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The stable carbon isotope fractionation of methanogenesis products at complete carbon consumption

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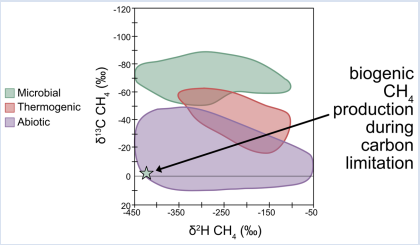
Abstract



The stable carbon isotope signature ($\delta^{13}C$) of methane (CH_4) is used to discriminate between biological, thermogenic, and abiotic sources. Methanogens, or methane producing archaea, inhabit a broad range of chemical conditions. Many of these environments are replete in dissolved inorganic carbon (DIC), causing isotopically depleted $\delta^{13}C$ biogenic CH_4. However, some extreme environments inhabited by methanogens, such as serpentinising systems, exhibit low carbon dioxide (CO_2) availability, replete H_2, and isotopically enriched $\delta^{13}C$ CH_4 that is outside the known biogenic range. We measured the $\delta^{13}C$ of CO_2, biomass, lipids, and CH_4 during hydrogenotrophic methanogenesis under hydrogen replete conditions with a limited carbon pool to investigate carbon isotope dynamics at complete DIC consumption. As theory predicts, we found that the final, accumulated methane $\delta^{13}C$ values closely reflect the $\delta^{13}C$ of the initial DIC supply, and that methane is more ^{13}C enriched than biomass and lipids. This provides the first experimental evidence that methanogens can achieve complete carbon consumption and thus can produce accumulated CH_4 products that isotopically reflect the initial CO_2. These data show that the range of possible $\delta^{13}C$ values from biogenic methane needs to be expanded for natural environments impacted by extreme carbon limitation.

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Introduction

Methane is an important energy source, greenhouse gas, and potential biosignature on Earth and other planetary bodies including Mars and Enceladus (Schulte *et al.*, 2006; Waite *et al.*, 2017). The stable isotope composition of methane is often used to distinguish between abiotic, thermogenic, and microbial sources on Earth (Schoell, 1980). However, there is ongoing debate about the isotopic range that is possible in biogenic methane (Etiope and Sherwood-Lollar, 2013), complicating interpretation of methane sources in disciplines such as natural gas exploration, origin of life studies, and extraterrestrial life detection.

Hydrogenotrophic methanogenesis, or the oxidation of H_2 to reduce CO_2 to CH_4, is the autotrophic mode of growth and most relevant methanogenesis pathway regarding the study of early Earth and the search for extraterrestrial life (Schulte *et al.*, 2006). Hydrogenotrophic methanogenesis usually results in methane with a $\delta^{13}C$ range of −110 ‰ to −60 ‰ (Elvert *et al.*, 1999; Conrad *et al.*, 2011). Factors including environmental stress, substrate availability, and metabolic reversibility control where biogenic methane plots within this range (Fuchs *et al.*, 1979; Valentine *et al.*, 2004) with metabolic net fractionation ($\varepsilon^{13}C$) estimated to range between 20 ‰ to −106 ‰ (Gropp *et al.*, 2021). In contrast, abiotic environmental methane is more ^{13}C enriched, with values as depleted as −47 ‰ to enriched positive values (Etiope and Sherwood-Lollar, 2013).

One example of environments where the source of methane remains ambiguous includes serpentinising systems, where water-rock reactions produce H_2 and CH_4 and cause extreme carbon limitation due to high alkalinity (Nothaft *et al.*, 2021). The $\delta^{13}C$ of CO_2/DIC found in natural serpentinites with high H_2 concentrations is −1.08 ‰ to −25.3 ‰ and methane detected in these systems can be relatively enriched in ^{13}C when compared to most natural environments, with $\delta^{13}C$ values as positive as +5 ‰ (Etiope and Sherwood-Lollar, 2013; Etiope *et al.*, 2016; Miller *et al.*, 2016; Nothaft *et al.*, 2021). The seemingly abiotic signal of methane in these serpentinites has sparked debate regarding the potential contribution of microbial methanogenesis since autotrophic methanogens have also been found in these systems (Miller *et al.*, 2016, 2018; Nothaft *et al.*, 2021). In theory, methanogens will produce methane with the same isotopic composition as the starting CO_2 at complete DIC consumption (Meister *et al.*, 2019). However, the lack of net carbon isotope fractionation at complete DIC consumption has not been experimentally shown. Here, we aim to address the question whether hydrogenotrophic methanogens will actually produce isotopically heavy methane in a carbon limited system.

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Lipids, which are utilised by all terrestrial life for energy storage and the construction of cellular membranes, are the most chemically stable polymer and can be preserved for over hundreds of millions of years within sediment (Sessions *et al.*, 2004). Like methane, lipids have carbon isotope signatures that store metabolic and/or environmental information. Carbon limitation has been seen to cause a smaller depletion in $\delta^{13}C$ of methanogen lipids when compared to carbon replete conditions, regardless of substrate (Londry *et al.*, 2008). $\delta^{13}C$ of lipids analysed from carbon limited serpentinising systems have shown ^{13}C isotopic enrichment, with an average $\delta^{13}C$ of +2 ‰ and a high of +14 ‰ compared to typically depleted values of ~−50 ‰ or less (Bradley *et al.*, 2009; Zwicker *et al.*, 2018). It is unknown whether lipids follow the same trend as methane with respect to carbon isotope fractionation under carbon limitation.

This study thus investigates the carbon isotope composition of methane, biomass, and lipids of hydrogenotrophic methanogen *Methanococcus maripaludis* S2 in a closed system under DIC limitation with excess H_2. We hypothesise that ^{13}C enriched methane should form from biological activity under extreme carbon limitation, giving rise to methane with $\delta^{13}C$ values indistinguishable from abiotic methane.

Methods

Experimental setup. Anaerobic batch cultures of *Methanococcus maripaludis* S2 were grown hydrogenotrophically in 160 mL serum vials in a modified DSMZ141 media devoid of yeast extract, cysteine, and other organic carbon sources. Cultures were given excess H_2 at 20 psi (7.4 mmol) as the electron donor and 1.08 mmol inorganic carbon ($NaHCO_3$) as the electron acceptor and sole carbon source. Cultures were continuously stirred at 625 rpm to increase the gas transfer rate between headspace and liquid. Cultures were grown at an initial pH of 6.7 and temperature of 37 °C. Optical density was measured continuously throughout growth at 630 nm. One vial was not inoculated, and the incubation was terminated immediately to capture initial DIC. Four incubations were terminated along various points of exponential growth phase. At termination, exponential cultures were injected with phosphoric acid to stop growth and release all remaining DIC into headspace. Three cultures were allowed to consume the entire DIC pool and sampled in early stationary phase. A small portion of stationary culture medium was acidified to determine if any DIC remained.

Headspace gas (CO_2, CH_4, and H_2) from acidified samples was transferred *via* gas-tight syringe to sealed serum vials filled with a 30 % NaCl solution for preservation until analysis (Gan *et al.*, 1998). After headspace sampling, biomass from stationary phase cultures was pelleted and freeze dried. Biomass pellets were divided in half for bulk biomass analysis and lipid extractions. Bulk biomass was oven dried to prepare for analysis. Lipids were extracted from biomass by acidic hydrolysis methanolysis (Zhou *et al.*, 2020). Phytane was extracted from the total lipid extract by ether cleavage and hydrogenation (Kaneko *et al.*, 2011).

Sample analyses. Headspace gases (CO_2, CH_4, and H_2) were quantified on a gas chromatograph with flame ionisation and thermal conductivity detectors (SRI GC-FID/TCD Multi-Gas #5 Configuration). $\delta^{13}C$ of CO_2 and CH_4 were measured on a Picarro Ring-Down Spectrometer G2201-I and $\delta^{2}H$ of CH_4 on a gas chromatograph isotope ratio mass spectrometry system (Thermo Scientific GC TraceGas Ultra system connected to a Thermo Scientific Delta V Plus).

Bulk biomass $\delta^{13}C$ was analysed on a Thermo Delta V continuous flow stable isotope ratio mass spectrometer attached to a Thermo Flash2000 Elemental Analyzer. Phytane was quantified on a GC flame ionisation detector (GC-FID Thermo TRACE 1310) and identified on a single quadrupole gas chromatography mass spectrometer (GC-MS Thermo ISQ LT with TRACE 1310). The $\delta^{13}C$ of phytane was measured on a GC pyrolysis isotope ratio MS (GC IsoLink II + MAT253 Plus IRMS, Thermo Scientific).

All carbon and hydrogen isotope measurements were corrected using standards of known isotopic composition and are reported in the conventional delta notation *vs.* the Vienna Pee Dee Belemnite (VPDB)/Vienna Standard Mean Ocean Water (VSMOW) international scales respectively: $\delta^{13}C = [^{13}C/^{12}C]_{sample}/[^{13}C/^{12}C]_{VPDB} - 1$; $\delta^{2}H = [^{2}H/^{1}H]_{sample}/[^{2}H/^{1}H]_{VSMOW} - 1$. Observed isotope fractionation between two reservoirs is reported in alpha and epsilon notation: $^{13}\varepsilon_{a/b} = {}^{13}\alpha_{a/b} - 1 = [^{13}C/^{12}C]_a/[^{13}C/^{12}C]_b - 1$. δ and ε values reported in per mille (‰) are implicitly multiplied by a factor of 1000 (Coplen, 2011).

Results and Discussion

During methanogenesis, CO_2 was fully consumed while H_2 remained in excess throughout the experiment. As CO_2 was consumed, the distillation process increased $\delta^{13}C$ CO_2 from −2.8 ‰ initially to +78.5 ‰ in late exponential phase (see Table 1). Conversely, methane started relatively depleted with $\delta^{13}C$ CH_4 −23.6 ‰ at the first measurement point (when ~42 % of the CO_2 was consumed) and increased to −2.5 ‰ (*i.e.* slightly above the starting value of CO_2) at the end of the distillation when the methanogens reached stationary phase and had consumed >99 % of the CO_2.

The $\delta^{13}C$ values for biomass and phytane measured in stationary phase were significantly more depleted than the methane that had accumulated at this point (Table 1), with $^{13}\varepsilon_{biomass/methane} = -5.3$ ‰ and $^{13}\varepsilon_{phytane/methane} = -16$ ‰. The biomass yield estimate from isotopic mass balance of the final

Table 1 $\delta^{13}C$ and $\delta^{2}H$ of methanogenesis products during complete carbon consumption. Stationary measurements represent 3 replicate cultures. All other measurements represent 1 culture. Errors represent the propagated standard error of the mean.

Samples	% CO_2 remaining	$\delta^{13}CO_2$ (‰)	$\delta^{13}CH_4$ (‰)	$\delta^{13}C$ (‰) phytane	$\delta^{13}C$ (‰) biomass	$\delta^{2}H$ (‰) CH_4
starting	100.0 ± 2.8	−2.8 ± 0.5				
early-exponential	57.9 ± 2.3	+15.7 ± 0.6	−23.6 ± 0.5			
early/mid-exponential	38.4 ± 2.3	+28.8 ± 0.9	−21.5 ± 0.7			
mid/late-exponential	23.6 ± 2.3	+51.2 ± 1.4	−16.1 ± 0.7			
late-exponential	13.2 ± 1.8	+78.5 ± 2.3	−12.0 ± 0.7			
stationary	0.6 ± 1.4		−2.5 ± 0.4	−18.5 ± 0.4	−7.8 ± 0.4	−437 ± 14

methane and biomass is 6.4 %, assuming no other significant sinks of carbon. This yield is lower than other estimates with abundant substrate but comparable to those with limited substrate (Londry *et al.*, 2008).

Carbon isotope fractionation between methanogenesis products. The net carbon isotope fractionation between biomass and methane measured in stationary phase is shown in Figure 1 together with literature data.

Overall, the data follows the trend that carbon limitation decreases the isotopic offset between biomass and methane. However, data from this study inverts the fractionation typically observed in laboratory experiments (Fuchs *et al.*, 1979; Summons *et al.*, 1998; Londry *et al.*, 2008; Nguyen *et al.*, 2020): methane in our cultures is more isotopically enriched than biomass (see Fig. 1; $\varepsilon < 0$ ‰/$\alpha < 1$). Fractionation between lipids and methane exhibits the same pattern (Fig. S-1).

We thus observe that extreme carbon limitation in a closed system causes the isotopic signature of accumulated biomass to be more ^{13}C depleted than methane. We hypothesise this could occur if biomass is primarily synthesised early on when there is abundant CO_2 available for both catabolism and anabolism. If methanogens prioritise the energy producing catabolic pathway of methanogenesis and reduce CO_2 fixation as CO_2 becomes limiting, the isotopic composition of biomass remains at relatively light values compared to the still accumulating methane that is produced from the increasingly enriched residual CO_2 (illustrated in Fig. 2 in the "anabolism stops" model). Although the impact of carbon limitation on biosynthesis inhibition has not been experimentally investigated in methanogens, inorganic carbon limitation has been found to increase energy producing metabolisms and decrease cell yield in ammonia oxidising bacteria to account for increased cellular maintenance energy requirements (Jiang *et al.*, 2015; Mellbye *et al.*, 2016). Additionally, hydrogenotrophic methanogens have been found to uncouple biosynthesis from methanogenesis during stressful situations, including phosphate limitation (Leigh *et al.*, 2008). As shown in Figure 2, such a decrease in biomass yield over time could cause the accumulated biomass in our experiments to be more isotopically depleted than final accumulated methane because it was predominantly produced from CO_2 early during the distillation when CO_2 was not yet as heavily ^{13}C enriched. The accumulated methane is isotopically heavier than the biomass because methane generation continued when CO_2 was sparse and ^{13}C enriched from the distillation process. This interpretation implies that the $\delta^{13}C$ of lipids and biomass may not reflect the final environmental state but rather reflect a time of high CO_2 availability.

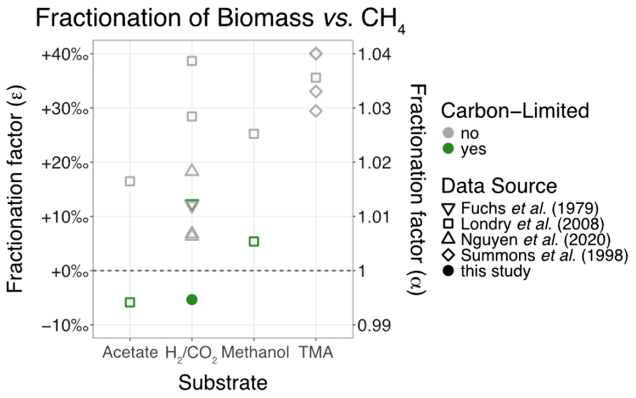

Figure 1 Carbon isotope fractionation between bulk biomass and methane from lab grown methanogens. TMA: trimethylamine.

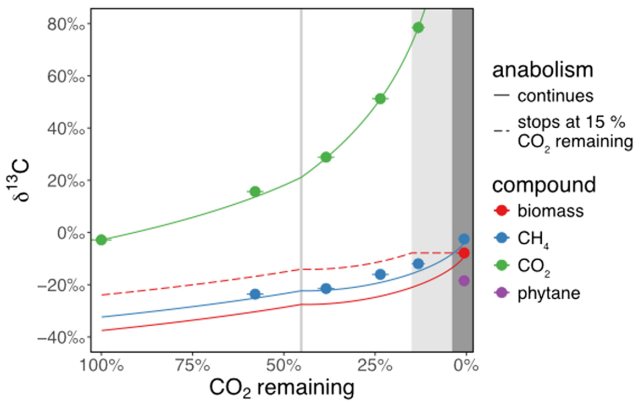

Figure 2 NLS model of CO_2 distillation during methanogenesis with $\delta^{13}C$ of substrate and accumulated products plotted against % CO_2 remaining over the course of culture growth. Lines represent modelled trends and points represent data from this study. The grey vertical line represents the step increase in metabolic fractionation that best fits the data (see text). The dark grey area represents stationary phase. The light grey area represents the stop of anabolism in the adapted model. Horizontal error bars represent standard errors. Vertical error bars are smaller than symbol sizes (Table 1).

Rayleigh distillation and CO_2 consumption. The observed isotopic compositions of methane and CO_2 fit a Rayleigh distillation model with increasing metabolic fractionation well. In its simplest form, this takes the shape of a two-step distillation process as illustrated in Figure 2 with an initial CO_2-CH_4 fractionation of -29.6 ± 2.3 ‰ that becomes more heavily fractionating (-44.0 ± 2.5 ‰) after ~55 % of CO_2 is consumed (all 3 parameters estimated simultaneously by non-linear least squares NLS data fitting in R; RMSE 2.2 ‰). This model reflects a closed system that starts with all the carbon as 100 % reactant (CO_2) and ends with 100 % products (CH_4 and biomass) and both methanogenesis and biomass production stop once all CO_2 is consumed. The total biomass yield is assumed to be the 6.4 % inferred from overall isotope mass balance. As expected from a Rayleigh distillation process, residual CO_2 and accumulated CH_4 and biomass systematically get isotopically heavier as CO_2 is consumed. The offset between the biomass and methane curves (−5.3 ‰) results from the constraint posed by the isotopic composition of the final products. At full DIC consumption, the accumulated methane is slightly enriched compared to the initial $\delta^{13}C$ of CO_2 (initial $\delta^{13}C_{CO2} = -2.8$ ‰, final $\delta^{13}C_{CH4} = -2.5$ ‰). This is the expected outcome from near complete consumption of CO_2 in a closed system for the majority product. By isotope mass balance, CH_4 will be necessarily enriched compared to CO_2 if biomass is more depleted than CO_2.

A modification of this model where anabolism stops as CO_2 becomes increasingly limiting can explain the observed isotopic composition of the accumulated biomass with a positive biomass CH_4 fractionation factor ($\varepsilon > 0$) that is consistent with literature data under non-carbon limiting conditions (Fig. 1). For example, if the methanogens stopped fixing carbon at a threshold of 15 % CO_2 remaining (example "anabolism stops" in Fig. 2), the metabolic fractionation factor between biomass CH_4 would be estimated at +8.9 ‰. The exact value of the fractionation factor depends on the threshold at which anabolism stops, which is not fully constrained by the available data (see Fig. S-2). However, based on the available literature data (Fig. 1), we hypothesise that this threshold model ("anabolism stops" in Fig. 2) is a more accurate representation of biomass

fractionation, with biomass more enriched than the accumulated methane during initial metabolism until anabolism stops and the accumulated methane continuing to get more enriched from the distillation process. The resulting estimates of the methanogenesis fractionation fall into a narrow range regardless of when anabolism stops and closely match the estimates from the simpler model ("anabolism continues" in Fig. 2): the initial fractionation is −30.0 to 29.6 ‰ and increases to −45.5 to −43.7 ‰ after ~55 % of CO_2 is consumed. These CO_2-CH_4 fractionation factors fall well within the possible range of methanogenic fractionation (−106 ‰ to −20 ‰, Gropp *et al.*, 2021). See SI for all equations and github.com/KopfLab/2025_batther_et_al._C_limitation for implementation.

Environmental implications. These experimental findings and comparison to model predictions show that biological CH_4 can span the full range of $\delta^{13}C$ CH_4 space depending on carbon availability and environmental conditions, such as hydrogen availability, rather than being constrained by the previously inferred microbial range (Fig. 3). The potential biogenicity of methane cannot be ruled out even if there is little isotopic fractionation between methane and the bulk carbon pool of any system. Rather, the lack of isotopic fractionation may be more indicative of extreme carbon limitation controlling the methane producing reaction pathway. Although such carbon limitation may be rare, environments such as serpentinising systems are an excellent example on Earth that may also be relevant to habitable rocky bodies in our solar system, and where the potential for microbial methanogenesis to produce ^{13}C enriched methane has proven to be controversial. Therefore, the $\delta^{13}C$ of CH_4 detected in the environment cannot be the sole measurement used to determine the source of CH_4, especially to rule out microbial activity. Given possible overlap with the large range of $\delta^{13}C$ CH_4 formed from Fischer-Tropsch type reactions (Etiope and Sherwood-Lollar, 2013), multiple measurements will be required to determine the biogenicity of CH_4, including analysis of the Schultz-Flory distribution of higher hydrocarbons, gene sequencing, lipidomics, or clumped CH_4 measurements (Nothaft *et al.*, 2021). However, if active biological CH_4 production can be confirmed, then the $\delta^{13}C$ of CH_4 can be used to infer if an environment is carbon limited or carbon replete.

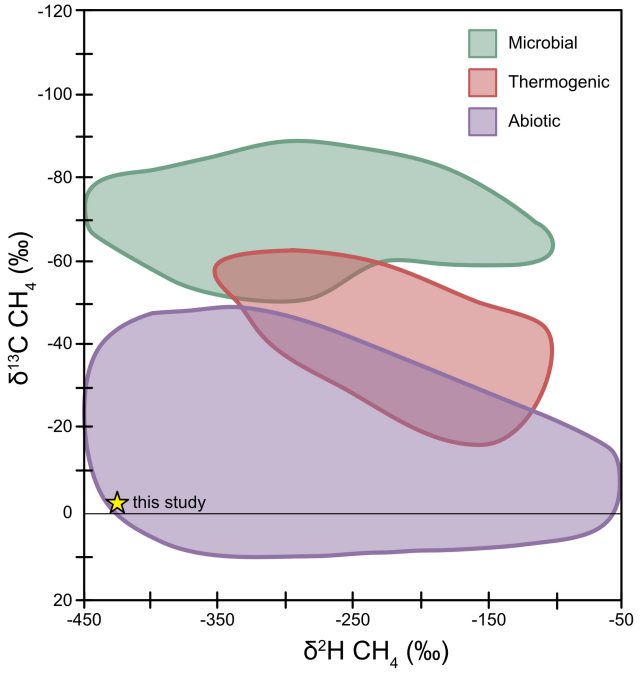

Figure 3 $\delta^{13}C$ *vs.* $\delta^{2}H$ plot of CH_4 based on Wilkes (2020) with data from Whiticar (1999); Etiope *et al.* (2016); Milkov and Etiope (2018); Miller *et al.*, (2018), and this study (yellow star).

Conclusion

This study experimentally demonstrates the impact of full carbon consumption on the carbon isotope signatures of CH_4, biomass, and lipids accumulated during purely autotrophic methanogenesis. The data show that carbon limitation causes accumulated CH_4 to isotopically reflect initial CO_2, which is supported by our Rayleigh Distillation model and has only been previously theorised. This can result in the production of biogenic methane tens of per mille more positive than traditionally assumed. Such ^{13}C enriched biogenic methane contains valuable information about the extent of C limitation, which is rarely utilised in environmental assessments. Instead, the detection of ^{13}C enriched methane has typically been attributed to abiotic sources, which may sometimes be erroneous. Additionally, we see a greater depletion of $\delta^{13}C$ biomass/lipids relative to CH_4 than expected, which could be caused by the inhibition of anabolism by carbon limitation and is an important physiological response worthy of further investigation. In summary, the data support the concept that biogenic methane, biomass, and lipid $\delta^{13}C$ values predicted for natural environments need to be significantly expanded to include the impact of extreme carbon limitation on isotope fractionation.

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Additional Information

Supplementary Information accompanies this letter at https://www.geochemicalperspectivesletters.org/article2543.

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