

Article

Optical Characteristics of Dissolved, Particulate and Sedimentary Organic Matter in Coastal *Porphyra* Cultivation Zone: A Case Study of Dayu Bay, China

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Abstract: Seaweed plays a critical role in marine carbon sequestration due to its high release rate of organic matter. However, the impacts of *Porphyra* cultivation on the concentration and composition of dissolved, particulate and sedimentary organic matter (DOM, POM and SOM) in coastal cultivation zones remain unclear. Herein, we investigated the optical properties of DOM, POM and SOM along a transect from the subtropical Chi River to the adjacent *Porphyra* cultivation zone in Dayu Bay (southeast China) during the late cultivation stage. The results revealed that all types of organic matter in coastal cultivation zones were predominantly characterized by highly autochthonous sources, contrasting sharply with the allochthonous, terrestrial sources observed at freshwater sites. The estuarine mixing model and principal component analysis further indicated that the organic matter dynamics in the coastal zone are primarily controlled by *Porphyra* cultivation, with relatively limited contributions from riverine inputs, coastal sediment and porewater sources. *Porphyra* cultivation leads to significant additions of protein-like components in the coastal water and sediment. Microbial degradation incubations of DOM and POM further demonstrated that *Porphyra* cultivation promotes the in situ production of humic-like components (peak M) in coastal water. DOM exhibited a higher microbial transformation efficiency into refractory components than POM, suggesting a more substantial role of DOM in coastal carbon sequestration. Our findings underscore the potential of *Porphyra* cultivation to enhance the carbon sequestration of coastal ecosystems.

Keywords: organic matter; *Porphyra* cultivation zone; recalcitrant dissolved organic matter; three-dimensional fluorescence; bioavailability



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1. Introduction

Seaweed cultivation contributes significantly to coastal carbon sequestration during its growth period, garnering global attention as a potential strategy to mitigate climate change [1,2]. Duarte et al. [3] reported that the primary production of global seaweeds is comparable to that of the Amazon forest. Over the past two decades, global seaweed cultivation has grown at an annual rate of 6.4%, reaching a production volume of 35 million

tons in 2020 [4]. Approximately 43% of seaweed biomass is released into the water column as dissolved and particulate organic matter (DOM and POM). For instance, Liu et al. [5] reported a significant increase in dissolved organic carbon (DOC) concentrations in Sanggou Bay driven by kelp cultivation, while Wada and Hama [6] estimated that kelp-derived DOM accounted for 20% of the total DOC in Oura Bay, Japan. Li et al. [7] documented similar variations in POM caused by *Ulva prolifera* blooms, leading to a 46.4% increase in particulate organic carbon (POC) concentrations compared to non-*Ulva prolifera* zones. These seaweed-derived DOM and POM are rich in bio-labile components, which are subject to mineralization and only partially long-term stored in the ocean [2]. More than 90% of seaweed-derived POM settles in sediments within cultivation zones or adjacent continental shelves, significantly altering the biogeochemical cycling of sedimentary organic matter (SOM) [1,8]. Coastal organic matter cycling is also shaped by other biogeochemical processes, including riverine inputs, primary production, microbial activity, photodegradation and sediment resuspension [9,10]. Therefore, understanding the eventual impacts of seaweed cultivation on coastal organic matter pools is critical for assessing its carbon sequestration potential.

Although extensive research through incubation experiments and field investigations has advanced our understanding of seaweed carbon cycling [6,11,12], most studies have predominantly focused on kelp species. This is limiting the scope for comprehensive assessments of other widely cultivated seaweeds. *Porphyra* is among the most important and high-yielding seaweeds, with a carbon content of 42% (dry weight), which is higher than that of kelp, *Undaria pinnatifida* and *Gracilaria* [13]. Chen [14] reported that *Porphyra* exhibits significantly higher DOC and POC release rates compared to these species, making it a critical contributor to carbon sequestration in seaweed cultivation. Therefore, understanding how *Porphyra* cultivation influences the concentration and composition of DOM, POM and SOM in coastal cultivation zones is essential. Additionally, evaluating the bioavailability of DOM and POM could provide valuable insights into the broader impacts of *Porphyra* cultivation on coastal organic matter cycling.

Optical measurements of absorbance and fluorescence are widely used to characterize the sources, composition and processing of DOM (i.e., CDOM and FDOM) due to their low cost and operation advantages [15]. For instance, specific ultraviolet absorbance at 254 nm ($SUVA_{254}$) and spectral slopes from 275–295 nm ($S_{275-295}$) are commonly linked to DOM aromaticity and relative molecular weight, respectively [16,17]. The application of the fluorescence excitation–emission matrix (EEM) allows quantification of humic-like and protein-like components from diverse sources [15]. Moreover, the introduction of alkaline extraction methods provides new opportunities to gain insights into organic matter pools from POM and SOM [18,19].

Herein, we conducted a comprehensive investigation of DOM, POM and SOM along a subtropical river to its adjacent coastal *Porphyra* cultivation zone (Chi River-Dayu Bay) during the late cultivation period. Our objectives were to (1) investigate the impacts of *Porphyra* cultivation on the spatial distribution of DOM, POM and SOM optical properties and (2) elucidate the bioavailability and transformation processes of DOM and POM to refractory DOM (RDOM). Our study aims to provide new insights about the characteristics and mechanisms driving organic matter cycling in coastal *Porphyra* cultivation zones.

2. Materials and Methodology

2.1. Study Area

Dayu Bay (120°03′–120°05′ E, 27°03′–27°04′ N) is located in southeastern Zhejiang Province, China, and is one of the largest *Porphyra* (*Haitanensis*) cultivation zones in the country (Figure 1). The cultivation area spans approximately 57,300 acres, accounting for

about 15% of China's total *Porphyra* production [20]. The cultivation period of *Porphyra* typically extends from late October to April of the following year. Dayu Bay is a semi-enclosed bay with an average water depth of 5 m. Its western region receives freshwater input from the Chi River, which has a small watershed area of 70 km². The freshwater discharge into Dayu Bay is limited, with an annual flux of approximately 3.8×10^7 m³. Dayu Bay supports extensive *Porphyra* activities, making it a critical area for exploring the impacts of seaweed cultivation on coastal carbon cycling.

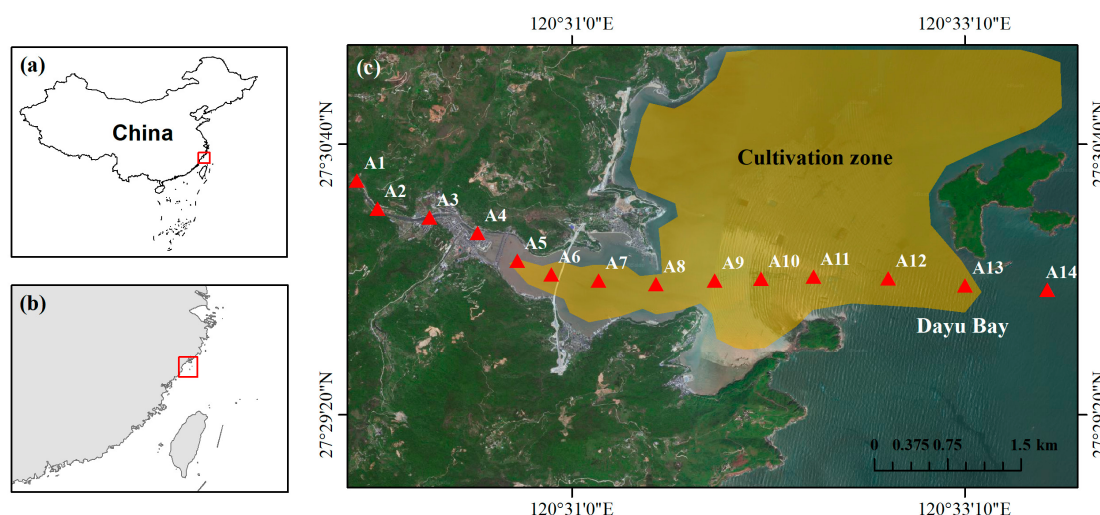


Figure 1. Study area (a–c) and sampling sites.

2.2. Sample Collection and Pre-Treatment

To better capture the seaweed-derived organic matter signal, field sampling was conducted at the aging stage of *Porphyra* (April 2023). Fourteen surface water samples (0.5 m depth) were collected using Niskin bottles along the river (A1–A4) and the coastal cultivation zone (A5–A14) at equal spatial intervals (Figure 1). Sediment samples were collected from 12 stations along the continuum (A3–A14). No sediments were collected from A1 and A2 due to the construction of anthropogenic impoundments.

After returning to the laboratory, water samples were immediately filtered through a pre-combusted (500 °C, 5 h) 0.7 µm GF/F filter for DOC and DOM optical parameter analysis. Retained particles on the filters were used for POC and POM optical parameter analysis. Sediment samples were freeze-dried, ground and sieved through 80 mesh for soil organic carbon (SOC) and SOM optical parameter analysis. In situ water temperature, salinity (Sal), dissolved oxygen (DO), turbidity (NTU) and chlorophyll (Chl *a*) were measured using a calibrated and integrated EXO2 sonde (YSI, Greene, OH, USA). All sensors were calibrated using the two-point method prior to the sampling campaign.

2.3. Incubation Experiment of DOM and POM

To assess the bioavailability of DOM and POM along the Chi River to Dayu Bay, two experimental groups were established: the BDOM group (DOM only) and the BTOM group (DOM and POM). We collected 500 mL filtered and unfiltered water samples in pre-combusted (500 °C, 5 h) brown glass bottles for the BDOM and BTOM groups, respectively. Samples were incubated in the dark at room temperature for 28 days, with daily shaking of BTOM bottles to avoid particulate settling. All samples were prepared and analyzed in triplicate.

2.4. Measurement of DOC, POC and SOC

DOC concentration was measured using a TOC-L (Shimadzu, Kyoto, Japan) by the high-temperature catalytic oxidation method. POC and SOC were measured using an elemental analyzer (Elementar, Frankfurt, Germany). POC and SOC samples were acidified with HCl to remove inorganic carbon before analysis.

2.5. Optical Analysis of DOM, POM and SOM

POM filters and SOM samples were extracted with 0.1 mol/L NaOH in the dark at 4 °C for 24 h. The extracts were neutralized with HCl to a pH of approximately 7.5 and filtered through 0.2 µm polycarbonate filters. The optical parameters (A) of POM were corrected using the initial filtered volume (V_1) and the extraction solution volume (V_2) using the following formula:

$$\frac{A \times (15 + V_2)}{V_1}$$

The absorption spectra and EEMs of DOM, POM and SOM were analyzed using an Aqualog fluorescence spectrometer (Horiba, Kyoto, Japan). The absorption spectrum was scanned over 200–700 nm with a 1 nm interval. EEMs were measured with excitation wavelengths (Ex) from 240 to 450 nm (5 nm intervals) and emission wavelengths (Em) from 240 to 600 nm (1 nm intervals), with an integration time of 1 s.

Peaks C, M and T were identified according to Fellman et al. [21]. Peak C represents terrestrial humic-like substances (Ex/Em ≤ 260 nm/448–480 nm). Peak M represents microbial-derived humic-like substances (Ex/Em = 290–325 nm/370–430 nm). Peak T represents autochthonous protein-like substances (Ex/Em = 270–280 nm/330–368 nm). Fluorescence intensity for each peak was expressed in Raman Units (RU) as the maximum value within its defined region. Additional optical indices, including $S_{275-295}$, $SUVA_{254}$, the humification index (HIX) and the biological index (BIX) were calculated as described by Hansen et al. [15]. The $S_{275-295}$ value is negatively correlated with the relative molecular weight of organic matter. Higher $SUVA_{254}$ values indicate greater aromatic organic content. Similarly, a higher HIX represents a greater degree of humification, while a higher BIX reflects a larger contribution from autochthonous sources.

2.6. Estuarine Mixing Analysis of DOM and POM

To identify potential addition or removal processes of DOM and POM in the water column, a theoretical mixing line was established based on the observed concentrations between a freshwater endmember and a marine endmember. The freshwater endmember was defined as the site closest to the estuary (A4), while the marine endmember was represented by the site with the highest salinity (A14). Samples plotted above the theoretical mixing line indicated net additions of organic matter, whereas those below the line represented removal processes.

2.7. Data Analysis and Visualization

The *t*-test was conducted using SPSS 22.0 (IBM, Armonk, NY, USA) to determine spatial differences of all parameters at a significance level of $p < 0.05$. Spearman correlation was assessed using Origin 2025 (OriginLab, Northampton, MA, USA) after data standardization. All figures were generated using Origin 2025 and ArcGIS 10.2 (Esri, Redlands, CA, USA).

3. Results

3.1. Spatial Variation of Water Quality Along the Chi River to Dayu Bay

Salinity exhibited a pronounced increase from 0–0.14 at freshwater sites (A1–A4) to 25.3–27.5 in coastal sites (A5–A14) (Figure 2). This sharp gradient reflects limited freshwater

inflows into Dayu Bay, likely attributed to the relatively small watershed area of the Chi River. COD concentrations ranged from 0.66 to 1.22 mg/L, showing a gradual increase from A1 to A3, followed by fluctuations at the coastal sites. Chl *a* (0.81–22.5 µg/L) remained at low concentrations in the freshwater sites, peaked at A5–A6 and gradually declined toward offshore sites. Turbidity (9.3–232 NTU) exhibited an overall increasing trend from freshwater to coastal zones, with notably high values recorded at sites A4 and A10.

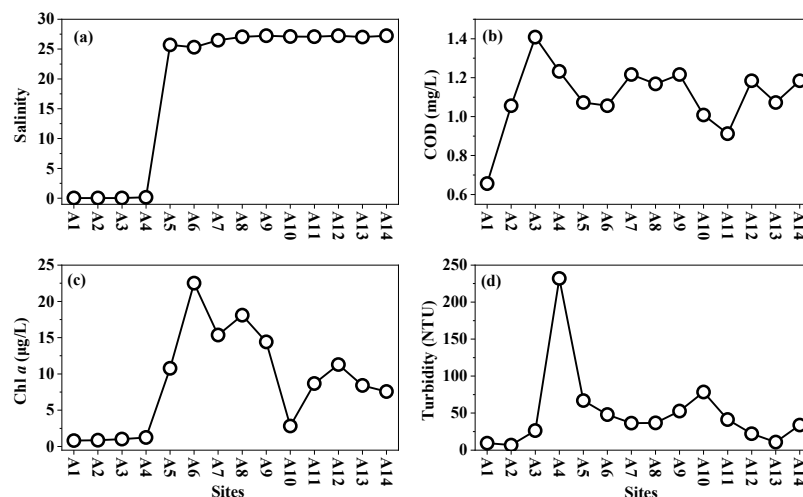


Figure 2. Distribution pattern of water quality from Chi River to Dayu Bay. (a) salinity; (b) COD; (c) Chl *a*; (d) Turbidity.

3.2. Spatial Variation of DOM Along the Chi River to Dayu Bay

DOC concentrations ranged from 0.84 to 1.92 mg/L (Figure 3), with no significant differences observed between freshwater sites and the cultivation zones ($p > 0.05$). Humic-like peak C_d (21.3–40.8%) and peak M_d (21.3–40.8%) were positively correlated with DOC ($r = 0.66$ – 0.76) and thus exhibited similar spatial distribution patterns. In contrast, the protein-like peak T_d (27.8–62.4%) showed a negative correlation with DOC ($r = -0.78$) and displayed an increasing trend from the freshwater to the coastal cultivation zone. HIX_d significantly declined from freshwater sites to the cultivation zones (0.6–0.95; $p < 0.05$), whereas the BIX_d showed a significant increasing trend (0.73–1.0; $p < 0.05$). $S_{275-295d}$ (0.0114–0.0262) and $SUVA_{254d}$ (1.59 – 5.16 L^{−1} mg C m^{−1}) both exhibited significantly higher values in the freshwater sites than in the cultivation zones ($p < 0.05$).

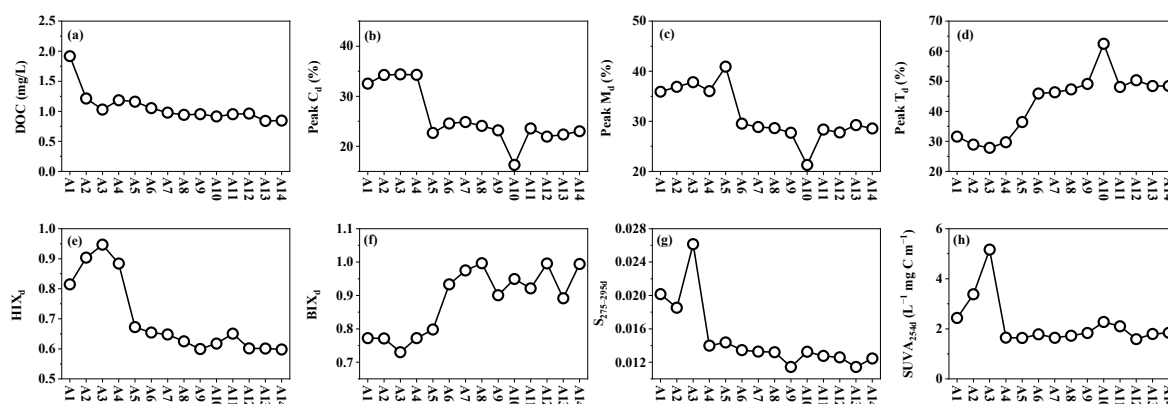


Figure 3. Spatial distribution pattern of DOM from Chi River to Dayu Bay. (a) DOC; (b) Peak C_d ; (c) Peak M_d ; (d) Peak T_d ; (e) HIX_d ; (f) BIX_d ; (g) $S_{275-295d}$; (h) $SUVA_{254d}$.

3.3. Spatial Variation of POM Along the Chi River to Dayu Bay

POC, peak C_p , peak M_p and peak T_p ranged from 0.74 to 3.26 mg/L, 10.3–30.9%, 23–52.5% and 24.4–60%, respectively (Figure 4). POC increased from site A2 to A9 and then gradually declined toward A14. Humic-like peak C_p showed a decreasing trend from A3 to A6, with a notable peak at A10. The relative abundance of humic-like peak M_p was significantly higher in the cultivation zone compared to freshwater sites ($p < 0.05$). The protein-like peak T_p fluctuated from the Chi River to Dayu Bay, with no significant differences ($p > 0.05$) observed between freshwater and coastal cultivation zones. HIX_p (0.27–0.73) and BIX_p (0.58–1.18) both decreased from A2 to A5 before exhibiting fluctuating increases toward offshore sites. $S_{275-295p}$ gradually decreased from the Chi River to Dayu Bay. $SUVA_{254p}$ (0.62–2.47) exhibited patchy high values at A4–A5 and A10.

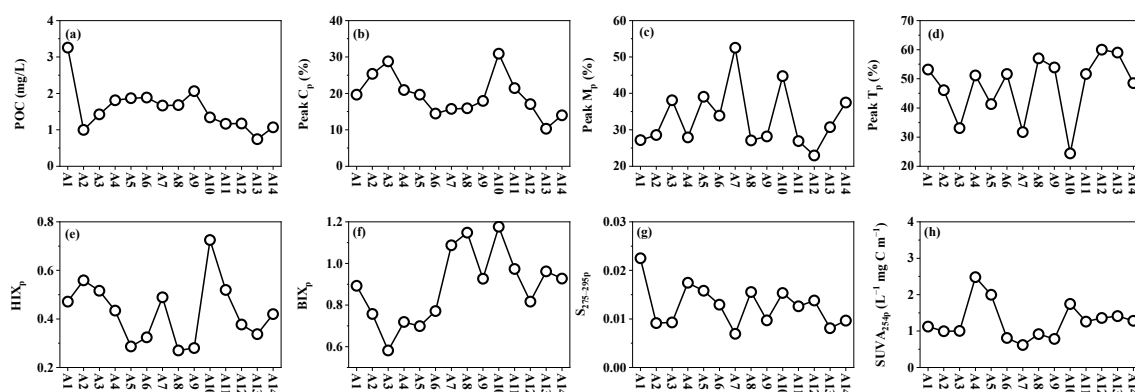


Figure 4. Spatial distribution pattern of POM from Chi River to Dayu Bay. (a) POC; (b) Peak C_p ; (c) Peak M_p ; (d) Peak T_p ; (e) HIX_p ; (f) BIX_p ; (g) $S_{275-295p}$; (h) $SUVA_{254p}$.

3.4. Spatial Variation of SOM Along the Chi River to Dayu Bay

SOC concentrations ranged from 5.72 to 8.35 g/kg and showed a decreasing trend from the Chi River to Dayu Bay (Figure 5). Humic-like peak C_s , M_s and protein-like peak T_s were positively correlated with SOC ($r = 0.81$ – 0.90), exhibiting similar spatial distributions. HIX_s (0.63–0.78) increased from freshwater sites (A3–A4) to coastal cultivation zones (A5–A9) and then gradually declined offshore. BIX_s (0.63–0.90) displayed fluctuating increases from freshwater sites to the cultivation zones. $S_{275-295s}$ (0.0114–0.0261) and $SUVA_{254s}$ (0.51 – $1.13 \times 10^{-3} \text{ L}^{-1} \text{ mg C m}^{-1}$) both decreased sharply from freshwater to cultivation zones.

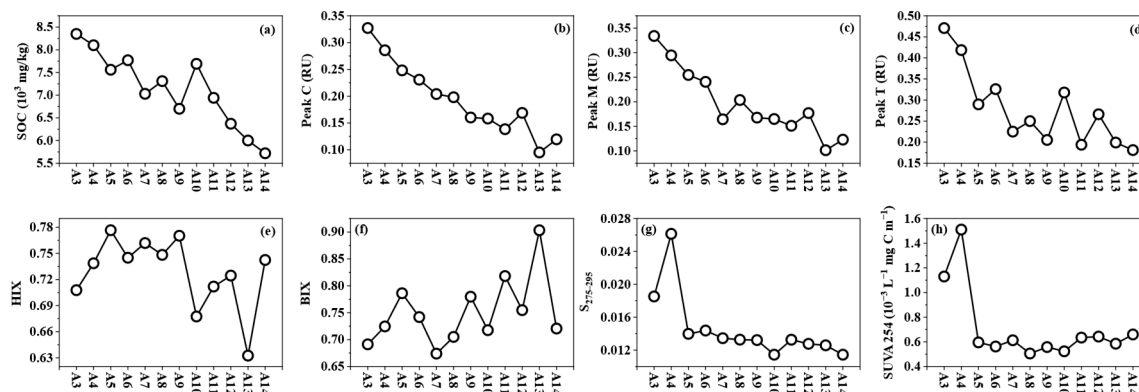


Figure 5. Distribution pattern of SOM parameters from Chi River to Dayu Bay. (a) SOC; (b) Peak C_s ; (c) Peak M_s ; (d) Peak T_s ; (e) HIX_s ; (f) BIX_s ; (g) $S_{275-295s}$; (h) $SUVA_{254s}$.

3.5. Principal Component Analysis for DOM, POM and SOM

To reveal the dynamics of *Porphyra* cultivation on the organic matter in the coastal zone, three principal component analysis (PCA) models were performed to trace the sources of DOM, POM and SOM, respectively (Figure 6). The first two principal components (PC1 and PC2) of the models explained 73.7%, 51.3% and 66.4% of the total spatial variability, respectively. In all three models, PC1 primarily reflected the river-to-sea gradient of organic matter. Terrestrial humic-like peak C, HIX and SUVA₂₅₄ exhibited high loadings on the positive axis of PC1, clustering with freshwater samples. In contrast, salinity, protein-like peak T and BIX showed higher loadings on the negative axis of PC1, corresponding to higher scores for samples from the cultivation zones. PC2 captured spatial variations in organic matter within the river and cultivation zones. For DOM and SOM, PC2 contributed only a limited additional explanation of this variation. In contrast, for POM, PC2 accounted for 22.7% of the variability, comparable to PC1 (28.6%). Notably, BIX and HIX displayed high loadings on the negative axis of PC2, where POM samples from the cultivation zones were clustered.

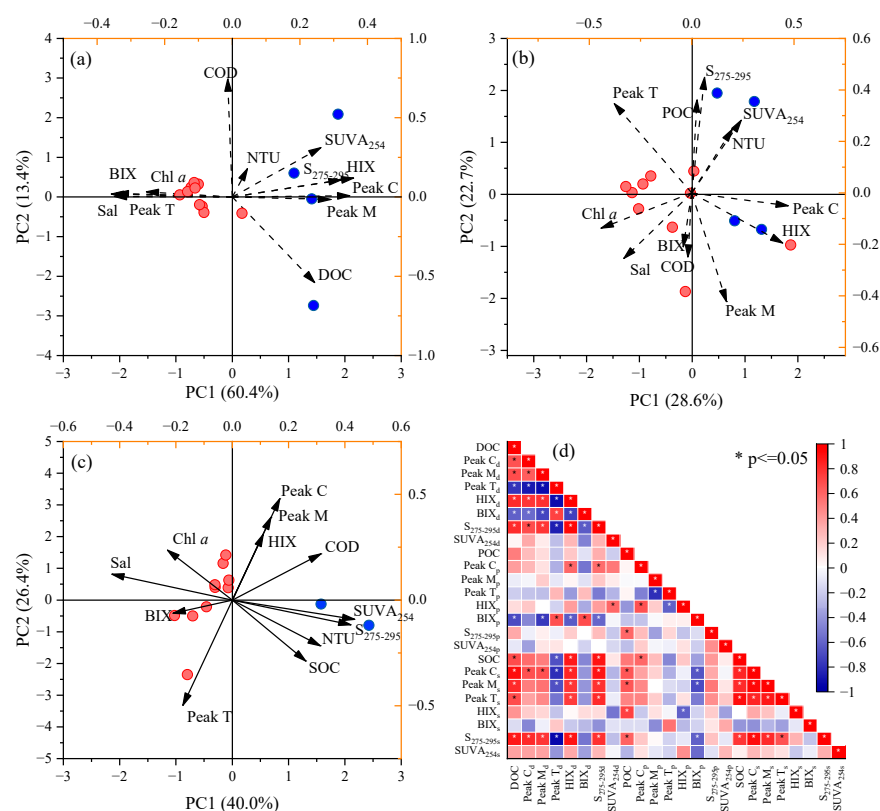


Figure 6. PCA analysis and Spearman correlation based on water quality and organic matter parameters. (a) DOM model; (b) POM model; (c) SOM model; (d) Spearman correlation matrix.

4. Discussion

4.1. Effects of *Porphyra* Cultivation on the Coastal DOM, POM and SOM

The optical characteristics of DOM, POM and SOM exhibited notable spatial variation from the Chi River to Dayu Bay (Figures 3–5). In freshwater sites, all three types of organic matter clustered along the positive PC1 axis in PCA models, where carbon concentrations and peak C showed higher loadings (Figure 6). This suggests that terrestrial inputs dominate organic matter composition in the river zones, as the Chi River watershed is primarily forested [22]. The flushing effect of riparian soil could provide abundant highly humified and aromatic DOM and POM [23]. This is supported by the elevated HIX and SUVA₂₅₄

values observed in freshwater sites [15]. Furthermore, the construction of anthropogenic impoundments in the Chi River slows water flow, accelerating the deposition of terrestrial POM and increasing SOC concentration in the river zones. The positive correlation between SOC and peak C_p ($r = 0.59$) corroborates this hypothesis.

In the coastal cultivation zone, decreases in DOC and peak C_d with increasing salinity reflect reduced contributions of terrestrial DOM, driven by limited freshwater inputs from the Chi River and dilution by offshore seawater [24]. However, higher DOC and FDOM components than the theoretical mixing line indicate substantial estuarine additions from multiple sources in the cultivation zone (Figure 7a–d). Similar patterns were also observed for POC and FPOM, with pronounced additions inferred (Figure 7e–h). Together with the increased POC concentration from freshwater sites to coastal water, we infer that the addition of POM in *Porphyra* cultivation zones may be more significant than DOM.

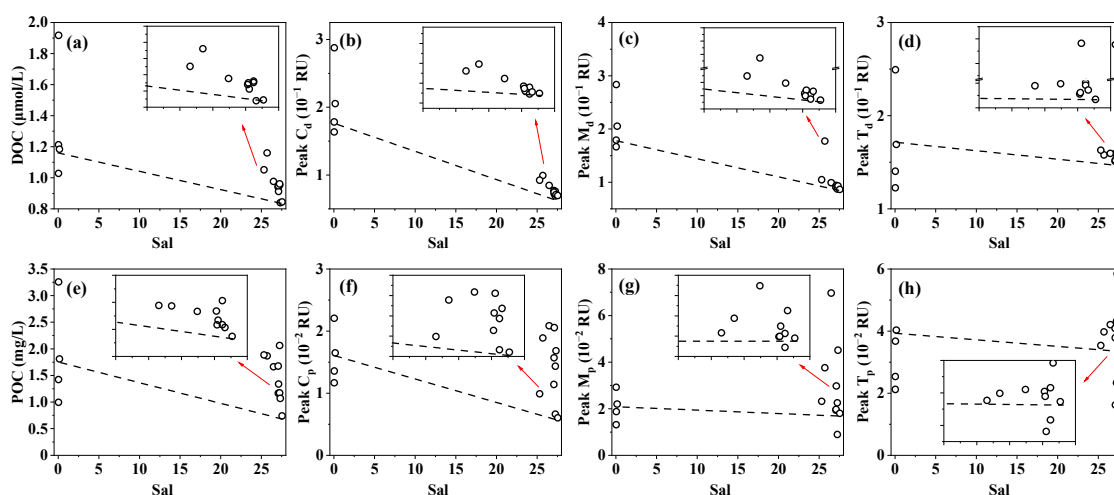


Figure 7. Estuarine mixing processes of DOM and POM parameters. (a) DOC; (b) Peak C_d ; (c) Peak M_d ; (d) Peak T_d ; (e) POC; (f) Peak C_p ; (g) Peak M_p ; (h) Peak T_p .

Moreover, DOM and POM in the cultivation zone were both clustered to the negative PC1 axis and were characterized by high protein-like peak T, BIX and Chl a , indicating a predominance of autochthonous bio-labile organic matter [25]. This is consistent with the significant additions of both protein-like peak T_d and peak T_p . Both *Porphyra* cultivation and algal blooms could serve as key sources of autochthonous bio-labile organic matter in the cultivation zone. Zhang et al. [26] reported that seaweed could competitively consume excess nutrients and inhibit microalgae growth. Furthermore, the relatively cold water temperatures during the investigation period (16.5 ± 0.3 °C) favor *Porphyra* growth over microalgae [27]. Therefore, the high bio-labile protein-like DOM and POM in the cultivation zone are likely primarily derived from *Porphyra* sources. Given the susceptibility of *Porphyra*-derived organic matter to microbial degradation, in situ microbial transformation could further enhance the accumulation of peak M_d and M_p in the cultivation zone [11,28]. Evidence from estuarine mixing models supports the significant addition of this bio-refractory DOM, underscoring the contribution of *Porphyra* cultivation to coastal carbon sequestration (further discussed in Section 4.2). The higher peaks C_d and C_p than the theoretical mixing line in the cultivation zone suggest there are additional contributions of refractory DOM from other pathways. The additional Peak C_d could be attributed to sediment porewater inputs, while peak C_p is possibly sourced from sediment resuspension driven by tidal exchange [29,30].

SOM in the coastal cultivation zone could be influenced by multiple sources, whereby the terrestrial input and deposition of *Porphyra* detritus are among the two most important

pathways [8,31,32]. The PCA results indicate that SOM in cultivation zones is characterized by high peak T_s and BIX_s , distinguishing it from freshwater sites (Figure 6c). This suggests that SOM in cultivation zones is primarily derived from settling *Porphyra*-sourced POM. During the late cultivation stage (April), aging *Porphyra* may cease carbon fixation and release detritus due to natural decay or wave-induced damage [33]. This is consistent with the previous investigations of kelp and *Gracilaria* cultivation zones, where macroalgal detritus contributed approximately 16% of sedimentary organic carbon, particularly in surface sediments [8,31]. Huang et al. [12] reported that kelp cultivation could enhance the microbial carbon and nitrogen metabolism genes in the sedimentary environment of cultivation zones, facilitating biogenic organic matter degradation and transformation. We speculate this process may also occur in the *Porphyra* cultivation zone. This could explain the higher HIX_s observed in cultivation zones compared to river zones.

4.2. Relative Contribution of DOM and POM to RDOM Production in the *Porphyra* Cultivation Zone

After 28 days of microbial degradation, DOC concentration and protein-like peak T_d in the BDOM group decreased significantly at all sites (Figure 8), while humic-like peak M_d increased. These results indicate that microbial processes produce bio-refractory DOM by utilizing bio-labile DOM components in both freshwater and coastal *Porphyra* zones [28]. The humic-like peak M is resistant to microbial degradation and can persist in the water column for years, making it a reliable proxy for refractory DOM (RDOM) [34]. Ligand exchange between humic-like DOM and metals on mineral surfaces may further enhance its preferential adsorption onto particles, facilitating their deposition into sedimentary carbon pools [35]. Notably, the ΔDOC and $\Delta peak T_d$ in the cultivation waters were lower than those in freshwater sites, whereas the $\Delta peak M_d$ was significantly higher than in the freshwater sites. This indicates that the microbial transformation rate of DOM in the *Porphyra* cultivation zone might be more efficient than in non-cultivation waters. This aligns with findings from Sanggou Bay, where the proportion of RDOM molecules in the kelp cultivation zones (58%) was much higher than in adjacent non-cultivation zones (33%) [28].

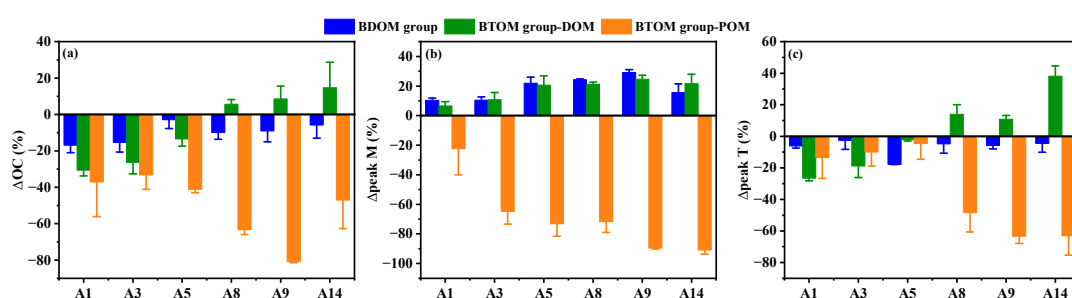


Figure 8. Dynamic changes of DOM and POM in BDOM and BTOM groups. (a) change in OC; (b) change in peak M; (c) changes in peak T.

In the BTOM group, DOC and protein-like peak T_d decreased in freshwater sites (A1–A3) after incubation, suggesting a similar microbial degradation of bio-labile DOM to the BDOM group. However, ΔDOC and $\Delta peak T_d$ shifted to a net increase in the coastal *Porphyra* cultivation zone (A8 to A14). This bio-labile DOM might be derived from the microbial degradation and release of POM, which is supported by the significant decreases in POC and protein-like peak T_p . Feng et al. [11] reported that some polymer hydrolyzers (e.g., *Clostridia* and *Bacteroidia*) could secrete extracellular enzymes to degrade biogenic detritus and convert it into DOM. Such microbial degradation tends to release protein-like DOM rather than humic-like DOM [36]. Further, the significantly higher ΔPOC and $\Delta peak T_p$ in the *Porphyra* cultivation zone compared to freshwater sites indicates that

microbial transformation of POM into bio-labile DOM is more pronounced in the *Porphyra* cultivation zone.

Moreover, the positive $\Delta\text{peak } M_d$ observed at all sites suggests the production of the RDOM component in the BTOM group, suggesting either (1) microbial transformation of bio-labile DOM and POM-derived bio-labile DOM [11], (2) direct dissolution from *Porphyra* detritus [36] or (3) a combination of both. Despite 65–91% of POC being dissolved or degraded by microbial activity in the *Porphyra* cultivation zone, $\Delta\text{peak } M_d$ in the BTOM group did not significantly exceed that in the BDOM group (Figure 8). This may reflect the underutilization of bio-labile DOM by microbial respiration due to limited incubation times, which is supported by the positive $\Delta\text{peak } T_d$. Another possible reason is the low transformation efficiency of *Porphyra*-derived POM into RDOM, with most POM being mineralized into CO_2 [11]. For instance, only 1.27% of kelp-derived POM was transformed into RDOM after 210 days of microbial degradation [11]. Similarly, for detritus from *Sargassum horneri*, only 2.71% of POM was transformed into RDOM [37]. Therefore, given the similar magnitudes of DOC and POC concentration in the *Porphyra* cultivation zone, *Porphyra*-derived DOM may play a more critical role in coastal carbon sinks.

5. Conclusions

Field investigations of DOM, POM and SOM along a subtropical river and its adjacent *Porphyra* cultivation zone indicate that coastal organic matter is influenced by multiple sources, including riverine input, *Porphyra* release, sediment and porewater sources. The combined analysis of PCA and estuarine mixing models reveals that the coastal DOM, POM and SOM are predominantly regulated by autochthonous, bio-labile protein-like components derived from *Porphyra* cultivation, with relatively limited contributions from other sources. Incubation experiments further demonstrate that *Porphyra* cultivation enhances the microbial transformation of bio-labile DOM into refractory DOM (RDOM) in coastal waters. Further, DOM plays a more significant role than POM in the microbial production of RDOM, highlighting its critical function in coastal carbon sequestration. Our study emphasizes the significant impact of *Porphyra* cultivation on coastal organic carbon dynamics and provides key insights into its role in enhancing carbon sequestration of coastal ecosystems.

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Data Availability Statement: Data will be made available on reasonable request.

Conflicts of Interest: The authors declare no conflict of interest.

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