Quantifying archaeal community autotrophy in the mesopelagic ocean using natural radiocarbon


*Department of Earth and Planetary Sciences, Harvard University, Cambridge, MA 02138; †Scripps Institution of Oceanography, University of California at San Diego, La Jolla, CA 92093; and *Department of Earth System Science, University of California, Irvine, CA 92697

Edited by John M. Hayes, Woods Hole Oceanographic Institution, Woods Hole, MA, and approved March 3, 2006 (received for review November 23, 2005)

An ammonia-oxidizing, carbon-fixing archaeon, *Candidatus Nitrosopumilus maritimus,* recently was isolated from a salt-water aquarium, definitively confirming that chemoaerotrophy exists among the marine archaea. However, in other incubation studies, pelagic archaea also were capable of using organic carbon. It has remained unknown what fraction of the total marine archaeal community is autotrophic in situ. If archaea live primarily as autotrophs in the natural environment, a large ammonia-oxidizing population would play a significant role in marine nitrification. Here we use the natural distribution of radiocarbon in archaeal membrane lipids to quantify the bulk carbon metabolism of archaea at two depths in the subtropical North Pacific gyre. Our compound-specific radiocarbon data show that the archaea in surface waters incorporate modern carbon into their membrane lipids, and archaea at 670 m incorporate carbon that is slightly more isotopically enriched than inorganic carbon at the same depth. An isotopic mass balance model shows that the dominant metabolism at depth indeed is autotrophy (83%), whereas heterotrophic consumption of modern organic carbon accounts for the remainder of archaeal biomass. These results reflect the in situ production of the total community that produces tetraether lipids and are not subject to biases associated with incubation and/or culture experiments. The data suggest either that the marine archaeal community includes both autotrophs and heterotrophs or is a single population with a uniformly mixotrophic metabolism. The metabolic and phylogenetic diversity of the marine archaea warrants further exploration; these organisms may play a major role in the marine cycles of nitrogen and carbon.

Results

Chemoaerotrophy in the marine archaea first was invoked to explain the stable carbon (δ13C) (20, 21) and radiocarbon (Δ14C) (13) isotope measurements of GDGT-derived lipids extracted from sediments. Incubation studies subsequently confirmed the presence of autotrophic capacity by demonstrating the uptake of isotopically labeled inorganic carbon directly into archaeal biomass (10, 11). However, other incubation experiments also demonstrated the incorporation of labeled amino acids by archaeal populations (9, 11), suggesting that some archaea are heterotrophic or mixotrophic. Most recently, an ammonia-oxidizing autotrophic crenarchaeon, *Candidatus Nitrosopumilus maritimus,* has been grown in culture (7). In addition, the gene for a subunit of a putative ammonia monooxygenase has been found in diverse locations throughout the ocean and appears to be affiliated with the archaea (8). Oxidation of reduced nitrogen may be highly prevalent or ubiquitous among marine archaea. Although these studies all demonstrate the presence of autotrophic metabolic potential within pelagic marine archaea, it has remained unknown to what extent these results are applicable to the environment. Direct in situ observation of the relative importance of heterotrophy and autotrophy among archaea in the oligotrophic ocean is lacking.

Here, we quantify the proportion of marine archaeal lipid that is synthesized by chemoaerotrophic production in mesopelagic waters. These results have important implications for biogeochemical cycles and for development of paleoceanographic proxies. Archaeal chemoaerotrophy fueled by oxidation of ammonia would result in a significant contribution to global water-column nitrification. Archaeal biomass also represents a source of recently fixed, but 14C-depleted, OC below the photic zone and possibly to the sediments.

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Abbreviations: AMS, accelerator mass spectrometry; DIC, dissolved inorganic carbon; DOC, dissolved OC; GDGT, glycerol dialkyl glycerol tetraethers; POC, particulate OC.

See Commentary on page 6417.

†A.E.I. and S.R.S. contributed equally to this work.

*Present address: School of Oceanography, University of Washington, Seattle, WA 98195.

To whom correspondence should be addressed. E-mail: pearson@eps.harvard.edu.

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Nonthermophilic archaea represent up to 40% of the free-living prokaryotic community in the water column of the world’s oceans (1–6), but until recently there has been limited information about the sources of carbon and energy that fuel these organisms (7–11). The characteristic membrane lipids of planktonic archaea include glycerol dialkyl glycerol tetraethers (GDGTs) (12). These compounds are ubiquitous in marine sediments and ocean water (12–15). The relative abundance of individual GDGTs recovered from sediments is used to reconstruct sea-surface temperatures (16–18). This distribution, known as TEX86, has been shown through experimental manipulation of surface-water mesocosm experiments to respond to changes in incubation temperature (18). In addition, the δ13C values of GDGTs display a remarkably constant offset from δ13C values of dissolved inorganic carbon (DIC) over a range of settings and geologic time (13, 19–21). The collective metabolic activities of the numerous archaea in the ocean are likely to play a significant role in the cycling of organic carbon (OC) and nutrients, and their membrane lipids show significant utility for paleoceanography. However, neither the metabolic requirements of the natural population of marine archaea nor the mechanisms by which these populations record sea-surface temperature are known.
relative abundances of uncyclized GDGT I and the pentacyclic
The most significant differences between the two depths are the
are published as supporting information on the PNAS web site).
and deep (670 m) water samples (Fig. 1; see also Figs. 3 and 4, which
analytical bias.
but overall these control samples are consistent with insignificant
measurement biases in our compound-specific analyses. The lower value
this value is
14C,*, values after correction for combustion blanks and sample processing
blanks as described in Supporting Text.
†AMS facility nos. all refer to University of California, Irvine, except for those
beginning with “OS,” which are for National Ocean Sciences Accelerator
Mass Spectrometry, and 115347–115348, which are from Lawrence Livermore
National Laboratory.

Table 1. Water temperature, values of Δ14C, sizes of samples,
and AMS facility sample numbers

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<th>Depth, m; temp., °C</th>
<th>Sample</th>
<th>Δ14C,*</th>
<th>Total Sample</th>
<th>Facility</th>
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<td>size, µg C</td>
<td>sample</td>
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<td></td>
<td>%</td>
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</table>

Italics symbolize samples excluded from the algebraic model. n.a., not available.

*Δ14C values after correction for combustion blanks and sample processing
blanks as described in Supporting Text.
†AMS facility nos. all refer to University of California, Irvine, except for those
beginning with “OS,” which are for National Ocean Sciences Accelerator
Mass Spectrometry, and 115347–115348, which are from Lawrence Livermore
National Laboratory.

The six different GDGTs typically detected in marine water
columns and sediments (12–16) were found in the surface (21 m)
and deep (670 m) water samples (Fig. 1; see also Figs. 3 and 4, which
are published as supporting information on the PNAS web site).
The most significant differences between the two depths are the
relative abundances of uncyclized GDGT I and the pentacyclic
marine archaeal compound, crenarchaeol (GDGT II). In the
surface, GDGT I accounts for 8% and GDGT II for 64% of total
archaeal lipids, but in deep water, they are 29% and 36% of the
total, respectively (Table 2). In addition, GDGT VI represents an
insignificant proportion of the total archaeal lipids in the surface
(2%), whereas the least abundant lipid in the deep sample is GDGT
V (1%). Two fractions of GDGTs were collected from the surface
sample (Figs. 1 and 3); compounds I, III, IV, and V were combined
to obtain sufficient carbon for 14C-accelerator mass spectrometry
(AMS) analysis (Δ14C = +77‰). Likewise, compounds II and VI
were collected together as a second fraction (Δ14C = +84‰). The
abundance-weighted average Δ14C value for the surface GDGTs is
+82‰. The difference between the Δ14C value of surface DIC
(+71‰) and the GDGTs is less than the measurement error for
the GDGTs.

Five fractions of GDGTs were collected from the deep sample
(Figs. 1 and 4). Values of Δ14C for individual GDGTs in the deep
sample ranged from −127‰ to −60‰ (Table 1). When replicate
14C measurements were available for the same compound, the
sample having a larger mass consistently has a more precise
measurement than the sample having smaller mass. Therefore, only
the values from the larger samples are used for the following
analysis and discussion. The abundance-weighted average Δ14C
value of the deep archaeal lipids was −77‰. This average was
calculated from 94% of total GDGTs from this depth, because
insufficient mass of sample was obtained from GDGTs V and VI
to measure accurate Δ14C values. Both GDGTs V and VI are
excluded from further discussion.

Discussion

The values of Δ14C for surface (21 m) archaeal lipids unambiguously
reflect production of biomass from DIC or from freshly produced
dissolved OC (DOC; solubilized from fresh POC and used by
microbes). In surface waters, it is not possible to distinguish
heterotrophy from autotrophy, because the
Δ14C values of the DIC
and fresh organic substrates are identical. However, the data do
confirm a short residence time and an in situ biosynthetic source for
GDGTs obtained from the upper water column. The data also
confirm that the GDGTs present in surface waters cannot derive from
relict microbial populations or from free lipids entrained
during occasional deep mixing events. It is difficult to assess the
relative contributions of Group I and II marine archaea to the total
surface GDGTs. Because many Euryarchaeota produce diether
lipids instead of tetraether lipids, the surface GDGT samples
probably underrepresent the contribution of marine Group II

Fig. 1. HPLC/atmospheric pressure chemical
ionization-MS total ion current chro-
matograms of GDGTs separated from the
surface filter (21 m) (A) and deep filter (670
m) (B) and molecular structures of the
GDGT lipids. GDGT VI is a regioisomer of
GDGT II (45).
Euryarchaeota. However, this bias toward the contribution of Group I Crenarchaeota in the surface sample also makes the comparison between surface and deep samples relevant in the algebraic model discussed below. The deep sample is expected to contain nearly exclusively the lipids of Group I organisms, reflecting the dominance of this population in deeper waters (1, 3–6, 11).

There are at least three possible sources of GDGTs that could contribute to the total archaeal lipids found at 670 m: (i) GDGTs that are produced at the surface, either autotrophically or heterotrophically, which subsequently sink in association with the sinking fraction of POC, (ii) in situ autotrophic production in the deep water column, and/or (iii) in situ heterotrophic production in the deep water column.

Because the average $\Delta^{14}C$ value of GDGTs at 670 m is $-77\%e$, all of these options can be eliminated as the sole source of GDGTs at this depth. Exclusive production of GDGTs by autotrophy at 670 m would yield $\Delta^{14}C_{\text{GDGT}} = -151\%e$, more negative than all of the observed values (Fig. 2). The $\Delta^{14}C$ values at depth also are not positive enough to derive solely from OC exported from surface waters. The $\Delta^{14}C$ value of sinking POC, which releases organic matter that can be used by microbial heterotrophs, is assumed to be equal to the $+71\%e$ value of surface DIC. In 1987, when there was more bomb $^{14}C$ in surface DIC than there is presently, sinking POC collected in nearby sediment traps at 4,800 m and suspended POC at 900 m both had $\Delta^{14}C$ values of approximately $+100\%e$ (24). A decadal residence time for GDGTs within the suspended or sinking POC pools would bias surface-derived GDGTs to more positive $\Delta^{14}C$ values. Therefore, the $\Delta^{14}C$ data suggest the true residence time is much shorter: the surface-derived GDGT I-fraction and GDGT II-fraction both are within 1‰ of the present $\Delta^{14}C_{\text{DIC}}$ value; and surface-derived material cannot be the sole source of the deep GDGTs.

The $\Delta^{14}C$ value of GDGT I provides further evidence that heterotrophic consumption of carbon derived from sinking POC does not contribute a large fraction of the in situ archaeal production at 670 m. This compound shows the largest increase in relative abundance in the deep sample (Fig. 1), indicating the greatest fractional contribution from in situ production at depth, and it has the most negative $^{14}C$-signature. Additionally, because there is no evidence for differential degradation of individual GDGT isomers in oxic sediments (25), presumably this finding also is true in the water column. It suggests the relative compositions and isotopic ratios of these samples would not be affected by degradation taking place in the water column. The GDGTs at 670 m are isotopically and compositionally different from the surface component.

To determine the maximum fraction of the total GDGTs in the deep sample that could be derived from material sinking directly from surface waters, a two end-member mixing model was created. The assumptions were as follows: (i) that GDGTs exported from the surface reach 670 m with the same relative abundance and $\Delta^{14}C$ values as were produced in the surface, and (ii) that all six of the GDGTs produced by archaea in situ at 670 m reflect utilization of the same source of carbon (or the same proportional mixture of multiple sources) having an isotopic value called $\Delta^{14}C_{\text{D}}$. This value is determined by the model and is not assumed to equal a purely autotrophic value of $-151\%e$. Because incorporation of both isotopically labeled DIC and leucine has been reported for the deep water column (11), we cannot assume a purely autotrophic community metabolism at 670 m. The model also assumes (iii) that none of the individual GDGTs is produced disproportionately by a subset of the archaea that may be expressing a metabolism vastly different
in isotopic composition from the mean community metabolism. This assumption can be evaluated by using the model and data below and appears to be valid.

The abundance of \(^{14}\text{C}\) in each GDGT collected from 670 m is the weighted average of two components, specifically

\[
\Delta T m_f = \Delta gm_S + \Delta pm_D, \tag{1}
\]

where \(m\) represents the molar quantity of carbon and \(\Delta\) represents the \(^{14}\text{C}\) value. The subscript \(T\) refers to the total material recovered at 670 m. The subscripts \(S\) and \(D\) refer to material produced at the surface \(S\) but that has been exported to 670 m and to material produced in situ at depth \(D\), respectively. \(^{14}\text{C}\) of \(D\) therefore becomes \(\Delta D\). The subscript \(i\) refers to the \(i\)th GDGT (i.e., I, II, III . . .). Thus, the relative abundance of each compound can be expressed in terms of a carbon mole fraction

\[
X_S = \frac{m_S}{\sum m_i}, \quad X_D = \frac{m_D}{\sum m_i}, \quad \text{and} \quad X_f = \frac{m_f}{\sum m_i}, \tag{2}
\]

Substitution for the \(m\) terms in Eq. 1 yields

\[
\Delta T X_T = \frac{\sum m_S}{\sum m_i} X_S + \frac{\sum m_D}{\sum m_i} X_D (1 - f_S), \tag{3}
\]

From the conservation of mass equations, \(\sum m_T = \sum m_S + \sum m_D\), and \(f_S = \sum m_S/\sum m_T\), we then obtain

\[
\Delta T = \frac{1}{X_T} \left[ \Delta S X_S f_S + \Delta D X_D (1 - f_S) \right], \tag{4}
\]

where \(f_S\) is the fraction of the total GDGT class collected at depth that was produced and exported from the surface. Table 2 shows the values of \(\Delta T\), \(X_T\), \(\Delta S\), and \(\Delta D\), which were obtained by laboratory analyses for compounds I–IV. Four equations (one for each of the GDGTs I–IV) thus can be used to obtain values for the two unknowns \(f_S\) and \(\Delta D\). The calculations also require values of \(X_S\). These values depend on the observed values of \(X_T\) and \(X_D\) and on the modeled variable, \(f_S\). Specifically, from rearrangement and simplification of

\[
X_D = \frac{m_T - m_S}{\sum m_T - \sum m_S} = \frac{X_T (\sum m_T - \sum m_S)}{\sum m_T - \sum m_S}, \tag{5}
\]

we obtain

\[
X_D = \frac{1}{1 - f_S} (X_T - f_S X_S). \tag{6}
\]

The model equations 4 and 6 were solved by iteration to determine values of \(f_S\) and \(\Delta D\) for which predicted values of \(\Delta T\) differ minimally from observed values of \(\Delta T\) (Table 2). This approach also allows evaluation of assumption (iii) above: none of the individual compounds, \(i\), generate significantly different values of \(f_S\) and \(\Delta D\). The final solution for \(f_S\) and \(\Delta D\) minimizes the absolute values of the differences between the predicted and observed values of \(\Delta T\) for compounds I–IV (see Fig. 5, which is published as supporting information on the PNAS web site). The solution reproduces all individual, measured values of \(\Delta T\) to within the reported 1σ uncertainties of the actual measurements (Table 2). Our approach was similar to previous uses of this algebraic model (26, 27).

We obtained the closest agreement between the model and the individual data points using the pair of values \(f_S = 0.14 \pm 0.07\) and \(\Delta D = -112 \pm 28\%\). The reported uncertainties reflect the range of values over which agreement was obtained between modeled values and the actual data to within the 2σ measurement precision of the values of \(\Delta T\), representing 95% confidence that \(f_S\) and \(\Delta D\) fall within this range. The model indicates that GDGTs sinking from the surface account for only 14% of the total GDGTs recovered at depth. The remaining 86% result from in situ production by an archaeal community that is using carbon sources having an average \(^{14}\text{C}\) value of \(-112\%\).

Therefore, even after removing the contribution of the \(^{14}\text{C}\)-enriched sinking fraction, the GDGTs at 670 m still contain more \(^{14}\text{C}\) than would be expected for a purely autotrophic population. The model does not permit the archaea to live by pure autotrophy at 670 m: \(\Delta D = -151\%\) is not an allowed mathematical solution at any value of \(f_S\). To produce the relatively positive \(^{14}\text{C}\) value of \(-112\%\), a portion of the archaeal population appears to be consuming organic material produced recently in surface waters by means of a heterotrophic or mixotrophic metabolism. Either form of heterotrophic activity is likely to contribute GDGTs relatively enriched in \(^{14}\text{C}\). Heterotrophic production fueled by the consumption of sinking, fresh POC (hydrolyzed to fresh DOC) would result in new production of GDGTs with the relative abundance distribution of the deep sample \((X_D)\) but with \(^{14}\text{C}\) values equal to +71\%. A mixture of 85% autotrophy at 670 m and 17% heterotrophic consumption of surface-derived organic matter is required to explain the \(\Delta D\) value of \(-112\%\).

The total mass balance based on the average isotopic endmembers and fractional contributions yields the following estimates: 71 ± 11% of the total archaeal lipids at 670 m are produced autotrophically in the deep water column near 670 m; 15 ± 10% are produced by heterotrophic feeding on modern DOC derived from sinking POC; and 14 ± 7% were produced and exported directly from the surface. Although the latter two components are identical in \(^{14}\text{C}\)-signature, they can be separated because the relative abundance distributions of the GDGTs are markedly different between the surface and deep samples (Fig. 1). The reported uncertainties again represent the 2σ or 95%, confidence intervals.

The relatively high values of \(^{14}\text{C}\) measured throughout this study make it unlikely that the aged, recalcitrant fraction of DOC contributes significantly to archaeal biomass. The \(^{14}\text{C}\) value of surface DOC obtained in 1987 was \(-191 \pm 9\%\) (24), and because of the dispersal of bomb-\(^{14}\text{C}\), the value of \(^{14}\text{C}\)-DOC currently is likely to be an even more negative value. If the surface DOC contains a 1:1 mixture of "fresh" DOC (+71\%) and recalcitrant end-member DOC (approximately −525\%), as suggested in refs. 23 and 28, recalcitrant DOC can contribute no more than 1% of archaeal carbon in surface waters. A similar assumption is plausible for the deep sample. The \(^{14}\text{C}\) value of DOC at 598 m in the North Central Pacific is −405 ± 5\%, and at 896 m it is −532 ± 3\% (Fig. 2 and ref. 24); both are much more negative than any of the values observed here. There is no reason a priori to think that the metabolic pathway of marine archaea would favor utilization of the old, recalcitrant fraction of DOC in deep waters. The total metabolic activity of archaea, including uptake of \(^{13}\text{C}\)-DIC and free amino acids, appears similar throughout the upper 1,000 m of the water column (11), and the primary trend with depth is a decreasing rate of leucine incorporation, consistent with a relatively greater importance of autotrophy in deeper waters (11). If the marine archaea live primarily as autotrophs (7, 10, 11, 13) but also are using a small amount of OC through mixotrophy or heterotrophy, such activity might be associated with the need to derive energy. In this case, it also would be likely that younger, more labile substrates are being used, possibly associated with the scavenging of reduced N species.

Additionally, if recalcitrant DOC were the source of the negative \(^{14}\text{C}\) values, up to 30% of the archaeal carbon would need to derive from this source to explain the values of \(\Delta T\) (assuming \(^{14}\text{C}\text{-DOC} = -532\%)\). By using an archaeal cell count of \(10^{13}\) cells/ml (6), carbon content of 8.4 fg-Cell\(^{-1}\) (11), average growth rate of 0.02 day\(^{-1}\) (11), and a DOC concentration of 42 \(\mu\)M (24), the archaea would consume the recalcitrant fraction of DOC with a turnover time of \(\approx 2,000\) years. This value is a factor of 3 too rapid to be consistent with the \(\approx 6,000\)-year radiocarbon age that is implied by
a value of $\Delta^{14}C_{\text{DOC}} = -532 \%$. Therefore, although it is possible that consumption of old DOC is the explanation for some of the $^{14}C$-depletion found at 670 m, several lines of emerging evidence (7–11, 13), in addition to the data here, suggest that incorporation of isotopically negative DIC is the more likely explanation for the $\Delta^{14}C_{\text{GDT}}$ values in the deep water column.

Because our model solves for the in situ concentration of GDGTs produced at 670 m, it is possible to compare the distribution of GDGTs in surface and deep samples without including the fraction of the deep sample that is contributed by sinking particles. Experiments using pure cultures show that thermophilic archaea increase the number of cyclopentane units in their membrane lipids in response to temperature or physical agitation (29, 30). Pelagic archaeal lipids show a similar response: the relative distribution of GDGTs III, IV, V, and VI defines the TEX$_{86}$ index, which has a calibrated relationship to temperature (16). Mesocosm incubations confirm this relationship when carried out at a range of temperatures using surface waters (18). Similarly, our surface sample (21 m) has a TEX$_{86}$ value of 0.69, corresponding to a calculated TEX$_{86}$ temperature of 28°C; this value is within the range of actual sea-surface temperature at this location. However, our deep sample (670 m) has a TEX$_{86}$ value of 0.65 for the modeled fraction produced in situ ($X_{\text{meq}}$ values). This value corresponds to a calculated temperature of 25°C. This value is far from the actual temperature of 6°C at 670 m. Our data are consistent with the suggestion that preferential export of GDGTs associated with surface-derived POC is responsible for the correlation between sea-surface temperature and TEX$_{86}$ (15, 18); but the data also suggest that GDGTs produced in the deep water column are not regulated by the same processes that control their distribution in surface waters. In the deeper population, the TEX$_{86}$ value would predict a warm temperature, yet the isotopic data preclude the presence of significant quantities of surface-derived material at 670 m.

Bulk prokaryotic metabolism in the mesopelagic ocean has been characterized as a process fueled by heterotrophic remineralization of organic matter recently produced at the surface (31, 32). In contrast, the definitive demonstration that a marine archaeon is chemoautotrophic (7) could be consistent with prior suggestions that pelagic crenarchaeota might be uniformly autotrophic (e.g., ref. 13). However, our compound-specific $^{14}C$ measurements of microbial lipids suggest that the deep archaea are not metabolically monolithic. The results confirm that there may be significant heterogeneity, including heterotrophic (9, 11) and autotrophic (7, 10, 11, 13) pathways, among the total archaea-mediated transformations of carbon in the mesopelagic ocean. Anaerobic carboxylation reactions may serve as an autotrophic mechanism in these environments (13), and autotrophic processes may be significant contributors to the carbon cycle in the mesopelagic ocean (11). Nevertheless, these results suggest that only 83% of the total community production is autotrophic and that the remaining carbon is derived from heterotrophic remineralization of organic C.

Herndl et al. (11) calculated that marine archaea produce biomass at a rate of 0.8 GtC/year by assuming that all archaea are 100% autotrophic, using an average fixation rate of 0.014 fmol-C/archaeon $^{-1}$day$^{-1}$ (11), and using an abundance of $1.3 \times 10^{28}$ archaeal cells in the whole ocean (6). The same approach, but considering only the 1.0 $\times 10^{28}$ deep pelagic cells (6), implies that the autotrophic fraction of archaeal biomass below the photic zone is produced at a rate of 0.6 GtC/year. However, our model suggests that only 83% of the total community production is autotrophic and that total biomass production by archaea in deep waters is 0.7 GtC/year. Although this 0.6–0.7 GtC represents only $\approx$1% of annual marine primary production (50 GtC/year), it is of a magnitude significant to the global carbon cycle and is greater than the 0.15 GtC/yr that is buried in marine sediments (34). The fraction of buried carbon that is derived from archaeal biomass remains unknown, but it could have the potential to influence the 13C (19) and 14C (13) contents of total sedimentary OC.

Significantly, these estimates of biomass production suggest that the archaea could be quantitatively the major nitrifiers in the ocean. If the archaea are living at the thermodynamic threshold, and assuming average production of CO$_2$ to the level of glucose ($\Delta G^\circ = +478$ kJ/molC), the oxidation of NH$_4^+$ to NO$_2^-$ ($\Delta G^\circ = -235$ kJ/mol) would require a minimum ratio of N oxidized per C fixed of 2:1. Thus, if archaeal autotrophy is fueled primarily by the oxidation of NH$_4^+$, these organisms correspondingly generate $\approx 1.2$ Gt/yr of N as NO$_2^-$. This estimate is enough to account for all of global new production, i.e., the nitrification of all of the export flux of N below the photic zone (10–20% of primary production (PP) (35)). This estimate suggests that the archaea are major participants in an extremely dynamic internal N$_2$, NO$_3^-$, and NH$_3$ cycle in the ocean. Given the current uncertainties in the oceanic N budget, including the rates of fixation of N$_2$, nitrification, conventional NO$_3^-$ reduction (detrnitrification), and ammonium, the total supply and demand for NO$_2^-$ remains poorly understood. However, if the oxidation of reduced N drives the majority of their autotrophic production, the crenarchaeota must have a major influence on the marine nitrogen cycle.

Methods

Sampling. The large-volume pumping capacity available at the Natural Energy Laboratory of Hawaii Authority (NELHA) was used to collect particulate organic matter from 104,000 liters of surface seawater (21-m depth) and 208,000 liters of deep seawater (670-m depth). The NELHA station pipeline supplies surface water at 0.6m$^3$/sec and deep water at 0.8 m$^3$/sec through 1-m diameter, high-density polyethylene pipes. Surface-water temperatures vary seasonally between 24 and 28°C and deep-water temperature is consistently 6°C (www.nelha.org/about/facilities.html). Organic matter was collected onto 0.2-μm Pall Supor filters from which lipids were extracted. The surface sample first was prefiltered (0.5-μm Millipore Opticap), although the lipid extracts from both filters subsequently were recombined for analysis and simulation of GDGTs to avoid partitioning of the community by size–class. The filtration was performed by using a parallel-flow apparatus, which was fed continuously and directly from the water supply (four filters in parallel for 670-m water; two in parallel for 21-m water). The individual filter cartridges (7 $\times$ 25 cm) contained spiral-wound filters of average surface area 4,650 cm$^2$ and were housed in stainless steel filter holders connected by Teflon tubing. The flow rate was 4 liters/min$^{-1}$-filter$^{-1}$. Filters were kept at the in situ temperatures of the respective water sources, and $\approx 52,000$ liters was passed through each. No significant reduction in flow rate was observed in any of the filters over the duration of the sample collection. Immediately upon recovery, the filters were frozen at $-70^\circ$C for return to the laboratory.

Lipid Extraction. Filters were stored at $-80^\circ$C until being excised by using a combusted hack saw, and all samples were lyzed in 1.5 M Na-perchlorate at 4°C for 48 h by using the method of R.L.H. and L.L.A. (unpublished data) after Blair et al. (36). Lysate and filter particles were extracted by using the method of Bligh and Dyer (37); the total lipid extract (TLE) was washed repeatedly against Barnstead Nanopure H$_2$O; each TLE was concentrated by evaporation and then dried and hydrolyzed in 5% H$_2$SO$_4$ (trans-esterification) for 4 h at 70°C to cleave polar head-groups; the transesterified products were extracted into CH$_2$Cl$_2$ and were dried onto precombusted quartz sand. Each sample was separated into compound-class fractions by SiO$_2$-gel chromatography (13).

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Archaeal Lipids. Individual compounds were separated by normal phase chromatography and detected between m/z 1,250–1,350 by using HPLC/atmospheric pressure chemical ionization-MS (38, 39). One-minute fractions were collected, and the GDGTs in each fraction were determined by flow injection analysis (FIA), monitoring m/z 350–1,400. For the deep archaeal lipids, the six most abundant compounds were separated into individual samples based on mass and retention time; for the surface samples, the GDGTs with m/z 1,302–1,296 were collected as one fraction, and those with m/z 1,292 were collected as a second fraction. Each subsequent GDGT fraction (six deep and two surface) was purified to remove pigmented impurities by RP-HPLC with an ZORBAX Eclipse XDB-C8 column (Agilent Technologies, Palo Alto, CA) at 30.0°C. GDGT fraction (six deep and two surface) was purified to remove most purely steroidal fractions were combusted, and Δ14C values for all GDGTs were measured at the Keck Carbon Cycle AMS facility at the University of California, Irvine by using the ultra-micro AMS methods of Santos et al. (42). Further methods for the quantification of sample processing blanks and error corrections made to measurements are reported in Supporting Text, which is published as supporting information on the PNAS web site.

Sterols. Sterols were obtained from the surface sample, >0.5-μm size class fraction only. SiO2-gel fraction 8 [75% hexane/25% ethyl acetate (13)] was separated isocratically by RP-HPLC by using a Develosil RP-Aqueous C8 column (Phenomenex, Mont, CA) at 30.0°C (4.6 × 150 mm; 5 μm). Sterols were separated with solvent A (98% methanol/2% water) over 45 min. The column was backflushed with 1:1 solvent A and ethyl acetate. Sterols were detected by atmospheric pressure chemical ionization-MS, monitoring m/z 300–500. The sterols were collected as 1-min fractions; the contents of each vial were determined by flow injection analysis, and the sterols were further purified by RP-HPLC as described above for GDGTs. The composition of the purified sterol fractions was determined by GC/MS (DB5-MS column; methods similar to ref. 13). The two most purely steroidal fractions were combusted, and Δ14C measurements of the captured CO2 were made by the AMS facility at Lawrence Livermore National Laboratories.

DIC. Five hundred-milliliter water samples were collected from the surface and deep Natural Energy Laboratory of Hawaii Authority pipelines according to the World Ocean Circulation Experiment (WOCE) protocol (42) for measurement of Δ14CDIC values. The values of Δ14CDIC were measured at the National Ocean Sciences Accelerator Mass Spectrometry facility on CO2 stripped from the water samples (43, 44).

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