamic conditions [11, 40], whereas specific amphipod epibionts have been linked to high wave exposure [41]. However, in our study, wave height was not identified as a significant driver of biofouling. The spatial resolution of the wave data (22 km radius) was broader than that of other environmental variables (4–8 km radius). This reduced spatial discreteness between sampling sites likely diminished the statistical power in our analysis. This is particularly the case because wave height and hydrodynamics are highly sensitive to local features such as topography (smooth beach, bay, cliff) and depth.

In conclusion, our results indicate that certain biofouling species are linked to environmental variables such as temperature (for bryozoans), salinity (for gastropods), and the type of kelp population (wild vs. not wild) for hydrozoans. Laminariales support richer and more diverse epibiont communities compared to other algal groups, emphasizing the need for further research

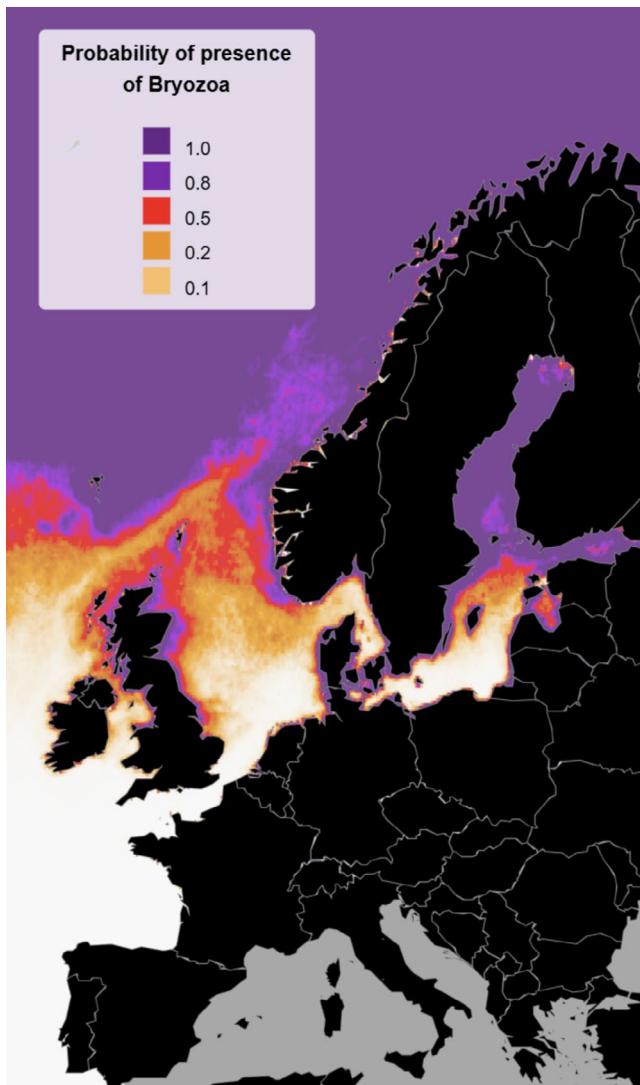


FIGURE 5 | Spatial distribution of kelp biofouling risk by bryozoans for the North-East Atlantic region where currently seaweed aquaculture is rapidly expanding. The spatial prediction was based on our binomial model of bryozoan presence as a function of salinity, SST, kelp condition (wild/not wild), wave height and chlorophyll-a, in which the variable SST was found to have a significant effect on the presence. A value of 1 indicates maximum risk of biofouling presence and 0.1 indicates minimum risk.

on the relationship between environmental conditions, community composition, and their effects on macroalgal development. Beyond Laminariales, the diversity in shape, size, and composition of other algae necessitates a focused approach to develop similar models. Given the challenges for food security and the need to protect coastal ecosystems, leveraging the relationship between biofouling and environmental conditions presents a promising approach to reduce farming costs and minimize the use of harmful chemicals. To enhance this approach, more *in situ* primary data are essential from a broader geographical scale, particularly regarding hydrodynamics. Additional variables, such as photoperiod, light intensity, pH, ship vessel traffic, slope, and substrate type, as well as larger geographical scales, should also be investigated.

Author Contributions

Victoria Delannoy: investigation, data curation, visualization, methodology, formal analysis, writing – original draft. **María Algueró-Muñiz:** supervision, project administration, writing – review and editing. **Eleni Christoforou:** supervision, project administration, writing – review and editing, methodology. **Yacob Haddou:** formal analysis. **Annabell Macphee:** data curation, investigation, methodology. **Keri McEachnie:** investigation, data curation. **Kyla Orr:** methodology, investigation, writing – review and editing. **Sofie Spatharis:** conceptualization, writing – original draft, resources, supervision, project administration.

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Data Availability Statement

The data that support the findings of this study are openly available in DRYAD at <https://doi.org/10.5061/dryad.sxksn03d8>.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.