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Vertical and latitudinal variations in amino acid fluxes and compositions of settling particles along 175°E in the North Pacific Ocean

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ABSTRACT

Settling particles collected by sediment traps deployed for about one year (1993–94) at four sites along 175°E longitude in the central North Pacific have been analyzed for amino acids (AA) and amino sugars (or hexosamines, HA). These compounds account for about 12.5–27.9% of particulate organic carbon flux to the deep ocean. Biogeochemical indicator parameters varied in the range comparable with similar studies conducted in other oceanic sites. Correlations between non-protein AA (β-alanine and γ-aminobutyric acid) and flux parameters indicate repackaging of settling particulate organic matter (POM) around intermediate water depth (below 1500 m) at all trap sites. Mean values of indicator parameters in the shallow trap differ significantly (Student's t-test; $p < 0.03$) from those in deep traps at the same site. Latitudinal trends in POM flux and its labile composition suggest that relatively fresh POM is being deposited at a higher rate in the subarctic area of the Pacific. However, this trend is not so clear in deep traps, probably due to the influence of bioactive transport and deposition of laterally advected particles in these traps. Total and particulate organic carbon fluxes normalized to primary productivity estimates show a sharp rise in efficiency of the biological pump towards the subarctic area, which is responsible for enhanced fluxes of particles with a high labile content to the deep ocean in this part of the Pacific.

1. Introduction

Amino acids (AA) and amino sugars (or hexosamines, HA) are among the labile components of organic matter. Their abundance in settling particulate organic matter (POM) in the ocean is a good indication of the relative freshness of the POM, and its potential for consumption by microbes as it sinks through the water column. Estimates of AA and HA, and parameters based on these two classes of compounds, have been used in a number of studies dealing with POM in marine water and sediments (Lee and Cronin, 1982; 1984; Ittekkot et al., 1984a,b; Müller et al., 1986; Haake et al., 1992; Cowie and Hedges, 1994; Wakeham et al., 1997; Dauwe and Middelburg, 1998). Such estimates also give important clues about processes affecting the flux of particulate organic carbon (POC) to the deep oceans. Depending upon the lability of POM, carbon may or may not be sequestered in sediments. This sequestration plays an important role in the global biogeochemical cycling of carbon and other associated elements. All over the world, oceans are being investigated for understanding the biogeochemical cycling of elements in general, and carbon, nitrogen and silicon in particular (e.g. Bronk et al., 1994; Mackey et al., 1997; Sabine et al., 1997; McCarthy et al., 1998; Dugdale and Wilkerson, 1998; Smetacek, 1998). Our current understanding of these cycles is as yet far from complete, which introduces considerable uncertainty into spredictions made by global climate change

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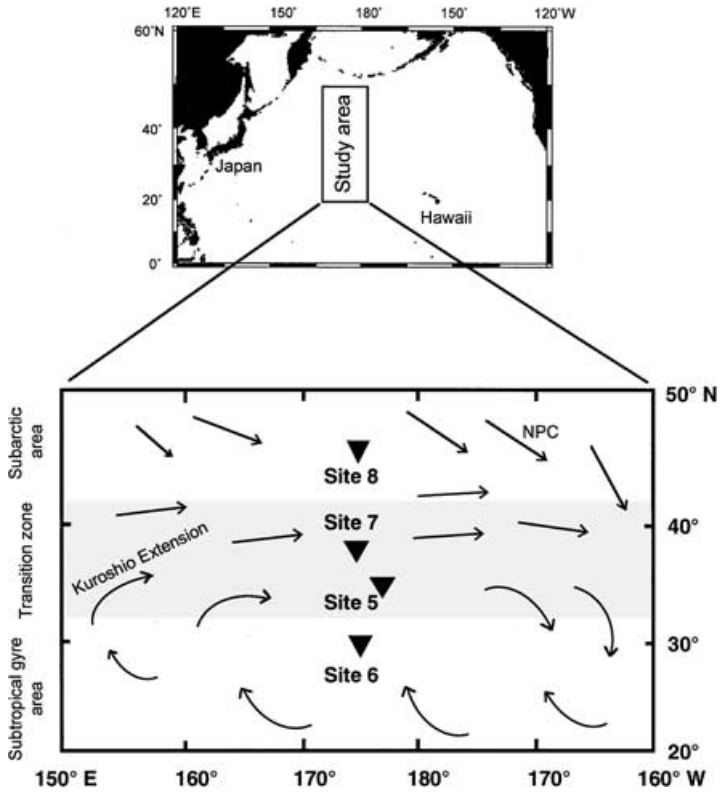

Fig. 1. Locations of sediment traps in the North Pacific Ocean and highly simplified ocean surface currents [NPC (north Pacific current) and Kuroshio current].

models (e.g. Sarmiento and Quere, 1996; Trenberth, 1997; Sarmiento et al., 1998; Falkowski et al., 2000). In order to minimize such uncertainties, more data on particle flux and the nature of settling POM need to be collected over the world ocean. The present work is a contribution in this direction.

Sediment traps have been used extensively in estimating particle fluxes from shallow to deep waters of the oceans. They provide new information on the reactivity of settling particulates. Here we describe and compare sediment trap data in terms of total mass and POM fluxes and parameters based on 20 common AA and 2 HA (glucosamine and galactosamine) from four trap sites along a north–south transect in the central North Pacific Ocean (Fig. 1). Subtropical gyre is the most saline watermass in the North Pacific, and is known for low primary productivity of ca. 70 mg C m^{-2} d^{-1} (Berger et al., 1989). Trap site 6 was located at the northern end of the gyre, adjacent to which lies the transition zone characterized by warm and saline water. This watermass expands up to 40°N latitude and includes the Kuroshio Extension, which shows interannual variations in its path across the latitudes (Qiu and Joyce, 1992). However, the extension has been rather stable latitudinally during the late Pleistocene (Kawahata and Ohshima, 2002). Primary productivity in this area has been estimated to be about 180 mg C m^{-2} d^{-1} (Berger et al., 1989). Trap sites 5 and 7 were located in the transition zone. Further north in the subarctic area, where trap site 8 was located, a high primary productivity of 220 mg C m^{-2} d^{-1} has been reported (Berger et al., 1989).

2. Materials and methods

Six SMD21-6000 (Nichiyu-giken-kogyou Ltd., Tokyo) time-series sediment traps, each with 0.5 m^2 collection area and 21 sampling bottles on a rotary collector, were deployed (Fig. 1) for a period of about one year during 1993–94 (Table 1). The sampling

Table 1. *Sediment trap site locations, water depths and sampling periods for this study*

Site	Location	Seafloor depth (m)	Trap depth (m)	Collection period
Site 6	30°00.1′N, 174°59.7′E	5390	3873	Jun 93–May 94
5, shallow	34°25.3′N, 177°44.2′E	3365	1342	Jun 93–Apr 94
5, deep	″ ″	″	2848	Jun 93–May 94
7, shallow	37°24.2′N, 174°56.7′E	5105	1482	Jun 93–Apr 94
7, deep	″ ″	″	4588	Jun 93–Apr 94
Site 8	46°07.2′N, 175°01.9′E	5435	1412	Jun 93–Apr 94

bottles were filled, prior to deployment, with filtered seawater (collected by a deep water cast) and a 3% solution of analytical grade formalin buffered with sodium borate/boric acid to retard microbial activity. The traps were programmed to collect samples in each bottle over an average period of about 2–4 wk. On recovery, the samples were refrigerated on board ship at 2–4 °C. In the laboratory, samples were passed through a 1 mm pore size sieve to remove swimmers and other large size debris, and the <1 mm fraction was split into aliquots with a high-precision rotating splitter. Desalted, dried and homogenized samples were used for chemical analyses (Kawahata et al., 2000a).

The AA and HA analysis has been described in detail in Gupta and Kawahata (2000). In brief, approximately 10 mg of sample was hydrolyzed with 6 N HCl at 110 °C under an argon atmosphere in a sealed glass ampoule for 22 h. The hydrolyzed sample was passed through a 0.45 μm filter and then the acid was removed using a rotary evaporator. The residue was then diluted to 500–1000 μL with a pH 2.2 solution, and 10 μL of the sample was injected by an autosampler into a Shimadzu amino acid analyzer. The analyzer was fitted with a 10 cm long strongly acidic cation exchange column, which was maintained at 60 °C during analysis. The AA and HA were eluted with binary solvents (pH 3.2 and 10.0). Post-column derivatives were reacted with *o*-phthaldialdehyde and quantified with a fluorescence detector. Peak areas were quantified using a Shimadzu Chromatopac C-R4A data system. Each sample was analyzed 2–3 times. The method has a relative standard deviation of less than 10% of the reported values. Although the data in this study were produced without using an internal standard, a subsequent use of the internal standard L-norleucine with other samples has shown a recovery of ca. 95% in this method. Based on the earlier analyses of the same samples, the data on annual mean settling flux of particulates and its major bulk components, such as carbonates, POM, opal and lithogens, have already been published (Kawahata et al., 1998).

AA and HA are among easily degradable constituents of POM and are metabolised during settling in a water column (Handa and Tominaga, 1969; Lee and Cronin, 1984). Some combinations of the individual AA and HA have been used in many studies to explore the biogeochemical status of POM (e.g., Izdar et al., 1987; Haake et al., 1992; Cowie and Hedges, 1994; Gupta et al., 1997; Hashimoto et al., 1998; Jennerjahn et al., 1999; Gupta and Kawahata, 2000; Suthhof et al., 2000; Gupta and Kawahata, 2002). The combined molar percentage of the two non-protein AA, β-ala and γ-aba, is an indicator of relative freshness of POM (Cowie and Hedges, 1994). The ratio between total AA and HA (AA/HA) is helpful in differentiating chitinous zooplankton (AA/HA, 9; Mayzaud and Martin, 1975) from phytoplankton (AA/HA >80; Strahlendorff, 1988). Low AA/HA ratios, with HA being mostly glucosamine (Glc-NH_2), indicate a large amount of chitinous material. The Glc-NH_2/Gal-NH_2 (galactosamine) ratio is used to differentiate chitinous zooplankton from microbial biomass. In many bacterial cell walls, both Glc-NH_2 and Gal-NH_2 are present (Wolla et al., 1984), and Glc-NH_2/Gal-NH_2 ratios of <4 were measured in various bacterial species (Kandler, 1979; Lehninger, 1982). The usefulness of the reactivity index (RI) and degradation index (DI) in interpreting diagenetic changes in POM has been described recently by Jennerjahn and Ittekkot (1997) and Dauwe and Middelburg (1998), respectively. Besides these parameters, variations in relative mole concentration of tyrosine (Tyr) can also be interpreted for the duration of oxic alteration of POM (Suthhof et al., 2000). These indicator ratios and other parameters have been used here to interpret the biogeochemical status of settling POM.

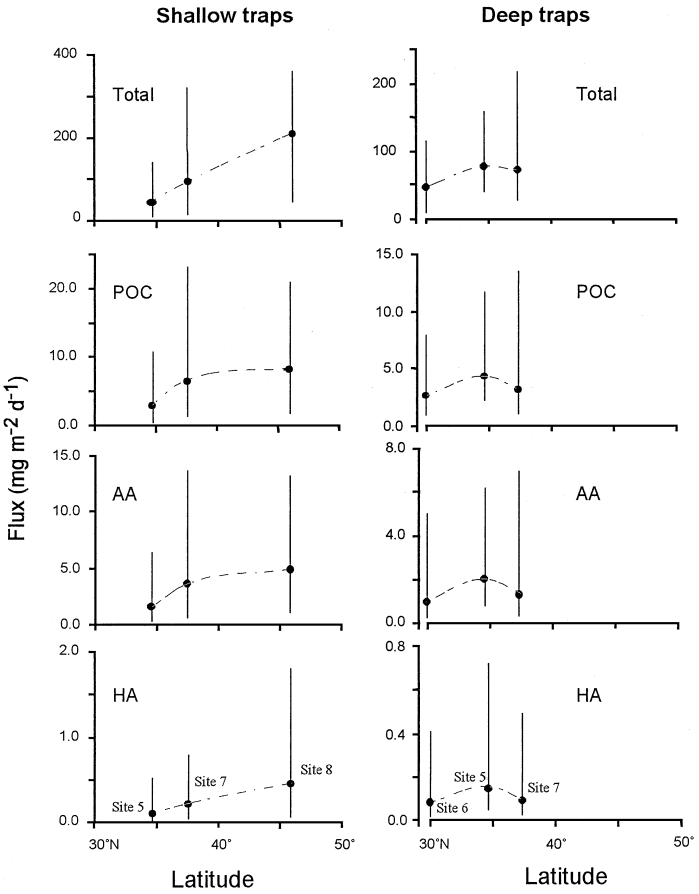

Fig. 2. Latitudinal trends in average daily fluxes of total mass, particulate organic carbon (POC), amino acid (AA) and hexosamine (HA) in shallow and deep traps. Total and POC flux data from Kawahata et al. (1998). Vertical lines depict minimum–maximum range.

3. Results and discussion

3.1. Average fluxes and contents of AA and HA

The AA and HA fluxes together accounted for 12.5–27.9% of the POC fluxes (Fig. 2). HA contents were 10–15% of AA content in all the traps. In general, about 45% of AA mass is carbon (Lee and Cronin, 1982). In the present study, AA carbon relative to POC (AA-C%) varied, on average (flux-weighted), from 22.6 at Site 5 to 25.9 at Site 8 among the shallow traps, and from 16.6 at Site 6 to 19.4 at Site 5 among the deep traps (Table 2). On average (flux-weighted), AA-N% varied from 49.5 at Site 5 to 52.6 at Site 8 among the shallow traps, and from 38.4 at Site 7 to 43.5 at Site 5 among the deep traps. Since microbial degradation of POM decreases concentrations of labile components at greater depths in the ocean (Lee and Cronin, 1982; Lee et al., 2000), AA, HA, AA-C% and AA-N% showed generally higher values in the shallow traps compared to respective deep traps (Fig. 3). Additionally, β-ala+γ-aba (mol%) content was lower in shallow traps compared to corresponding deep traps. At Sites 5 and 7, where shallow and deep traps were deployed in the same mooring, AA, AA-C%, AA-N%, β-ala+γ-aba, RI and Glc-NH_2/Gal-NH_2 showed the mean values to be significantly different between shallow and deep traps ($p < 0.03$; Student's *t*-test, two-tailed, heteroscedastic). At Site 5 mean total flux ($p < 0.03$), while at Site 7 mean AA/HA ratio and Tyr content ($p < 0.01$) were significantly different between the shallow and deep traps. These observations

Table 2. *Flux-weighted averages and range of variations in biogeochemical parameters of settling particles in the North Pacific*

Trap	AA (mg g^{-1})	AA-C%	AA-N%	Glc-NH_2/ Gal-NH_2	AA/HA	TYR (mol%)	Non-protein (mol%)	RI	DI
Shallow traps									
Site 5	**37.5**	**22.6**	**49.5**	**7.2**	**22.3**	**2.2**	**1.2**	**4.4**	**−0.2**
(1342 m)	24.4–55.0	19.5–32.6	43.6–65.1	4.1–9.0	16.9–31.5	1.1–2.6	0.7–1.6	3.1–6.5	−2.1–1.4
Site 7	**38.1**	**23.9**	**50.1**	**6.4**	**26.4**	**2.5**	**1.2**	**5.0**	**−0.4**
(1482 m)	25.7–62.2	20.0–28.6	43.1–58.8	3.6–8.6	19.5–39.8	2.1–3.5	0.8–1.6	3.8–7.4	−2.0–1.5
Site 8	**22.6**	**25.9**	**52.6**	**10.6**	**25.8**	**2.1**	**1.2**	**4.3**	**−0.3**
(1412 m)	14.1–36.2	22.2–31.7	45.5–63.6	2.8–33.0	6.2–45.5	1.5–2.4	0.9–1.6	3.1–6.2	−1.9–1.7
Deep traps									
Site 6	**23.1**	**16.6**	**40.6**	**5.3**	**19.4**	**2.2**	**1.5**	**3.6**	**−0.5**
(3873 m)	12.7–46.4	12.8–27.1	31.8–65.9	3.4–8.1	16.6–23.3	2.0–2.6	1.1–2.1	2.3–5.1	−1.7–1.5
Site 5	**26.7**	**19.4**	**43.5**	**7.2**	**23.9**	**2.1**	**1.6**	**3.2**	**−0.2**
(2848 m)	14.9–41.8	15.0–24.2	36.1–50.8	3.5–15.1	12.4–35.3	1.9–2.5	1.1–2.2	2.2–4.9	−2.1–1.0
Site 7	**17.9**	**17.2**	**38.4**	**4.2**	**20.4**	**2.9**	**2.3**	**2.7**	**−0.4**
(4588 m)	9.4–32.2	13.6–22.4	31.6–50.0	3.2–5.0	16.9–28.1	2.5–3.4	1.3–3.3	1.6–4.4	−2.3–1.0

AA, amino acid; AA-C%, AA carbon percent of particulate organic carbon; AA-N%, AA nitrogen percent of particulate nitrogen; Glc-NH_2/Gal-NH_2, glucosamine/galactosamine; HA, hexosamine; Tyr, tyrosine; RI, reactivity index; DI, degradation index.

indicate that the settling particles in the shallow and deep traps differ from each other in biogeochemical terms. At comparable depths, the AA fluxes (shallow traps 0.3–13.6, deep traps 0.1–7.0 mg m^{-2} d^{-1}) recorded in this study are lower than those recorded in the Drake Passage (Müller et al., 1986) and at the VERTEX II Mexico site (Lee and Cronin, 1984), but are close to those recorded in the central Arabian Sea (Haake et al., 1992). AA contents (shallow traps 14.1–62.2, deep traps 9.4–46.4 mg g^{-1}) are comparable with those from the deep Sargasso Sea, the deep Panama Basin and the Drake Passage. The AA/HA ratios (shallow traps 6.2–44.9, deep traps 7.6–34.9) recorded in this study are comparable with those from the Arabian Sea, the Drake Passage and the deep Panama Basin (Ittekkot et al., 1984b). The Glc-NH_2/Gal-NH_2 ratios (shallow traps 2.8–33.0, deep traps 3.2–15.1) are comparable with those from the Arabian Sea and Drake Passage. This comparison of data indicates that labile contents and their flux to deeper depths in the North Pacific are almost similar, or are within the range observed at other sites in the world ocean.

Indicator parameters were evaluated simultaneously to find clues about origin, decompositional status of the settling POM and biogeochemical processes operating in deep ocean. Only a few of these parameters showed significant correlations among themselves for very obvious reasons. For instance, AA content was positively correlated with AA-C% and AA-N% and RI, but negatively correlated with β-ala+γ-aba content (Table 3). However, when individual trap data were subjected to regression analysis, many new correlations became statistically significant. At Sites 5 and 7, where shallow and deep traps were deployed in the same mooring, significant inverse correlations ($r = -0.8$ to -0.9) between total flux and β-ala+γ-aba content (mol%) of particles collected by deep traps suggest that particles deposited during high total flux are relatively fresher than those during low flux periods (Fig. 4). Moreover, AA concentrations in deep traps covary positively with total flux ($r = 0.7$–0.8) and RI ($r = 0.8$–0.9). Similar correlations are nonexistent in the case of shallow traps ($r = 0.3$ to -0.2), although significant coupling ($r > 0.8$) of total fluxes exists between the shallow and deep traps. These correlations suggest that during higher fluxes, some kind of repackaging of particles occurs at intermediate water depths of about 1500 m, so that particles settle faster and deposit relatively fresher POM to the deeper depths. This repackaging can be nothing but a result of the 'Bioactive Transport' as proposed earlier by Walsh et al. (1988) for the settling particles in the North Pacific.

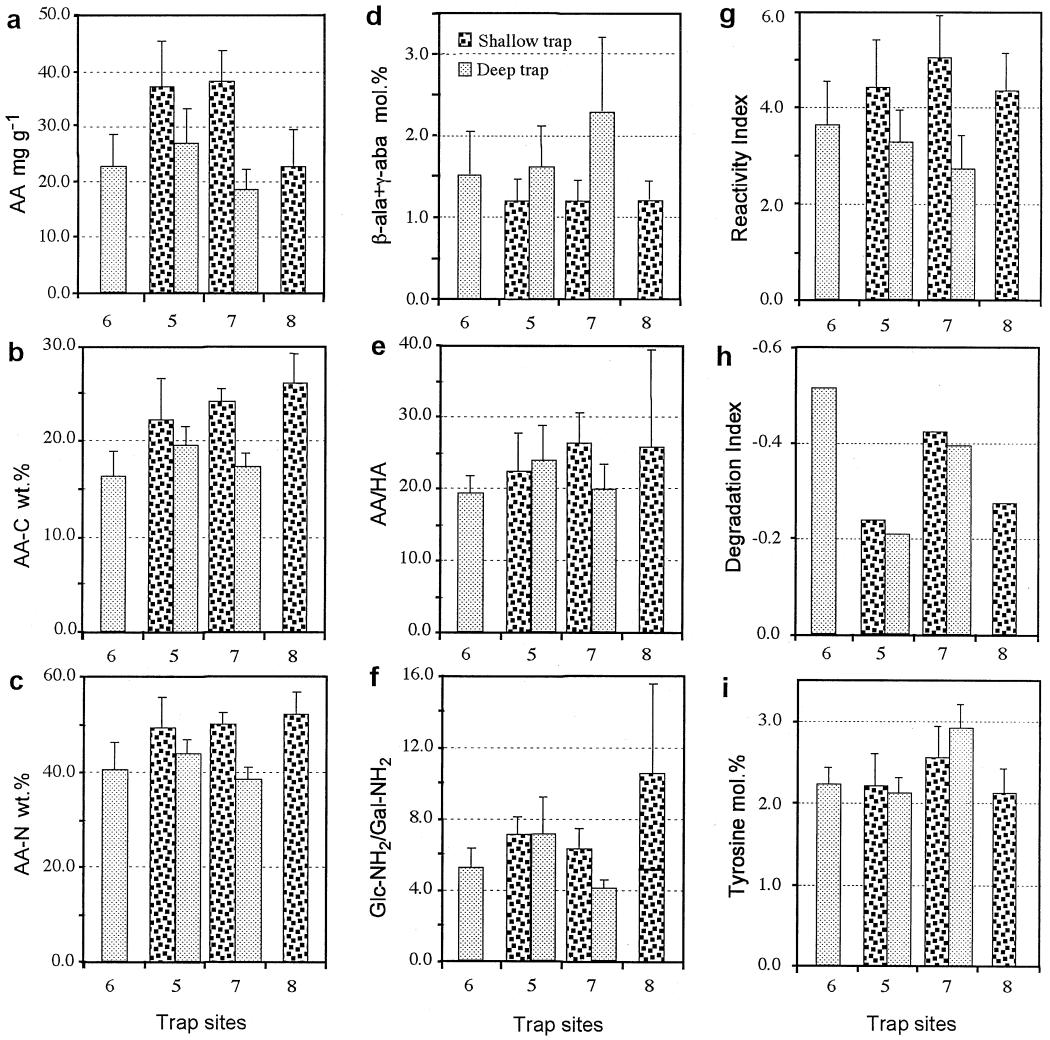

Fig. 3. Latitudinal variations in flux-weighted averages of: (a) amino acid (AA); (b) AA carbon relative to POC (AA-C%); (c) AA nitrogen relative to total nitrogen (AA-N%); (d) β-alanine and γ-aminobutyric acid (β-ala+γ-aba); (e) ratio of AA and hexosamine (AA/HA); (f) ratio of glucosamine/galactosamine (Glc-NH_2/Gal-NH_2); (g) reactivity index (RI); (h) degradation index (DI); and (i) tyrosine content. Standard deviations are shown, which is 1 in the case of DI.

In this mode of particle sinking, zooplankton living in intermediate water depths feed on settling particles and move to deeper depths to defecate. Biogeochemical signature of ingested POM is significantly altered due to zooplanktonic metabolism (Cowie and Hedges, 1996). As a result of enhanced particle flux from surface waters, the feeding rate of these zooplankton may be positively influenced, so that they graze excessively and defecate quickly to inadvertently transport less digested (or degraded) POM to deeper depths as compared to that during low flux periods. This scenario can explain coupling of higher fluxes in deep traps with low β-ala+γ-aba content, high AA content and high RI of settling particles in the deep central North Pacific Ocean. The planktonic activities in intermediate water may be closely associated with relatively deeper mixed layer and thermocline (>1000 m deep) between 30–40°N latitudes in the Pacific (Fig. 1.7-5 in Kennish, 1994). In contrast, during the low flux period, the settling speed may be low, which will offer

Table 3. *Correlations among selected biogeochemical indicator parameters for all samples* (n = *107) from shallow and deep traps*

	Total flux (mg m^{-2} d^{-1})	β-ala+γ-aba (mol%)	RI	AA (mg g^{-1})	Glc-NH_2/ Gal-NH_2	AA/HA	AA-C%	AA-N%	Tyr (mol%)
DI	−0.41	0.19	−0.04	−0.37	−0.17	−0.02	−0.27	−0.31	0.19
Tyr	−0.21	0.56	−0.24	−0.41	−0.30	−0.17	−0.38	−0.45	
AA-N%	0.41	−0.78	0.76	0.80	0.27	0.42	0.96		
AA-C%	0.40	−0.74	0.74	0.71	0.25	0.54			
AA/HA	−0.03	−0.29	0.27	0.19	−0.37				
Glc-NH_2/Gal-NH_2	0.50	−0.36	0.29	0.26					
AA	0.18	−0.72	0.71						
RI	0.23	−0.89							
β-ala+γ-aba	−0.29								

Abbreviations same as in Table 2.

a longer span for enzymatic/microbial degradation of settling POM.

3.2. *Latitudinal trends in various parameters*

In the case of shallow traps, all flux parameters showed an increase towards higher latitudes, although total and HA fluxes increased at a faster rate than POC and AA fluxes, especially between Sites 7 and 8 (Fig. 2). Similar increase was shown by AA-C%, while AA-N% showed only marginal increase (Fig. 3). In contrast, AA concentration decreased after a slight increase, while β-ala+γ-aba content was nearly unchanged. AA/HA, RI and tyrosine content initially increased followed by a decrease. Glc-NH_2/Gal-NH_2 and DI decreased initially followed by an increase. The latitudinal increase in fluxes can be attributed to a higher lithogenic content at Site 7, but to a higher opal content (Boyd and Harisson, 1999) at Site 8. In the central North Pacific, aerosols are the major contributor to pelagic sediments. Based on their quartz content and the ^{210}Pb content of seawater, the maximal input of aerosols has been estimated to occur between 30 and 40°N (Nozaki and Tsunogai, 1973; Windom, 1975). Aeolian dust was attributed to a high lithogenic content around Site 7 trap (Kawahata et al., 1998; 2000b). Higher lithogenic content intensifies ballast formation in surface water and particles sink rapidly due to enhanced density (Ittekkot, 1993). Further, an excess of phytoplanktonic biomass originating from high primary production might not be completely consumed by zooplankton, as a result of which fresh phytoplanktonic POM can arrive at trap depth possibly through formation of large, rapidly settling aggregates of phytoplankton (Peinert et al., 1989). At Station PAPA (50°N, 145°W) diatom-dominated spring blooms have been shown to be a driving factor behind sedimentation of phytoplankton (Boyd and Harisson, 1999). A high settling speed of diatoms brings cytoplasm-rich cells to the deep ocean (Scharek et al., 1999). Besides this, the higher efficiency of the 'Biological Pump' has been attributed to enhanced sedimentation of biogenic silica in higher latitudes of the North Pacific (Buesseler et al., 2001). These processes can possibly explain the supply of fresh POM with higher AA-C% and AA-N% values at Site 8, where the biogenic silica flux is much higher (Kawahata et al., 1998) relative to that at other sites in this study.

Nearly constant β-ala+γ-aba content suggests that the degree of degradation of settling POM does not depend upon the absolute amount of AA, which does decrease towards higher latitudes. Trends in the average AA/HA ratio and RI and Tyr content imply that settling POM is fresher and more reactive at Site 7. However, DI and Glc-NH_2/Gal-NH_2 values are not consistent with this inference. The average DI value for a data set turns out to be 0, because it is calculated from the data standardized to give an average value of 0 and a standard deviation of 1. In the process of flux-weighted average calculation, DI attained a value different from 0, which probably has no practical meaning. The Glc-NH_2/Gal-NH_2 ratio is highly skewed due to the large Glc-NH_2 content relative to Gal-NH_2 during a phenomenal rise in flux (possibly due to planktonic bloom) at Site 8. Samples during this rise show a Glc-NH_2/Gal-NH_2 value of ca. 33, which brought the average value to >10. If the extremely high values are

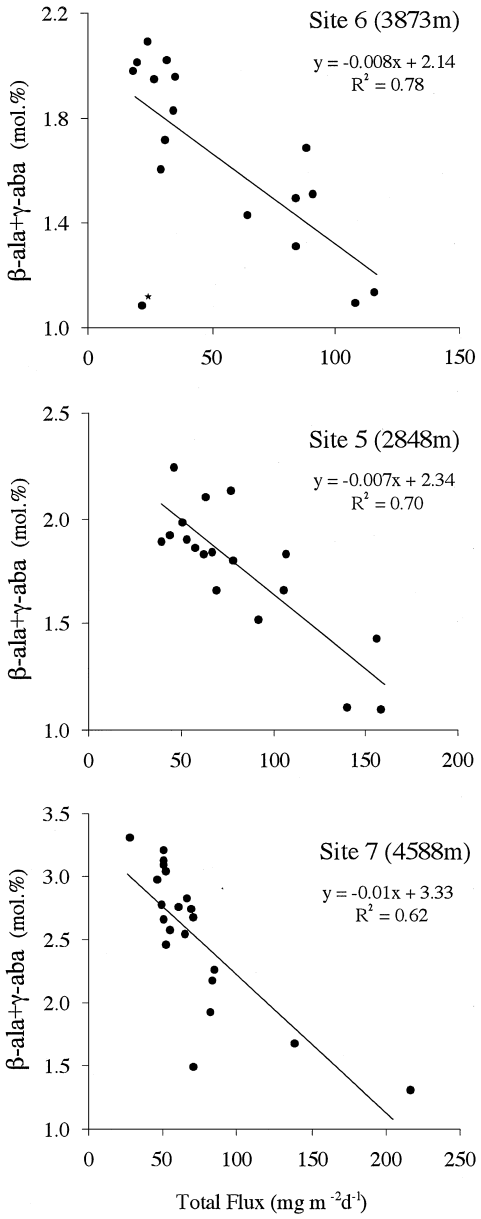

Fig. 4. Inverse relationship between non-protein AA (β-ala+γ-aba) content and total flux in deep trap samples. For Site 6, $*$ denotes a data point excluded from the regression.

omitted, the average falls to ca. 5, which then depicts a decreasing trend in Glc-NH_2/Gal-NH_2 ratio towards higher latitudes. This trend implies a decrease in zooplanktonic component relative to microbial mass in the settling particles.

All deep traps exhibited a poleward increase in β-ala+γ-aba (mol%) and a corresponding decrease in RI (Figs. 3d and g). Other parameters, including fluxes, showed an initial increase followed by a decrease towards higher latitudes. Only the Tyr content showed an opposite trend of a decrease followed by an increase; however, the decrease is analytically insignificant. Similarly, a small increase in β-ala+γ-aba content between Sites 6 and 5 is insignificant. The higher β-ala+γ-aba content and lower RI at Site 7 suggest settling POM to be more degraded than that at Sites 6 and 5. However, this may have nothing to do with the latitudinal trend as the Site 7 deep trap was located at the deepest water depth (4588 m) relative to that at Site 6 (3873 m) and Site 5 (2848 m). Particles settling to deeper depths are expected to have a longer exposure to enzymatic/microbial degradation than those at shallower depths. This significantly large difference in trap deployment depth also explains the trend of initial increase followed by a decrease in the rest of the parameters, except for the Tyr content, which is unusually higher in the deepest trap. The high Tyr content is slightly higher than that in the shallow trap at the same site (Site 7). Some sedimentary deep-sea bacteria contain as much as 2.7 mol% Tyr (Suthhof et al., 2000), which is still lower than the maximum value of 3.4 mol% recorded in this study. However, plankton net samples showed a Tyr content in the range 3.8–5.5 mol% (Suthhof et al., 2000). These high Tyr values suggest that Tyr in the deep trap at Site 7 may predominantly be of planktonic origin rather than bacterial origin. The higher Tyr content in the deeper trap relative to the shallow trap may be a result of lateral advection, as mentioned before. Besides this, deep traps have possibly collected sediments under the influence of 'Bioactive Transport'; therefore any inference on the latitudinal trends, based on deep traps, is likely to be biased due to these processes.

3.3. Implications of the latitudinal trends

Since the higher-latitude oceans are more influenced by glacial–interglacial variations (CLIMAP, 1976), and they are a sink of CO_2 (Takahashi, 1998), the observed latitudinal variations can be evaluated for their influence on the carbon cycle, especially in the central North Pacific. AA/POC ratios in shallow traps show a steady rise from ca. 52% in the Kuroshio Extension to ca. 60% in the subarctic area. This small poleward rise in AA/POC ratios is an indication of enhanced

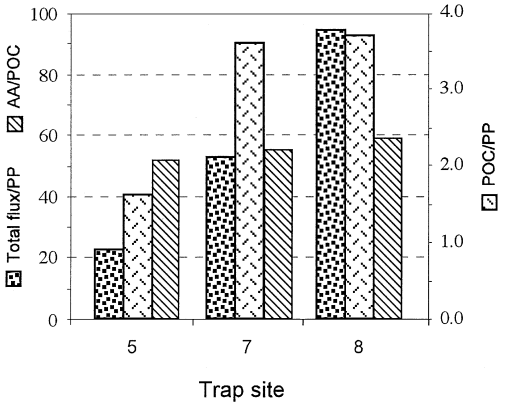

Fig. 5. Latitudinal variations in amino acid/particulate organic carbon (AA/POC), POC/PP (primary productivity) and Total flux/PP ratios in shallow traps. Total and POC flux data from Kawahata et al. (1998); PP data from Berger et al. (1989).

freshness of settling POM in the subarctic area relative to that in the Kuroshio Extension area (Fig. 5). Recently, Rivkin and Legendre (2001) have reported the bacterial growth efficiency to be inversely proportional to the ambient temperature. Based on this relationship, they showed that a greater proportion of the primary production can be exported to the deep ocean at higher latitudes relative to low latitudes. This finding is in line with the higher flux rates observed by us in the subarctic area, and corroborates the enhanced availability of fresh POM at the trap depths. Average total fluxes in shallow traps normalised to primary productivity values from Berger et al. (1989) depict a sharp rise in efficiency of the biological pump towards the subarctic area (Fig. 5). An almost similar trend is shown by average POC fluxes normalised to the primary productivity values. Thus, higher fluxes coupled with higher lability of settling POM is the current scenario at the mid-latitude North Pacific. A similar inference on the latitudinal trend of efficiency of the biological pump can be made on the basis of the opal/carbonate ratio, which increased from 0.14 in the subtropical gyre to 3.72 in the subarctic water (Kawahata et al., 1998). Given the understanding that plankton biomass was an order of magnitude higher during the last glacial maximum than it is today in the North Pacific (Sancetta, 1992), this scenario implies that enhanced availability of labile components (food) to benthic organisms might have led to a proportionate rise in the benthic biomass and burial of POC during the same time period.

4. Conclusions

This study deals with a wide region of the central North Pacific Ocean covering latitudinal and vertical variations in the labile components of settling particle fluxes. The AA and HA carbon fluxes together account for 12.5–27.9% of the POC flux, with AA predominating by an order of magnitude. The average daily fluxes of AA and HA recorded by shallow traps generally increase from subtropical gyre towards the subarctic area. Latitudinal trends in biogeochemical parameters are prominent, with greater variations in the case of shallow traps. The deep traps at all sites show some kind of repackaging of settling particles under the influence of bioactive transport below a depth of 1500 m. This repackaging may be responsible for the statistically significant differences between shallow and deep traps in terms of biogeochemical indicator parameters. In the subarctic area, a higher portion of primary production with higher contents of labile compounds is being exported, indicating a higher efficiency of the biological pump. This efficiency is further enhanced by the increasing opal/carbonate ratio at the northern site. The POM burial rate may have been much higher during the last glacial maximum, when planktonic biomass was one order of magnitude higher around the northern site (Site 8), and therefore might have supported higher benthic biomass and deposition of POM in this part of the Pacific.

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