RACER: Bacterial abundance and thymidine incorporation in the Bransfield Strait, 1986–1987

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One of the primary objectives of the microbiology and vertical flux component of the Research on Antarctic Coastal Ecosystem Rates (RACER) program was to examine the role of bacterioplankton in the Antarctic Peninsula coastal ecosystem. Thus we measured bacterial abundance and biovolume by direct epifluorescence microscopy and rates of ^{3}H-thymidine incorporation during shipboard incubations. Our data on ^{3}H-thymidine incorporation were used to estimate bacterial production and specific growth rates using existing laboratory and field derived extrapolation factors.

Bacterial cell abundances and production were obtained for both the fast and slow grid sampling modes of four RACER cruises from December 1986 to March 1987 (Huntley et al., *Antarctic Journal*, this issue). During the fast-grid sampling mode, surface waters were collected using a tethered bucket sampler and during the slow grid, water column vertical profiles were obtained at stations 13, 20, 39, 43, and 48 using 10-liter Niskin bottles. Subsamples were processed for quantitative epifluorescence microscopy after staining with DAPI (Porter and Feig 1980). Bacterial production was estimated using ^{3}H-thymidine (Fuhrman and Azam 1980).

The rate of ^{3}H-thymidine incorporation in December was uniformly low (figure 1) and did not display the strong coastal-to-open ocean spatial trends that were observed for chlorophyll *a*, total microbial biomass (ATP concentrations), or primary production (Tien et al., *Antarctic Journal*, this issue; Holm-Hansen, Letelier, and Mitchell, *Antarctic Journal*, this issue.) Throughout the study area there was a large increase in the rate of ^{3}H-thymidine incorporation between December and January, especially in the northern sector of the Gerlache Strait (figure 1). An unexpected result was the fact that ^{3}H-DNA averaged only 10–30 percent of the total radioactivity incorporated into cellular macromolecules (total = ^{3}H-DNA + ^{3}H-RNA + ^{3}H-protein; figure 2). The January results show a slight increase in the proportion of the total radioactivity which appears as DNA, but on average, it was still ≤50 percent (figure 2).

We present vertical profiles (0–200 meters; figure 3) for two contrasting environments in the RACER study area: station 20,

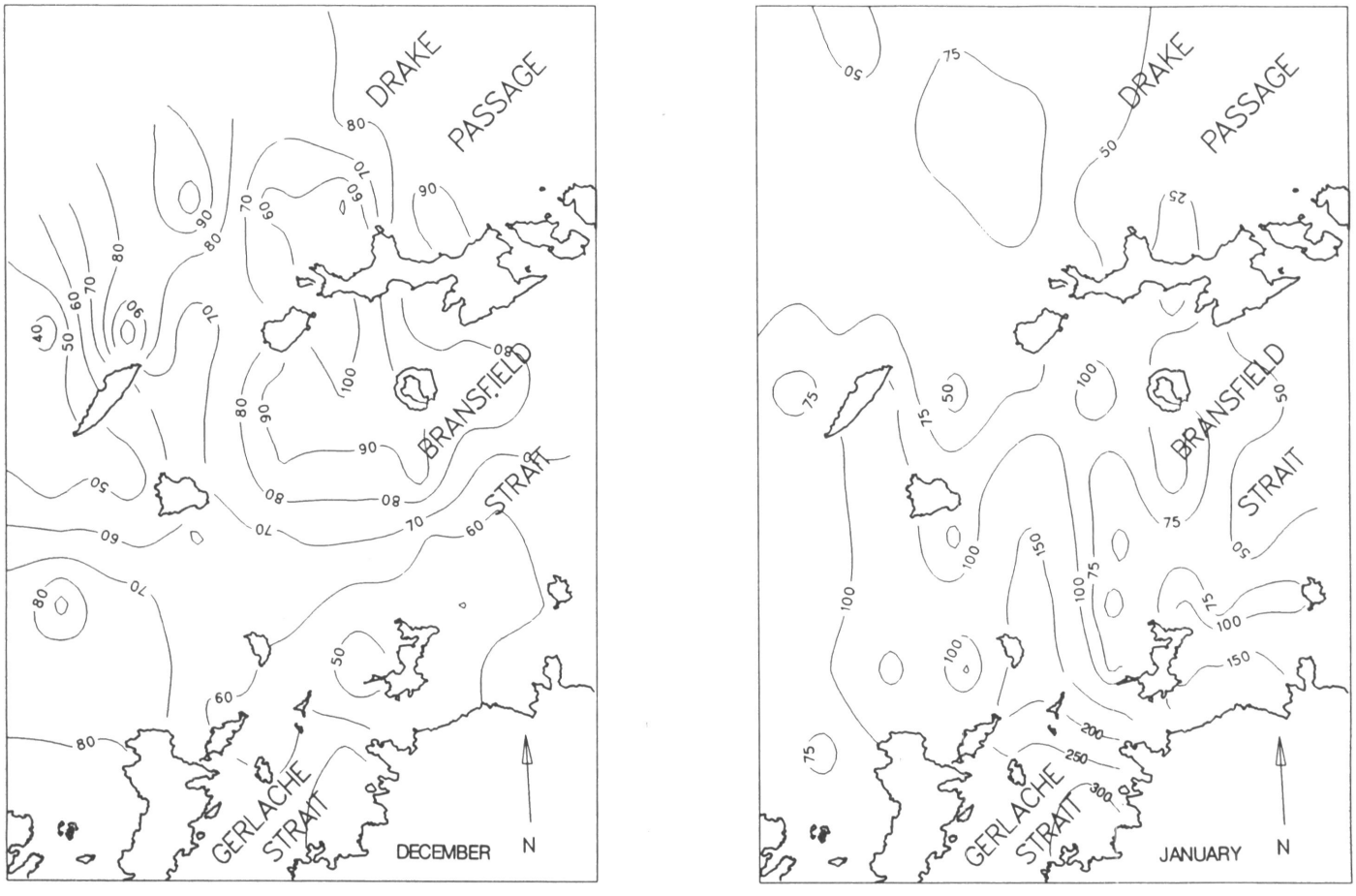
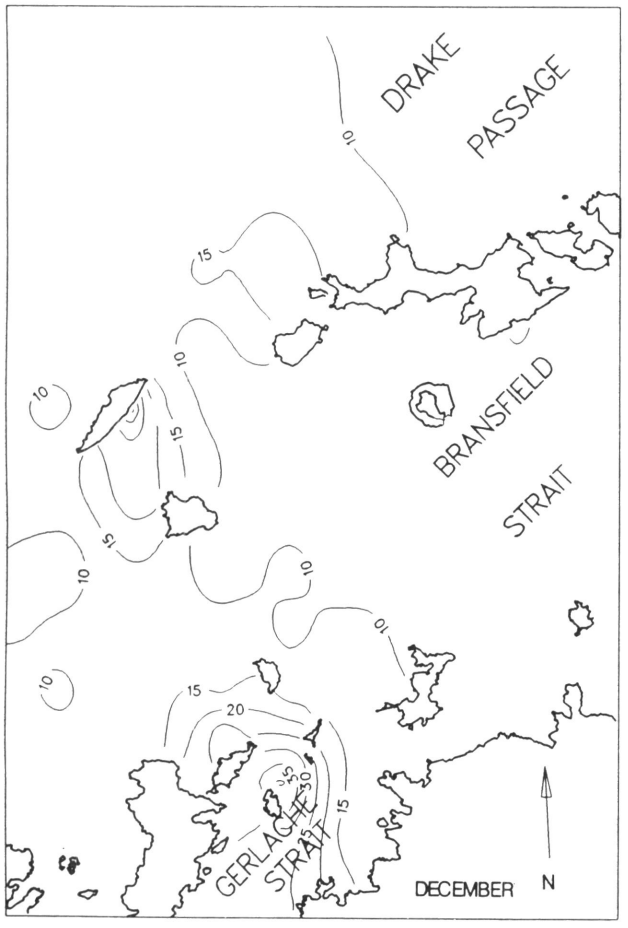


Figure 1. The spatial distribution of thymidine assimilation (in units of nanocuries per liter per hour) for samples collected in the RACER study area during December 1986 and January 1987. All data are for surface water samples.



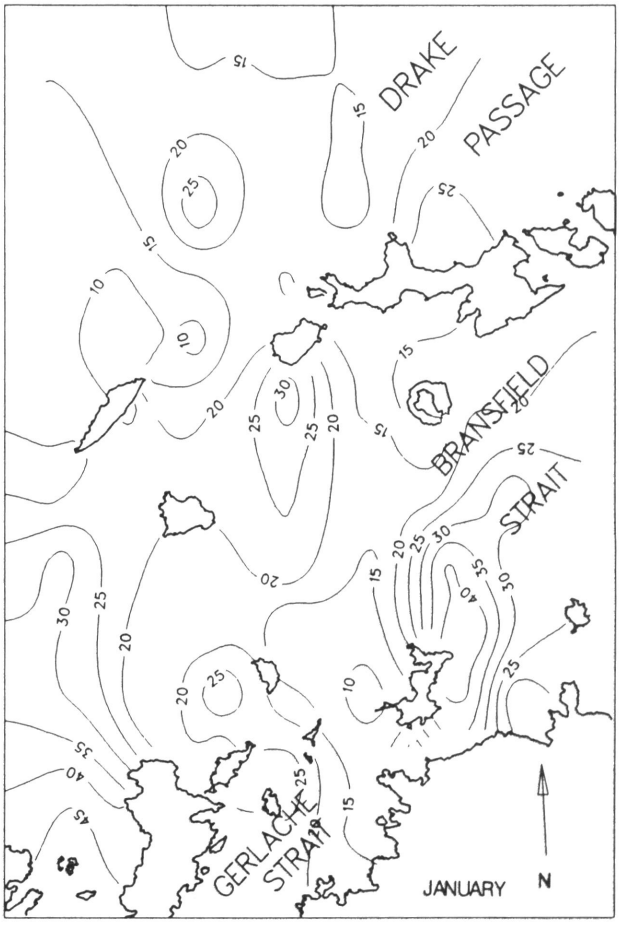
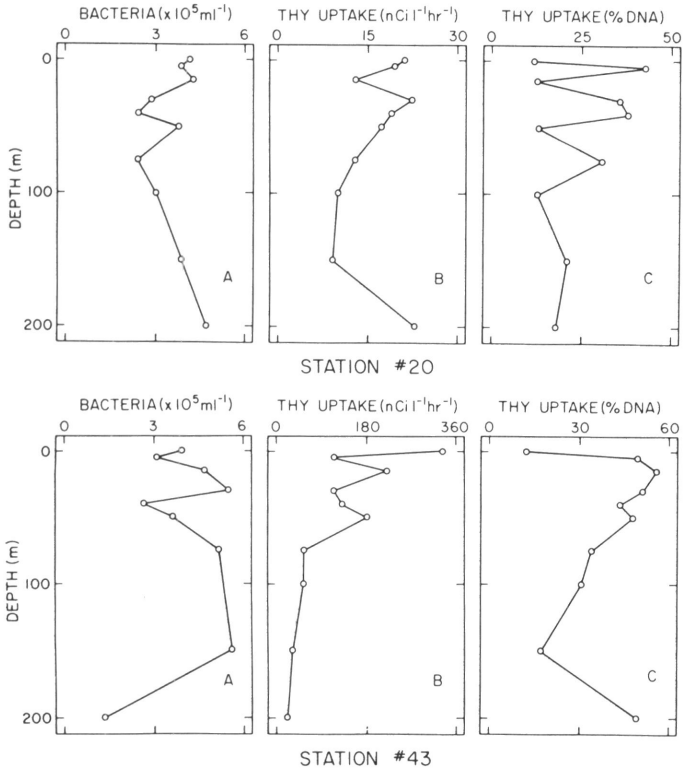


Figure 2. The spatial distribution of the ^{3}H-DNA as a percentage of total ^{3}H incorporated into cellular macromolecules for samples collected in the RACER study area during December 1986 and January 1987. All data are for surface water samples.



located in the Drake Passage, and station 43, located in a well-protected portion of the northern Gerlache Strait. Substantial differences were observed in upper water column physics (Amos, *Antarctic Journal, this issue) and phytoplankton production rates (Holm-Hansen et al., Antarctic Journal,* this issue) at these two stations. Neither station 20 nor station 43 displayed a strong correlation between bacterial cell number and thymidine incorporation (figure 3a, b). Station 20 exhibited a uniform distribution of both bacterial abundance and total thymidine incorporation throughout the water column, and the degree of non-specific ^{3}H-thymidine labeling was not correlated with depth. At station 43, there was a marked vertical gradient in the rate of thymidine incorporation with values up to an order of magnitude greater than those measured at station 20 (figure 3b). The highest rates of ^{3}H-thymidine incorporation were observed in the upper 30 meters of all the RACER samples analyzed to date, the DNA/total incorporation never exceeded 60 percent, an observation which contradicts the assumption that DNA comprises ≥90 percent of total thymidine incorporation (Fuhrman and

Figure 3. Vertical profiles of: (A) bacterial cell number, (B) total incorporation of ^{3}H-thymidine, (C) percentage of ^{3}H-Total which is incorporated into DNA. Top: station 20. Bottom: Station 43. ("ml^{-1} denotes "per milliliter." "nCi l^{-1}hr^{-1}" denotes "nanocuries per liter per hour.")

Azam 1980). Our data on bacterial abundances (table) are similar to previous measurements made in antarctic waters (Fuhrman and Azam 1980; Azam, Ammerman, and Cooper 1981; Hanson et al. 1983a, 1983b; Zdanowski 1985). Despite the elevated rates of ^{3}H-thymidine incorporation at station 43 relative to station 20, both sites had comparable bacterial populations (table).

Riemann et al. (1987) have recently reviewed the range of extrapolation factors currently available for DNA per bacterial cell and provided an average value for coastal marine ecosystems (1.1×10^{18} cells per mole thymidine incorporation). If we apply this relationship to our data, we can extrapolate our measured uptake rates to estimates of bacterial production. To estimate the rate of total bacterial carbon production (table), we have selected three biovolume-to-biomass (carbon content) extrapolation factors, each independently derived (Bratbak and Dundas 1984; Bratbak 1985; Lee and Fuhrman 1987). The bacterial production rates for station 20 are within the range of values previously reported for antarctic ecosystems (Fuhrman and Azam 1980; Hanson et al. 1983a; Kottmeier et al. 1987) using similar methodologies. However, the rates measured for the northern Gerlache Strait (station 43; table) are among the highest production estimates measured for any marine ecosystem studied to date. We believe this reflects environmental conditions present during our field program (spring-summer bloom) and the fact that the Bransfield Strait maintains a high rate of primary production (Holm-Hansen et al. *Antarctic Journal*, this issue). A comparison of primary production rates to our depth-integrated (0–200 meter) bacterial production rates, indicates that at station 20, bacterial production (84 milligrams of carbon per square meter per day) was approximately 17 percent of contemporaneous net primary production. At station 43 bacterial production (564 milligrams of carbon per square meter per day) was closer to 70 percent of the measured rate of primary production. The specific growth rates (μ) of the bacterial assemblages also varied considerably between the two contrasting sites (table). The several-fold variation in mean specific growth rates (μ), especially for the near surface waters, between these two contrasting sites is most likely due to the higher rates of primary production and greater water column stability present at station 43. At the present time we do not know whether the algal and bacterial rate processes are coupled in space or time or whether

Bacterial abundance and total thymidine incorporation rate

NOTE: The production rate was calculated using the extrapolation factor 1.1×10^{18} cells per mole thymidine incorporated (Reimann et al. 1987) and a range of current biovolume estimates: (a) 2.2×10^{-13} grams of carbon per cubic micrometer (Bratbak and Dundas 1984), (b) 3.8×10^{-13} grams of carbon per cubic micrometer (Lee and Fuhrman 1987), and (c) 5.6×10^{-13} grams of carbon per cubic micrometer (Bratbak 1985). All data given for stations 20 and 43 depth profiles were obtained during the RACER January cruise.

Depth[a]	Bacterial cell number[b]	Thymidine uptake[c]	Bacterial production rate[d]			Mean rate[e]	Specific growth rate[f]
			(a)	(b)	(c)		
Station 20							
0	4.18	21.05	0.34	0.59	0.87	0.60	0.03
5	3.90	19.40	0.36	0.61	0.90	0.62	0.03
15	4.30	12.91	0.26	0.45	0.67	0.46	0.02
30	2.90	22.32	0.38	0.66	0.97	0.67	0.05
40	2.46	18.87	0.16	0.27	0.40	0.50	0.05
50	3.80	17.23	0.26	0.45	0.66	0.45	0.03
75	2.43	12.82	0.24	0.41	0.60	0.42	0.03
100	3.04	9.94	0.20	0.35	0.51	0.35	0.02
150	3.89	9.04	0.15	0.26	0.38	0.26	0.01
200	4.73	22.82	0.32	0.56	0.82	0.57	0.03
Station 43							
0	3.99	332.23	8.14	14.05	20.17	14.12	0.48
5	3.14	114.74	2.28	3.93	5.80	4.00	0.21
15	4.73	220.57	4.40	7.60	11.20	7.73	0.27
30	5.52	114.57	2.21	3.82	5.63	3.89	0.12
40	2.71	130.75	2.37	4.10	6.03	4.17	0.28
50	3.60	180.61	3.95	6.82	10.05	6.93	0.18
75	5.21	54.83	1.13	1.95	2.86	1.98	0.06
100	—[g]	53.72	—	—	—	—	—
150	5.62	31.00	0.64	1.10	1.62	1.12	0.03
200	1.33	20.36	0.50	0.86	1.26	0.87	0.09

[a] In meters.
[b] Times 10^8 per liter.
[c] In nanocuries per liter per hour.
[d] In micrograms of carbon per liter per day.
[e] In milligrams of carbon per cubic meter per day.
[f] Per day.
[g] Sample lost in preparation of slide.

there is a succession from an autotroph-dominated to a heterotroph-dominated ecosystem as the spring bloom matures and then dissipates. However, the design of the RACER program was such that this information will be available following the completion of our sample analyses.

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RACER: Dissolved free amino acid concentrations, molecular composition, and microbial uptake rates in the Bransfield Strait

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A fundamental hypothesis of the Research on Antarctic Coastal Ecosystem Rates (RACER) project is that upper ocean physical dynamics favor high productivity at all trophic levels of the Antarctic Peninsula coastal food web (Huntley et al., *Antarctic Journal*, this issue). One component of the RACER program examined microbial production processes and vertical flux of biogenic matter relative to the physical regimes of the Bransfield Strait. In this report, we present preliminary data on the composition and concentration of dissolved free amino acids in the water column and the rates of its uptake by microheterotrophs, in particular, bacteria. Selected data are presented from two contrasting stations in our study area: station 20 (located in the southern Drake Passage) was characterized by deep vertical mixing and a moderate-to-low rate of primary production, and station 43 (located in the northern Gerlache Strait) was characterized by a well-stratified water column and a high rate of primary production (Amos, *Antarctic Journal*, this issue; Holm-Hansen, Letelier, and Mitchell, *Antarctic Journal*, this issue).

Water samples for dissolved free amino acid analyses (5 milliliter), initially collected with 10-liter Niskin bottles (vertical profiles) or a tethered bucket sampler (surface samples), were gravity filtered through a stacked filter column containing 20-micrometer and 1-micrometer Nitex mesh, followed by vacuum filtration through a combusted glass fiber filter (Whatman, GF/F). The filtered samples were stored frozen for analysis at the University of Hawaii by reverse-phase high-pressure liquid chromatography (Mopper and Lindroth 1982; Haberstroh and Ahmed 1986). Dissolved free amino acid uptake and turnover rates were estimated using [3,4-^{3}H]L-glutamic acid as a model substrate.

The spatial distributions of the ambient glutamate pool turnover time (in hours) in the RACER study area measured during