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Hidden Bioavailable Dissolved Organic Matter in the Deep Northwestern Pacific Ocean

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Key Points:

- A cross-latitude field survey reveals patchy occurrence of bioavailable dissolved organic molecules in the deep Pacific Ocean
- The bioavailable organic molecules are confined to 1,000–4,000 m in the 30°N–36°N region and exhibit a semi-labile character
- The presence of deep-sea semi-labile molecules is a sporadic event likely arising from actively settling particles

Supporting Information:

Supporting Information may be found in the online version of this article.

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Abstract

The deep ocean is widely viewed as a stable reservoir of dissolved organic carbon (DOC) that is highly resistant to microbial degradation. However, this paradigm may be oversimplified. In a cross-latitude survey conducted in the northwestern Pacific Ocean (155°E, 28.5°N–41.5°N), bulk DOC concentrations were found to be relatively constant below 1,000 m with little variation across latitude. Despite this stability, compound-specific analyses revealed unexpectedly high abundance of hydrolyzable amino acids, up to 1.1% of DOC, at depths of 1,000–4,000 m between 30°N and 36°N. This amino acid enrichment, doubling the typical levels observed in other deep-sea basins and comparable to upper ocean values, reflected episodic inputs of semi-labile DOC likely derived from actively settling fresh particles. These findings reveal hidden reservoirs of bioavailable DOC in the deep ocean, a feature not captured by bulk analysis, challenging the conventional view of deep-sea DOC as predominantly refractory and stable.

Plain Language Summary

The deep ocean is a large and long-term reservoir of dissolved organic carbon (DOC) on Earth. Traditionally, scientists believed that DOC in the deep ocean is highly resistant to microbial degradation and can persist for millennia. However, recent research suggests that this view may be oversimplified and that some organic molecules in the deep ocean are younger and more dynamic than previously thought. Understanding whether parts of this deep-sea DOC are still available for microbial utilization could reshape how we view deep-sea carbon cycling. We addressed this question by tracing DOC across a latitudinal and productivity gradient from 28.5°N to 41.5°N in the northwestern Pacific Ocean. We specifically analyzed amino acids, a class of bioavailable organic molecules, as a proxy for DOC bioavailability. We found that certain regions at depths greater than 1,000 m (mostly between 30°N and 36°N) had unexpectedly high levels of hydrolyzable amino acids, reflecting a localized input of semi-labile DOC in the deep ocean. These findings reveal hidden, patchy hotspots of bioavailable organic molecules in the dark ocean, suggesting that the deep sea plays a more active role in the carbon cycle than previously recognized.

1. Introduction

Marine dissolved organic carbon (DOC) constitutes the largest reservoir of reduced carbon in the ocean (662 Pg), roughly equivalent to the size of atmospheric carbon dioxide (Hansell et al., 2009; Hedges, 1992). The majority of this DOC is sequestered in the dark, deep ocean, where radiocarbon dating indicates its persistence for millennia (Bauer et al., 1992; Williams & Druffel, 1987; Zigah et al., 2017). Bioassay experiments assessing microbial utilization of deep-sea DOC have typically shown negligible changes in bulk DOC concentrations during incubation (Barber, 1968; Hopkinson et al., 2002; Kähler et al., 1997). As a result, deep-sea DOC has traditionally been viewed as a long-term stable carbon reservoir with limited bioavailability to microbial communities.

Accumulated studies, however, challenge the notion of uniformity within the deep-sea DOC pool (Dittmar et al., 2021; Follett et al., 2014; Walker et al., 2016). Emerging research has revealed heterogeneity in deep-sea DOC concentrations, compositions and ^{14}C ages, suggesting the deep ocean DOC reservoir is more dynamic than previously thought. Global surveys have revealed significant gradients in DOC concentrations across major deep-sea basins, indicating DOC losses in certain regions of the deep ocean (Hansell & Carlson, 1998, 2013). Radiocarbon measurements have also noted spatial and temporal differences in DOC ^{14}C ages in deep waters, suggesting varying DOC turnover rates (Bauer et al., 1998; Druffel et al., 2018, 2019, 2021). These observations imply potential fluctuations in the bioavailability of deep-sea DOC.

Accurately evaluating the bioavailability of DOC in the deep ocean has been challenging. The traditional approach relies on bioassay experiments that detect changes in bulk DOC concentrations over incubation periods

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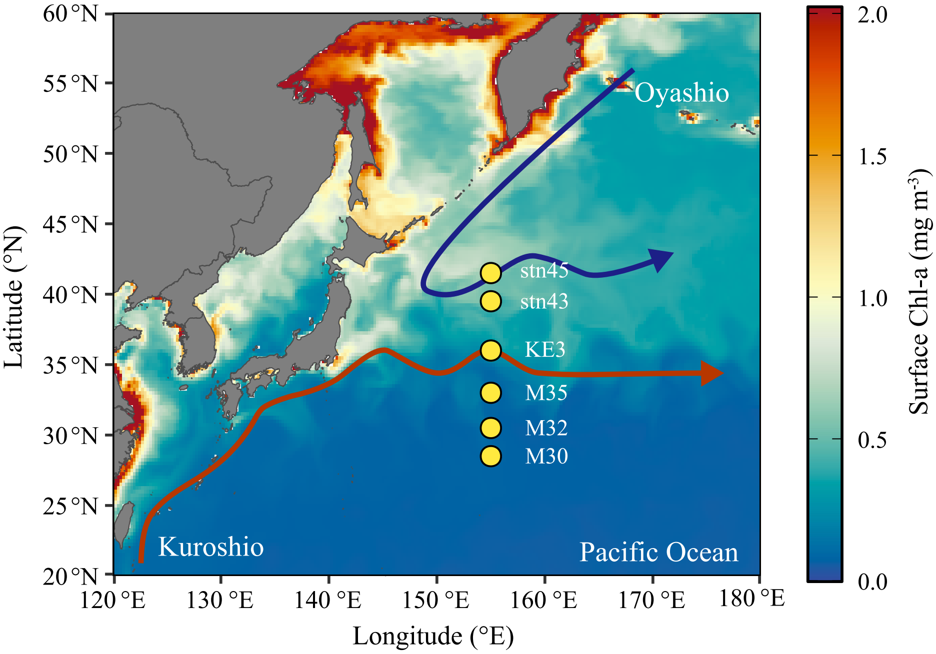

Figure 1. Sampling sites in the northwestern Pacific Ocean during the KK2202 cruise in June–July 2022. The major currents in the sampling region include the Kuroshio Current (red line) and the Oyashio Current (blue line). Color bar represents the average chlorophyll-*a* (Chl-*a*) level during the sampling period. Chl-*a* data were obtained from E.U. Copernicus Marine Service Information (CMEMS, https://marine.copernicus.eu).

(Lønborg et al., 2009; Ortega-Retuerta et al., 2021; Søndergaard & Middelboe, 1995). While informative, this method is limited in sensitivity. It detects changes in DOC concentration only on the order of several μmol C L^{-1} and may overlook subtle but ecologically important DOC degradation processes (Barber, 1968; Hopkinson et al., 2002; Kähler et al., 1997). An alternative approach involves molecular-level analysis, specifically targeting bioavailable compounds of the organic carbon pool, such as amino acids and carbohydrates (Benner, 2003; Cowie & Hedges, 1994; Kirchman et al., 2001). Among these, amino acids stand out as a sensitive and informative indicator of DOC bioavailability. Amino acids are preferentially utilized by microorganisms over bulk DOC, leading to their rapid depletion as DOC degrades (Amon et al., 2001; Davis et al., 2009; Stephens et al., 2025). The relative abundance of amino acids, commonly expressed as DOC-normalized yields (%DOC), serving as a qualitative or quantitative proxy for assessing marine DOC bioavailability (Davis & Benner, 2007; Shen et al., 2016, 2018). This method circumvents the necessity of conducting bioassay experiments and can provide a more efficient and sensitive measure of bioavailable DOC, as amino acids can be detected at nanomolar levels (nmol L^{-1}) (Kaiser & Benner, 2005; Shen et al., 2015).

In this study, we leverage the sensitivity of amino acids as molecular proxies to investigate the bioavailability of DOC in the deep open ocean. We measured concentrations of DOC and hydrolyzable amino acids across a broad latitudinal and productivity gradient in the northwestern Pacific Ocean, mainly focusing on depths exceeding 1,000 m. By calculating DOC-normalized yields of amino acids, we assessed DOC bioavailability across three depth layers (1,000–2,000 m, 2,000–4,000 m, >4,000 m) between 28.5°N and 41.5°N. Our results reveal unexpected presence of localized areas with high bioavailable DOC confined to 1,000–4,000 m between 30°N and 36°N, providing new insights into the variability and dynamics of the deep-sea carbon reservoir.

2. Materials and Methods

2.1. Sample Collection

Water samples were collected in the northwestern Pacific Ocean aboard the R/V *Tan Kah Kee* (KK2202 cruise) from 9 June to 25 July 2022. Sampling was conducted at six stations across a 13° span in latitudes from the subtropical to near subarctic regions along the 155°E transect (across the Kuroshio-Oyashio Extension): M30 (28.5°N), M32 (30.5°N), M35 (33.0°N), KE3 (36.0°N), Stn 43 (39.5°N), and Stn 45 (41.5°N) (Figure 1). All samples were collected using Niskin bottles mounted on a rosette sampler equipped with a Conductivity–Temperature–Depth (CTD) system. The collected water was filtered using an acid-cleaned in-line polycarbonate filter with pre-combusted (450°C, 4.5 hr) GF/F filter membranes. The filtrate was transferred into pre-combusted 40 mL glass bottles and immediately frozen at −20°C until analysis. Depth profiles of temperature and salinity were determined with a Sea-Bird 911 CTD.

2.2. Chemical Analyses

Concentrations of DOC were measured using the high-temperature catalytic oxidation method with a Shimadzu Total Organic Carbon TOC-V CPH analyzer. DOC samples were acidified to pH 2–3 using 25% H_3PO_4, and each sample was injected 3–5 times at a volume of 100 μL. Deep seawater reference was measured every five samples to assess instrumental performance. The coefficient of variation for all measured references was <2%.

Concentrations of dissolved hydrolyzable amino acids were determined using an Agilent 1260 ultrahigh performance liquid chromatography (HPLC) system. Water samples (100 μL) were dried under N_2 and hydrolyzed using a microwave-assisted gas-phase technique with 6 mol L^{-1} HCl at 150°C for 32.5 min (Kaiser & Benner, 2005). Post hydrolysis, the samples were derivatized with *o*-phthaldialdehyde (OPA) and *N*-isobutyryl- L-cysteine (IBLC), separated on a Poroshell 120 EC-C18 column, and detected with a fluorescence detector (Ex/Em:330/450 nm). A linear binary gradient program was used for elution, starting with 100% potassium phosphate monobasic (KH_2PO_4; 48 mM L^{-1}, pH = 6.25) and 0% methanol-acetonitrile (13:1, v/v), then progressing to 61% KH_2PO_4 at 13.3 min, 46% at 19.2 min, 40% at 21.3 min, and 20% at 22 min (Shen et al., 2015). Twenty amino acids were quantified, including D- and L-asparagine + aspartic acid (Asx), D- and L-glutamine + glutamic acid (Glx), D- and L-serine (Ser), L-histidine (His), L-threonine (Thr), glycine (Gly), L-arginine (Arg), *β*-alanine (*β*-Ala), D- and L-alanine (Ala), *γ*-aminobutyric acid (*γ*-Aba), L-tyrosine (Tyr), L-valine (Val), L-phenylalanine (Phe), L-isoleucine (Ile), L-leucine (Leu), and L-lysine (Lys). Acid-catalyzed racemization was corrected as described by Kaiser and Benner (2005). Total hydrolyzable amino acids (THAA) concentrations were calculated as the sum of the 20 quantified hydrolyzable amino acids.

DOC-normalized yield values of THAA were calculated as the percentage of amino acid carbon to the total DOC using the following formula (Equation 1):

$$\mathrm{THAA(\%DOC)} = \frac{[\mathrm{THAA-C}]}{[\mathrm{DOC}]} \times 100, \tag{1}$$

where [THAA-C] and [DOC] represent the concentrations of carbon in total hydrolyzable amino acids and bulk DOC, respectively. *β*-Ala and *γ*-Aba are non-protein amino acids and were excluded from the yield calculation.

D-Asx, D-Glx, D-Ser, and D-Ala determined here represent the most abundant and mostly used D-amino acids (Dittmar et al., 2001; Kaiser & Benner, 2008; Tremblay et al., 2015). In this study, concentrations of D-amino acids were reported as the sum of D-Asx, D-Glx, D-Ser, and D-Ala.

Degradation Index (DI) was calculated using the principal component analysis (PCA)-based approach of Dauwe et al. (1999) with PCA score values adapted for marine DOM (Kaiser & Benner, 2009), according to following equation (Equation 2):

$$\text{Degradation Index} = \sum_i \left(\frac{\mathrm{var}_i - \mathrm{AVG}_{\mathrm{var}_i}}{\mathrm{SD}_{\mathrm{var}_i}}\right) \times \mathrm{fac.coef}_i \tag{2}$$

where var_i is the mole percentage of amino acid i in the sample; $\mathrm{AVG}_{\mathrm{var}_i}$ and $\mathrm{SD}_{\mathrm{var}_i}$ are the mean and standard deviations of mole percentage of amino acid i in marine DOM data set, and $\mathrm{fac.coef}_i$ is the factor coefficient (loading) of amino acid i on the PC1 axis. Parameters used for DOM DI calculation were reported in Peter et al. (2012).

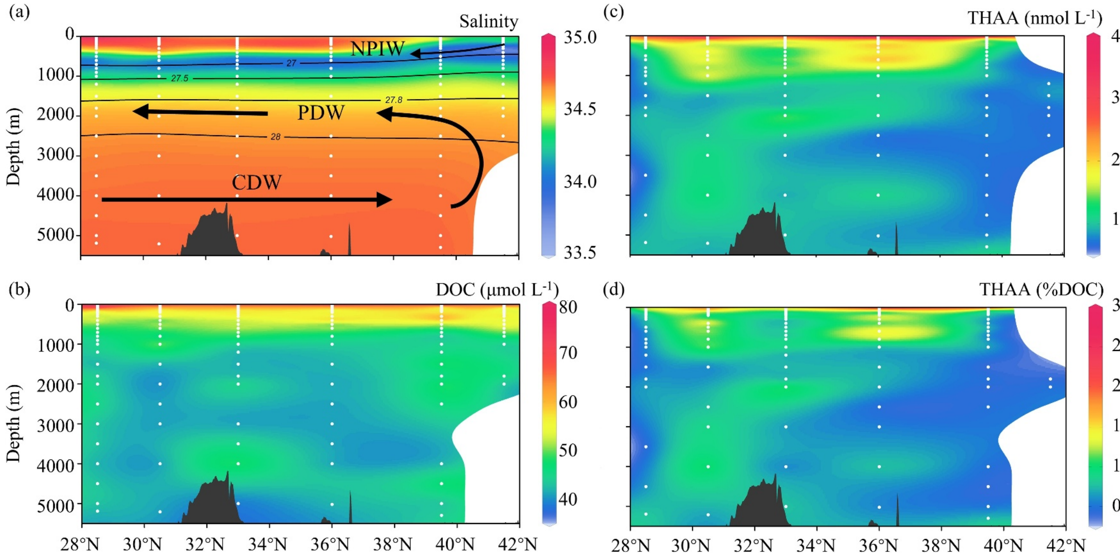

Figure 2. Meridional sections of (a) salinity, (b) DOC, (c) total hydrolyzable amino acids (THAA) concentrations and (d) DOC-normalized yields of THAA along the 155°E in the NW Pacific Ocean (28.5°N–41.5°N). Contour lines and black arrows in (a) represent neutral density and major mid-depth to deep-water masses, respectively. Abbreviations: NPIW = North Pacific Intermediate Water; PDW = Pacific Deep Water; CDW = Circumpolar Deep Water. This figure was generated with Ocean Data View.

3. Results and Discussion

3.1. Cross-Latitude Variation in Concentrations and Compositions of DOC in the NW Pacific

The northwestern (NW) Pacific Ocean is a dynamic and heterogeneous region characterized by strong spatial variability in hydrographic conditions, nutrient supply, and biological productivity (Dai et al., 2023; Hu et al., 2015; Yasuda, 2003) (Figure 1). Along the 155°E meridional transect, where our sampling was conducted, a clear south-to-north gradient in nutrient and Chl-*a* concentrations was observed (Figure 1), with higher values occurring north of 35°N indicative of enhanced primary production. These surface patterns contrast sharply with the relatively uniform hydrographic conditions in the deep water column. Deep waters (≥1,000 m) along the 155°E transect were dominated by the southward Pacific Deep Water (PDW) (1,000–3,000 m) and the northward Circumpolar Deep Water (CDW) (>3,000 m) with minimal variation in temperature and salinity (Figure 2a).

The concentrations of DOC in the NW Pacific Ocean exhibited a ~2-fold decrease from surface to depth, ranging from 67 to 72 μmol L^{-1} in the surface layer (≤20 m) to 39–48 μmol L^{-1} below 1,000 m (Figure 2b; Table S1 in Supporting Information S1). A sharp decline in DOC concentrations occurred within the upper 1,000 m, consistent with global patterns of DOC attenuation with depth (Hansell & Orellana, 2021; Kaiser & Benner, 2009). Contrary to the trend of Chl-*a* and previously observed particulate organic carbon (POC) flux in the upper NW Pacific Ocean (Zhong et al., 2021), surface DOC concentrations did not display a significant latitudinal gradient from 28.5°N to 41.5°N ($R^2 = 0.06$, $p > 0.1$; Figure S1 in Supporting Information S1), despite clear increases in productivity at higher latitudes. This decoupling suggests that enhanced primary production at higher latitudes did not necessarily translate to a significant net DOC accumulation. One explanation is the preferential partitioning of fixed carbon into POC rather than DOC, a phenomenon commonly observed in other high-latitude regions dominated by large phytoplankton such as diatoms (Carlson et al., 1998, 2000; Huang et al., 2023). It has been observed in the NW Pacific that the abundance of diatom increased markedly from the oligotrophic subtropical gyre to the nutrient-rich subpolar region (Z. Chen et al., 2021; Lin et al., 2020). At depths ≥1,000 m, DOC concentrations remained relatively constant across depth and latitude, adding to the conventional view of the presence of a refractory DOC pool that is largely resistant to microbial degradation in the deep ocean (Hansell, 2013).

In contrast to the relatively stable DOC concentrations, total hydrolyzable amino acids (THAA; a class of organic compounds more readily utilized by microbes), displayed substantially greater variability across depth and latitude (Figure 2c; Table S1 in Supporting Information S1). THAA concentrations spanned a 7-fold range from

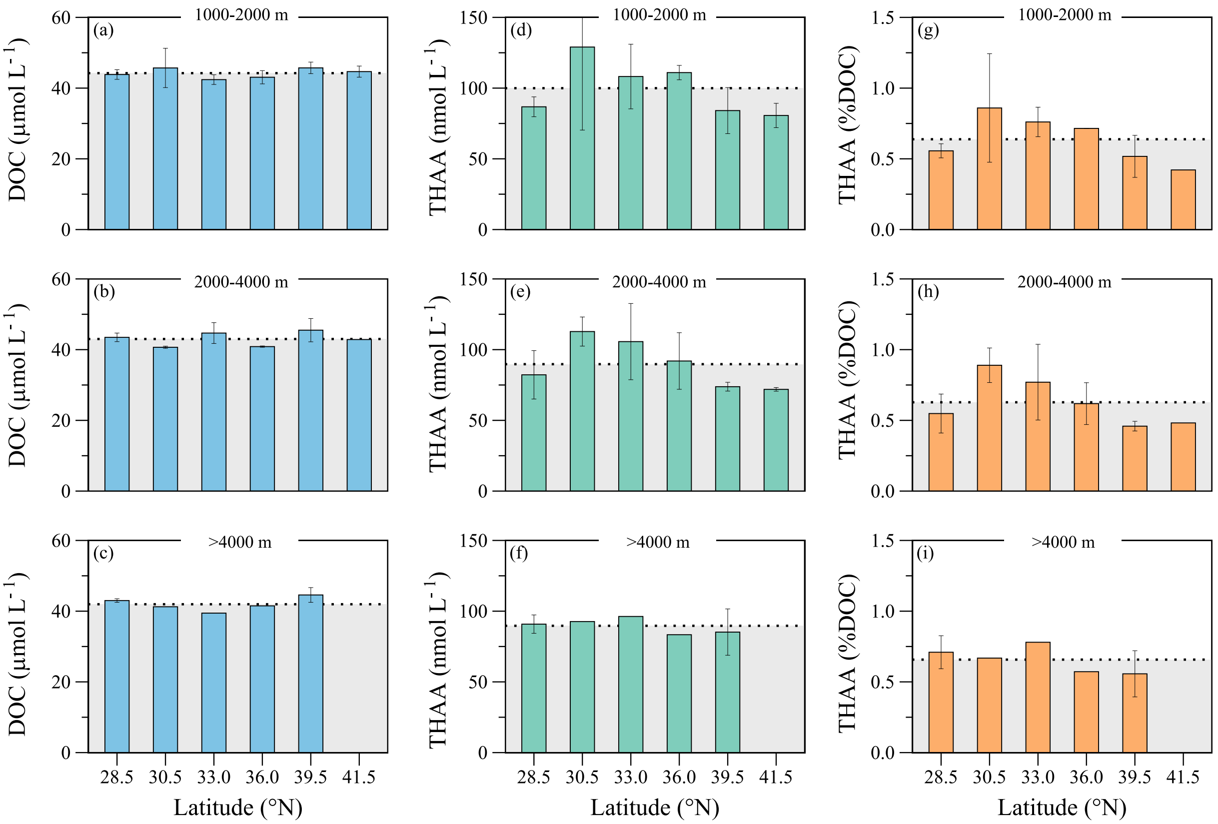

Figure 3. Concentrations of DOC (a–c) and THAA (d–f) and THAA yields (g–i) in deep waters across different latitudes in the northwestern Pacific Ocean. The dashed line and gray shading represent the average concentration values of DOC and THAA, respectively, at the corresponding depth range. Error bars indicate one standard deviation.

70 to 486 nmol L^{-1}, mirroring the vertical distribution of bulk DOC but showing greater sensitivity to environmental gradients. In surface waters, THAA concentrations increased significantly with latitudes ($R^2 = 0.71$, $p < 0.05$; Figure S1 in Supporting Information S1). This suggests that amino acid content more sensitively tracks the trend of primary production than bulk DOC measurement alone. At depths ≥1,000 m, THAA concentrations also exhibited greater variability (70–171 nmol L^{-1}; Figure 2c) than bulk DOC, across both depth and latitude, highlighting heterogeneity in deep ocean DOC at a molecular level.

THAA yields (THAA normalized to DOC, expressed as %DOC or %) were calculated to evaluate DOC bioavailability (Figure 2d; Table S1 in Supporting Information S1), with higher yields indicating a higher bioavailability (Davis & Benner, 2007; Davis et al., 2009). THAA yields decreased with depth and exhibited a 7-fold variability, ranging from 0.4% to 2.8%, suggesting a broad spectrum of DOC bioavailability across depth. In surface waters, THAA yields increased significantly with latitude ($R^2 = 0.58$, $p < 0.05$; Figure S1 in Supporting Information S1), paralleling Chl-*a* trend (Figure 1) and supporting the view that primary production modulates DOC quality/bioavailability more than its total concentration (Shen et al., 2018; Tremblay et al., 2015). In the deep ocean (≥1,000 m), THAA yields exhibited a ∼3-fold variation (0.4%–1.1%), indicating a wide range of deep-sea DOC bioavailability. This suggests that even in deep waters, where DOC is typically considered refractory, substantial variability exists in the potential for microbial utilization of DOC. These observations overall emphasize the importance of considering compositional aspects of DOC when assessing carbon cycling, as bulk measurements may obscure spatial variations in bioavailable organic matter.

3.2. Hidden Patches of Bioavailable DOM in the Deep NW Pacific

To further resolve spatial patterns in deep-ocean DOC composition and bioavailability, we examined DOC and THAA concentrations and across three depth layers along the 155°E transect: 1,000–2,000 m, 2,000–4,000 m, and >4,000 m (Figure 3). While bulk DOC concentrations below 1,000 m remained relatively uniform

(43 ± 2 μmol L^{-1}; $n = 49$) and exhibited no significant latitudinal trends ($R^2 = 0.05$, $p > 0.1$; Figures 3a–3c), THAA concentrations showed pronounced latitudinal variability. Significantly elevated THAA concentrations (92–129 nmol L^{-1} on average) were observed between 30°N and 36°N in the 1,000–2,000 m and 2,000–4,000 m depth ranges, compared to values at corresponding depths at other latitudes (Mann-Whitney U test, $p < 0.01$; Figures 3d–3f). This pattern diminished at depth below 4,000 m. Previous investigations of deep-sea THAA concentrations in open oceans were often limited at single station (e.g., BATS and HOT) (Ianiri et al., 2022; Kaiser & Benner, 2009; Lee & Bada, 1977), which restricts insights into spatial variability within or across ocean basins. Our cross-latitude survey provides new evidence of spatial heterogeneity in deep-sea DOM composition, revealing regional "hotspots" of bioavailable substrates in the NW Pacific basin.

DOC-normalized yields of THAA varied ~3-fold at 1,000–4,000 m (0.4%–1.1%), with consistently elevated values (range: 0.6%–1.1%) occurring between 30°N and 36°N (Mann-Whitney *U* test, $p < 0.01$; Figures 3g–3i). These elevated deep-ocean THAA yields are striking, as previous studies have typically reported low THAA yield values below 1,000 m, such as 0.4%–0.5% in the deep Pacific and 0.6%–0.7% in the deep Atlantic (Kaiser & Benner, 2009). The observed elevated yields (~1.1%) exceeded the typical range for deep-sea DOC but were below the ~1.6% threshold characteristic of DOC containing labile compounds, indicating a semi-labile nature of this amino acid enrichment (Davis & Benner, 2007). Semi-labile DOC is generally thought to occur in the upper ocean and turn over on timescales of months to years (Hansell, 2013), although the actual turnover rates depend on various influencing factors, such as temperature, dissolved oxygen concentration, and microbial community (M. Chen et al., 2023).

For context, THAA yields in surface waters elsewhere commonly fall within similar ranges, including 0.9%–1.9% in the Atlantic Ocean, 0.6%–1.3% in the Pacific Ocean (Kaiser & Benner, 2009), 0.9%–2.7% in the Southern Ocean (Tremblay et al., 2015), 0.4%–4.2% in the Arctic shelf regions (Shen et al., 2018), and 0.5%–2.0% in marginal seas such as the Japan Sea (0.5%–1.3%) (Kim et al., 2017) and Louisiana margin (mostly 0.7%–2.0%) (Shen et al., 2016). Thus, the unusually high THAA yields observed at depth in this study are comparable to those typically found in the upper ocean of other regions, implying the presence of relatively fresh, semi-labile organic molecules in deep waters between 30°N and 36°N. These results suggest that this latitude band may harbor previously unrecognized patches of semi-labile DOC. The findings challenge the prevailing notion that deep-sea DOC is predominantly recalcitrant, instead revealing that bioavailable DOC can occur in patchy distributions at depth.

3.3. Potential Sources of Bioavailable DOM in the Deep Ocean

To investigate the origin of the elevated THAA observed in the mid-latitude deep Pacific, we analyzed the compositional signatures of the excess THAA relative to background levels (Figure 4 and Table S2 in Supporting Information S1). Sample handling artifacts were ruled out based on amino acid composition. Contamination from human-derived proteins (e.g., keratin) would yield distinct amino acid compositions (e.g., higher percentages of glycine, leucine, serine) than natural marine DOM (Strnad et al., 2011). Furthermore, no concurrent increases in bulk DOC were detected, which would be expected if contamination had occurred.

The elevated THAA observed in the 30°N–36°N region differed markedly in composition from surrounding THAA and were characterized by lower proportions of glycine and bacterially-derived D-amino acids (Figures 4a and 4b, and Figure S2 in Supporting Information S1), both of which typically accumulate during microbial degradation or reworking of DOM (Kaiser & Benner, 2009; McCarthy et al., 1998; Shen et al., 2015, 2025). A broader indicator of degradation, Degradation Index, was calculated based on the relative abundance of individual amino acids, leveraging their differences in diagenetic reactivity (Dauwe et al., 1999; Kaiser & Benner, 2009). This index was significantly higher (indicating fresher, less degraded material) in the mid-latitude deep Pacific compared to surrounding waters ($p < 0.001$, Mann–Whitney *U*-test; Figure 4c and Table S2 in Supporting Information S1). These compositional traits, together with elevated THAA yields, support the interpretation that the excess material in the deep NW Pacific is relatively fresh and bioavailable.

Several mechanisms may contribute to the observed mid-latitude enhancement in deep-ocean bioavailable DOC. One involves physical processes, such as vertical mixing from upper water mass (e.g., North Pacific Intermediate Water; NPIW) or horizontal advection of deep water (Pacific Deep Water; PDW) (Figure 2a). Vertical transport via NPIW is unlikely, as this water mass is often restricted to depths of 300–800 m (You, 2003). Similarly, southward advection of PDW at 1,000–3,000 m brings water from the north (Kawabe & Fujio, 2010), where DOC

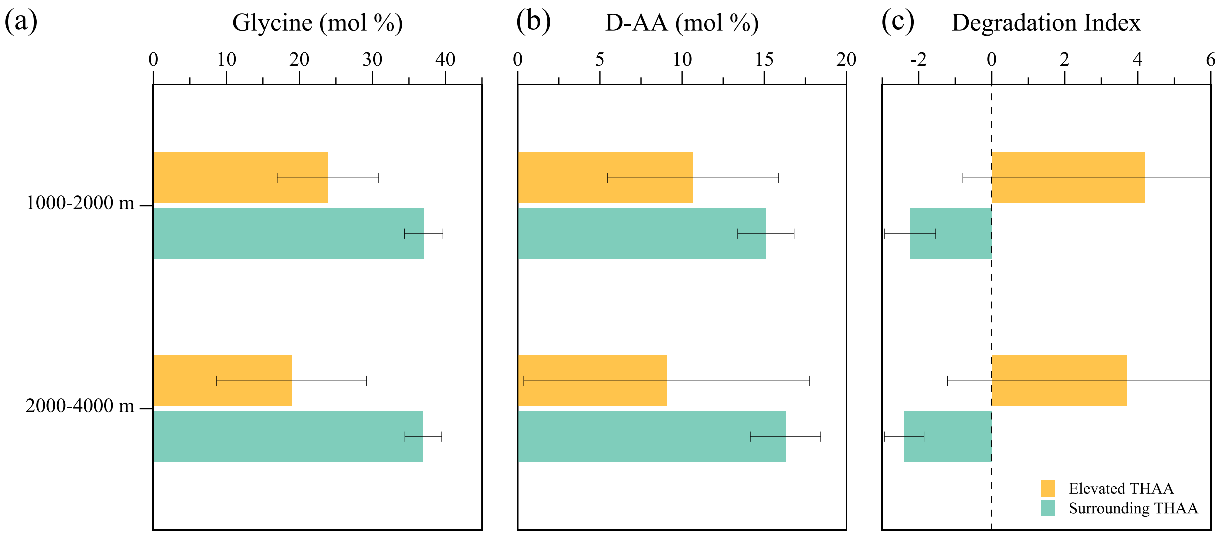

Figure 4. Comparison of molecular indicators (a: Glycine mol%; b: D-AA mol%; c: Degradation Index) between the elevated THAA at 30°N–36°N (relative to the average values at other sampling latitudes) and surrounding THAA (average values at other sampling latitudes) in the 1,000–2,000 m and 2,000–4,000 m depth range. Error bar represents one standard deviation ($n = 8$–11 per group).

is depleted in THAA (Figure 3), making this pathway inconsistent with the THAA enrichment at the 30°N–36°N mid-latitudes.

Another potential source is the supply of fresher material from surrounding suspended particles or/and sinking particles to the deep ocean. However, suspended particles are unlikely sufficient. THAA concentrations in deep suspended particles rarely exceed 10 nmol L^{-1} (Lee et al., 2000; Sheridan et al., 2002). Even if fully solubilized, they could not account for the observed excess of THAA (22–49 nmnol L^{-1}; Figures 3d–3f). Likewise, passive sinking particles may contribute only partially. Data on amino acid fluxes in the deep ocean are limited. Using the few available measurements from the North Pacific Ocean, which show amino acid fluxes decreasing from 4.5 mg m^{-2} d^{-1} at 1,000 m to 1.9 mg m^{-2} d^{-1} at 3,600 m (Lee et al., 2000), we could estimate a flux loss of 2.6 mg m^{-2} d^{-1} over this depth range. Assuming that this entire loss is converted to the dissolved phase and remains unaltered by degradation or transport, it would result in an average increase of ~0.01 nmol L^{-1} d^{-1} in dissolved THAA. Further assuming that this input persists over an annual timescale (e.g., ~360 days), the cumulative increase would be around 2–3 nmol L^{-1}. Even under this generous scenario, the contribution from sinking particles accounts for only a small portion of the observed THAA anomaly, suggesting that additional sources or mechanisms are involved.

A more plausible mechanism involves active input of protein-rich organic matter from diel vertical migrators. The active carbon flux by migrators can bypass traditional sediment traps (Steinberg et al., 2008; Turner, 2015) and may represent an overlooked yet significant source of bioavailable organic matter in the deep ocean. Recent radiocarbon (^{14}C) and molecular characterizations in the North Atlantic Ocean detected an elevated occurrence of ^{14}C young, labile, high-molecular weight proteinaceous organic material in deep waters, attributed to active transport of sinking particles from migrating zooplankton (Shen et al., 2025). Pulsed fluxes of zooplankton fecal pellets have been observed at a depth of 3,500 m in the northeastern Pacific (Wilson et al., 2013), and similar inputs might have occurred in the northwestern region. The biologically mediated replenishment provides a plausible explanation for the observed amino acid enrichments in deep Pacific waters, linking episodic biological inputs to the presence of protein-rich DOM at depth.

The localized enrichment of bioavailable dissolved organic molecules in the deep NW Pacific likely reflects a sporadic and episodic event, particularly if it is linked to the delivery of fresh organic particles by migrating zooplankton. THAA enrichment was also observed in the mesopelagic zone (500–1,000 m) between 30°N and 36°N, whereas adjacent regions showed no such signal, suggesting a localized input of bioavailable material from the upper water column to depth. However, zooplankton abundance and biomass in the NW Pacific generally increase with net primary productivity from low to high latitudes (Xu et al., 2025). Copepods and Malacostracans are the dominant groups, and the active carbon flux mediated by zooplankton diel vertical migration also exhibits a south-to-north increasing trend (Xu et al., 2025). This cross-latitude pattern in zooplankton biomass and active flux appears decoupled from the observed spatial enrichment in dissolved amino acids. These observations suggest that the deep delivery of migrant-derived material is an intermittent process that may not always be captured in or reflected by the dissolved organic pool.

Independent lines of radiocarbon provide additional evidence for the sporadic input of fresh organic matter to depth. Previous surveys conducted along nearby transects have documented spatial and temporal variability in the apparent age of deep waters in the NW Pacific, inferred from radiocarbon analysis of dissolved inorganic carbon (Δ^{14}C-DIC) taken from 1993 to 2019 (149.3°E in 1993, 149.3°E in 2005, and 150°E in 2019) (Ge et al., 2022; Key et al., 2004; Kumamoto et al., 2013). Notably, elevated Δ^{14}C-DIC values observed between 30°N and 40°N at 1,000–4,000 m in 2019 were absent in earlier years (Ge et al., 2022), suggesting intermittent deep inputs of fresher carbon in this region.

The confinement of THAA hotspot to 30°N–36°N in the NW Pacific is intriguing. In the eastern side of the North Pacific, deep DOC enrichment has been reported beneath major frontal zones (~34°N, ~42°N) along the P16 transect (25°N–50°N, 151°W), attributed to the deep introduction of DOC via sinking particles (Lopez & Hansell, 2021). In contrast, we did not observe similar enrichment in bulk DOC in the western basin, possibly due to varying particle export. This lack of deep-sea DOC enrichment may appear inconsistent with the observed increase in THAA concentrations. However, it is important to note that even a substantial rise in THAA (on the order of 22–49 nmol L^{-1} as observed here) would translate to only a minor increase (~0.1 μmol C L^{-1}) in total DOC, given the low carbon contribution of amino acids (1 nmol L^{-1} of THAA ≈ 0.004 μmol C L^{-1}). Such a minor change would fall well below the detection threshold of most DOC measurement techniques and could easily escape notice in bulk analyses.

Regardless of the exact mechanism, our results reveal the presence of spatially discrete pools of bioavailable DOC in the deep ocean. The relatively high THAA yields in the deep ocean imply that a portion of this DOC is semi-labile, with turnover times of months to years. These "hidden" bioavailable organic patches are not easily captured by conventional bulk DOC measurements but represent important subsidies for microbial communities in the dark, energy-scarce deep ocean (Arístegui et al., 2009; Herndl & Reinthaler, 2013). Identifying the drivers behind these episodic and localized enrichments remains an important avenue for future research.

Conflict of Interest

The authors declare no conflicts of interest relevant to this study.

Data Availability Statement

All data used in this study are provided in Supporting Information S1 and have been archived on Figshare (Li et al., 2025).

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