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Stable Carbon Isotope Signature of Methane Released from Phytoplankton

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Abstract

Aquatic ecosystems play an important role in global methane cycling and many field studies have reported methane supersaturation in the oxic surface mixed layer (SML) of the ocean and in the epilimnion of lakes. The origin of methane formed under oxic condition is hotly debated and several pathways have recently been offered to explain the 'methane paradox'. In this context, stable isotope measurements have been applied to constrain methane sources in supersaturated oxygenated waters. Here we present stable carbon isotope signatures for six widespread marine phytoplankton species, three haptophyte algae and three cyanobacteria, incubated under laboratory conditions. The observed isotopic patterns implicate that methane formed by phytoplankton might be clearly distinguished from methane produced by methanogenic archaea. Comparing results from phytoplankton experiments with isotopic data from field measurements, suggests that algal and cyanobacterial populations may contribute substantially to methane formation observed in the SML of oceans and lakes.

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Key Points:

- Stable carbon isotope values of methane emitted from six phytoplankton cultures incubated in the laboratory
- Isotope fractionation between methane source signature and biomass of widespread algal and cyanobacterial species
- Isotopic patterns of methane released by phytoplankton may be clearly distinguished from methane formed by methanogenic archaea

Abstract

Aquatic ecosystems play an important role in global methane cycling and many field studies have reported methane supersaturation in the oxic surface mixed layer (SML) of the ocean and in the epilimnion of lakes. The origin of methane formed under oxic condition is hotly debated and several pathways have recently been offered to explain the 'methane paradox'. In this context, stable isotope measurements have been applied to constrain methane sources in supersaturated oxygenated waters. Here we present stable carbon isotope signatures for six widespread marine phytoplankton species, three haptophyte algae and three cyanobacteria, incubated under laboratory conditions. The observed isotopic patterns implicate that methane formed by phytoplankton might be clearly distinguished from methane produced by methanogenic archaea. Comparing results from phytoplankton experiments with isotopic data from field measurements, suggests that algal and cyanobacterial populations may contribute substantially to methane formation observed in the SML of oceans and lakes.

Plain Language Summary

Methane plays an important role in atmospheric chemistry and physics as it contributes to global warming and to the destruction of ozone in the stratosphere. Knowing the sources and sinks of methane in the environment is a prerequisite for understanding the global atmospheric methane cycle but also to better predict future climate change. Measurements of the stable carbon isotope composition of carbon – the ratio between the heavy and light stable isotope of carbon – help to identify methane sources in the environment and to distinguish them from other formation processes. We identified the carbon isotope fingerprint of methane released from phytoplankton including algal and cyanobacterial species. The observed isotope signature improves our understanding of methane cycling in the surface layers of aquatic environments helping us to better estimate methane emissions to the atmosphere.

1 Introduction

Methane (CH_4) plays an important role in atmospheric chemistry and physics as it contributes to global warming and the destruction of ozone in the stratosphere. Aquatic environments including oceans, lakes, rivers, estuaries, and wetlands have recently been estimated to contribute to around half of annual global CH_4 emissions to the atmosphere (Rosentreter et al., 2021), although a large portion of the CH_4 produced in these individual ecosystems is oxidized by methanotrophic bacteria in the sediment or water column before escaping to the atmosphere (Reeburgh, 2007; Weber et al., 2019). Despite CH_4 losses through oxidation and release at the water surface to the atmosphere, numerous field studies have shown CH_4 supersaturation in the oxic surface mixed layer (SML) of the ocean (e.g. Karl et al., 2008; Kolomijeca et al., 2022; Scranton & Brewer, 1977; Scranton & Farrington, 1977; Sosa et al., 2019; Taenzer et al., 2020; Weber et al., 2019) and in the epilimnion of lakes (e.g. Donis et al., 2017; Grossart et al., 2011; Günthel et al., 2019; Hartmann et al., 2020; Tang et al., 2016; Thottathil et al., 2022). Maintaining the CH_4 supersaturation state requires frequent CH_4 production in the oxygenated water column, though it has been postulated for decades that microbial CH_4 production by methanogenic archaea is prevented by oxygen. Several sources and processes have recently been

proposed to explain the so called "methane paradox" occurring in oxic waters in oceans and lakes which we summarize in the following. (1) Methane might be produced by photochemical degradation of the algal metabolite dimethyl sulfide (DMS) or acetone and chromophore organic matter (Bange & Uher, 2005; Li et al., 2020; Zhang et al., 2015). (2) Methane is formed by microbes including (a) methanogenic archaea in anoxic microsites (de Angelis & Lee, 1994; Karl & Tilbrook, 1994; Oremland, 1979; Schmale et al., 2018; Stawiarski et al., 2019; Zindler et al., 2013), (b) bacterial degradation of the algal metabolites dimethylsulfonium propionate (DMSP) and its degradation products dimethyl sulfoxide (DMSO) and DMS (Damm et al., 2010; Damm et al., 2008; Florez-Leiva et al., 2013), (c) N_2-fixing bacteria, carrying Fe-only nitrogenase (Zheng et al., 2018), (e) bacterial conversion of methylamine (Wang et al., 2021) and (d) bacterial degradation of methyl phosphonates (MPn) via the C-P lyase reaction pathway, with MPn serving as an alternative source of P under phosphate-limiting conditions (del Valle & Karl, 2014; Karl et al., 2008; Metcalf et al., 2012; Repeta et al., 2016; Taenzer et al., 2020). (3) Phytoplankton produces CH_4 *per se* (Bižić et al., 2020a; Ernst et al., 2022; Klintzsch et al., 2019; Klintzsch et al., 2020; Lenhart et al., 2016; McLeod et al., 2021), (4) and specifically for surface waters of lakes physical transport processes from shallow water zones to the open surface waters (Encinas Fernández et al., 2016, Peeters et al., 2019). For a more detailed overview of the different sources and processes please refer to recent review articles (e.g. Bižić et al., 2020b; Bižić, 2021; DelSontro et al., 2018; Liu et al., 2022; Reeburgh, 2007; Tang et al., 2016).

Interestingly, a very recent study (Perez-Coronel & Beman, 2022) that applied freshwater incubation experiments under different treatments suggested multiple sources act simultaneously to explain aerobic CH_4 production in aquatic environments. Several recent studies have applied stable isotope techniques to better constrain the origin and fate of CH_4 in lakes (Einzmann et al., 2022; Hartmann et al., 2020; Taenzer et al., 2020; Thottathil & Prairie, 2021; Thottathil et al., 2022; Tsunogai et al., 2020). The stable carbon isotope ratio ($^{13}C/^{12}C$) of CH_4 (expressed as $\delta^{13}C$-CH_4 values) depends on the production, degradation, and transport processes within the aquatic system. Thus, a comprehensive temporal and spatial $\delta^{13}C$-CH_4 data set of the water column is useful to disentangle sources and sinks. Their inclusion together with CH_4 concentration data allows for improved modelling of the regional and global CH_4 budget (Sherwood et al., 2017). As phytoplankton might contribute to CH_4 production in both oxic marine and freshwater environments, we measured $\delta^{13}C$-CH_4 values from phytoplankton including three widespread marine haptophite algal, and three cyanobacteria species. The six phytoplankton species were incubated under controlled laboratory conditions and the apparent isotopic fractionation between phytoplanktonic CH_4 and biomass was calculated. The importance of the observed isotopic patterns for our understanding of aquatic CH_4 cycling is discussed in relation to recent results from field experiments and to well-known isotope patterns of biotic and abiotic CH_4 sources.

2 Results and Discussion

2.1 Stable carbon isotope signature and isotopic fractionation of CH_4 emitted from phytoplankton.

Six phytoplankton cultures were cultivated under sterile conditions, including three different marine algal species (haptophytes) and three cyanobacteria species. We determined CH_4 mass and $\delta^{13}C$-CH_4 values in the cultures' headspace at the end of the incubation period. In addition, stable carbon isotope values of particulate organic matter ($\delta^{13}C$-POC) were measured (a detailed

methodical description is given in the Supporting Information Text S1-Text S5 and Figure S1). At the end of the incubation period, the CH_4 mass in the headspace of all studied cultures increased compared to the medium control group. The latter remained at the initial measured atmospheric background CH_4 levels (all culture vessels were closed in atmospheric air and thus contained background CH_4). The amount of CH_4 produced correlated positively with the amount of initial inoculated phytoplankton biomass (Figure S2). Simultaneously, the $\delta^{13}C$-CH_4 values in five cultures shifted towards to more positive values with increasing CH_4 production when compared to the control group, i.e., atmospheric background values, while a shift towards more negative values was observed for one culture only. To determine the isotopic source signature of CH_4 ($\delta^{13}C$-CH_{4_source}) of the phytoplankton cultures the Keeling plot method (Keeling, 1958) was used as described in the Supporting Information (Text S2). Figure 1 shows the Keeling plots for each species in which the intersection of the extrapolated regression between $\delta^{13}C$-CH_4 values and the inverse CH_4 mass yields the CH_4 source signatures. Five cultures produced CH_4 that was clearly enriched in ^{13}C relative to the $\delta^{13}C$-CH_4 values of atmospheric CH_4 (≈ -47‰) yielding $\delta^{13}C$-CH_{4_source} values ranging between -19 ‰ and - 43 ‰ (Figure 1,a, b, c, e, f), while a slight depletion in ^{13}C relative to atmospheric CH_4 was found only for *Prochlorococcus* strain (-54 ‰; Figure 1, d). Based on the discrepancy between $\delta^{13}C$-CH_{4_source} values (Figure 1) and the $\delta^{13}C$-POC values (Table S1) the apparent stable carbon isotopic fractionation during CH_4 formation ($\varepsilon_{CH4/POC}$) was calculated for each phytoplankton species. The corresponding isotopic fractionations are shown for each species in Figure 2. The observed negative values for $\varepsilon_{CH4/POC}$ ranging from -29.8 ± 1.7 ‰ to -1.4 ± 0.7 ‰ exhibited a ^{13}C depletion of released CH_4 when compared to the biomass expressed as POC, with the exception of *Synechococcus* WH8102, where no fractionation occurred (+ 0.5 ± 1.0 ‰). Thus, CH_4 formation by phytoplankton followed the general isotope fractionation rule that in kinetic reactions the lighter isotopes tend to react faster, resulting in a ^{13}C-depleted product compared to the substrate (see e.g., Fry, 2006). However, based on the degree of fractionation, the calculated $\varepsilon_{CH4/POC}$ values obviously suggest two different CH_4 formation patterns of the phytoplankton species. On the one hand, CH_4 formation by *E. huxleyi*, *P. globosa*, and *Prochlorococcus* resulted in a substantial depletion of ^{13}C in the formed CH_4 compared to their $\delta^{13}C$-POC values, with an average fractionation of -23 ± 4 ‰. On the other hand, *Chrysochromulina* sp. and both *Synechococcus* strains showed average $\varepsilon_{CH4/POC}$ values of -1 ± 1 ‰ (Figure 2). Thus, the $\delta^{13}C$ values of CH_4 emitted by these strains are nearly the same as those measured for POC. Currently, we can only speculate about the reasons of the observed different $\varepsilon_{CH4/POC}$ values. It is known that different metabolic pathways are accompanied by specific kinetic isotope fractionation that leads to specific $\delta^{13}C$ values of the cellular compounds (e.g., see Hayes, 2001). Thus, the different $\varepsilon_{CH4/POC}$ values calculated for the six investigated species may indicate that these organisms used different pathways and/or precursor compounds to produce CH_4. This is well known for CH_4 formation pathways of methanogenic archaea: the CO_2-reducing pathway fractionates significantly stronger against ^{13}C than the acetoclastic pathway, with apparent isotopic fractionations of around -49 ‰ and -19 ‰, respectively (see Conrad, 2005 and references therein). Analogously, the CH_4 formation by marine algae, with isotopic fractionations of *P. globosa* and *E. huxleyi* (-22.6 ± 0.9 ‰ and -17.9 ± 1.2 ‰) distinct from those of *Chrysochromulina* sp. (-2.1 ± 2.5 ‰) might be the result of conversion of different CH_4 precursors compounds. This hypothesis is supported by recent studies (Klintzsch et al., 2019; Lenhart et al., 2016), showing that methylated sulfur compounds such as DMS, DMSO, methionine sulfoxide and methionine are potential CH_4 precursor compounds in marine algae. It has been shown that the investigated algal species

produce these compounds in mM cellular concentrations (Liss et al., 1994; Sunda et al., 2002) with the synthesis of these compounds requiring individual enzymatic steps (Bullock et al., 2017; Stefels, 2000). Therefore, a different isotopic composition of the methyl precursors might cause different isotope fractionation in CH_4 produced by phytoplankton as observed in our study (Figure 2). This might also explain the larger differences in isotopic fractionation between phytoplankton cultures even though δ^{13}C-POC values were similar (Table S1). Please note that within this study it was not possible to extract potential methyl precursor compounds such as DMS or DMSO from the incubation experiments and measure their δ^{13}C values.

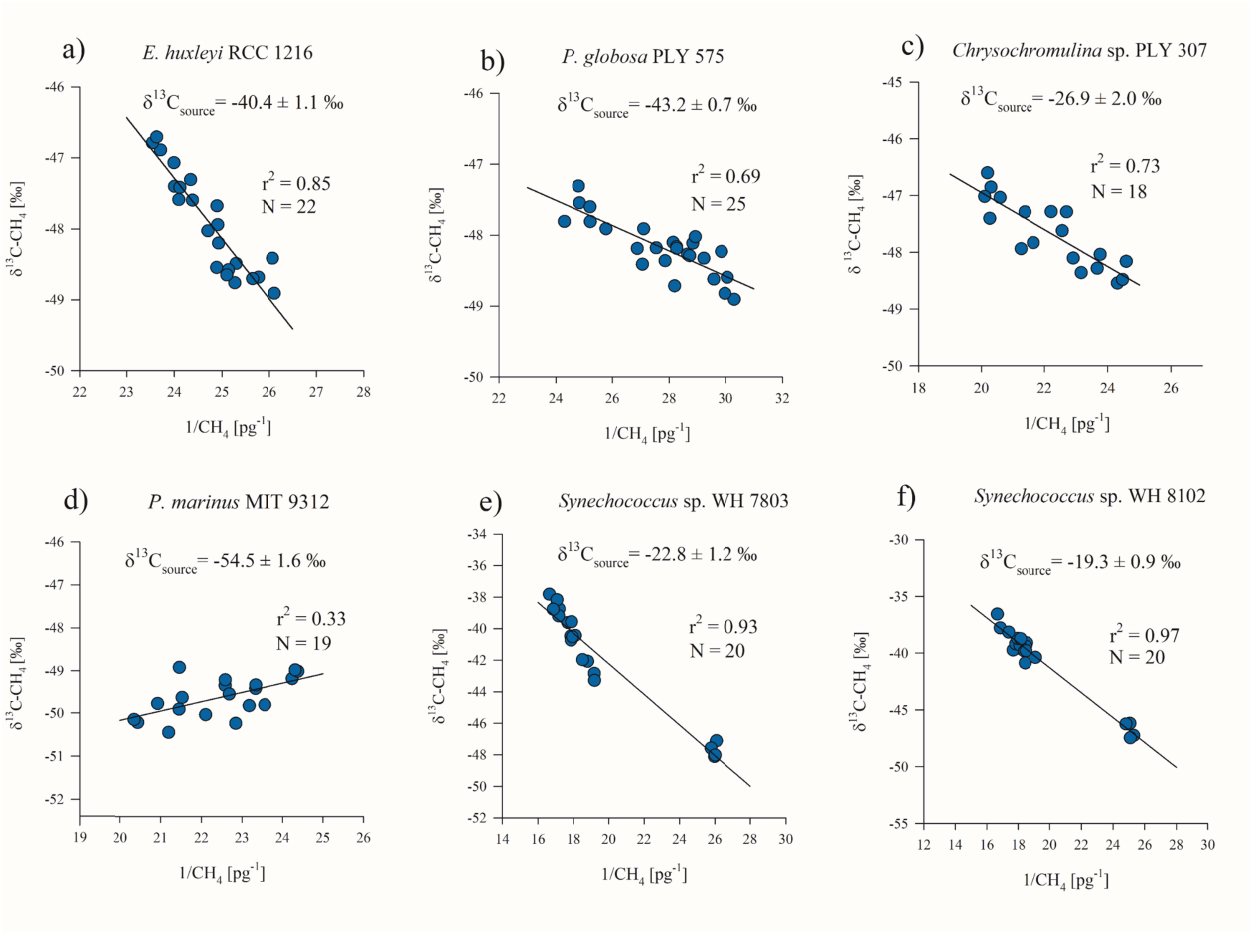

Figure 1. Keeling plots from three haptophytes (**a, b, c**) and *Cyanobacteria* species (**d, e, f**). The calculated δ^{13}C-CH_{4_source} values of each species are given by the extrapolated intercept with the y axis CH_4 ($1/[CH_4] = 0$). The correlation between CH_4 mass (given as reciprocal) and the δ^{13}C-CH_4 values of all incubations is shown in detail for each plot. N refers to the total number of observations from independent incubation experiments.

Cyanobacteria including the investigated genera *Synechoccocus* and *Prochlorococcus* have been shown to produce methylated sulfur compounds but in extremely low-intracellular concentrations (Corn et al., 1996; McParland & Levine, 2019). In contrast, MPn associated with esters are common in many bacteria strains (Metcalf et al., 2012). Methylphosphonates can be metabolized by several marine bacteria as an alternative phosphorus source via the C-P lyase

pathway whereby CH_4 is released (del Valle & Karl, 2014; Karl et al., 2008; Repeta et al., 2016; Taenzer et al., 2020). Taenzer et al. (2020) showed that the MPn cleaving by freshwater and marine bacterial strains leads to marginal isotopic fractionation between substrate MPn and produced CH_4 with average ε values of 1.3 ‰. Based on the observed isotopic pattern, the research team concluded that MPn is a likely source of CH_4 in the surface waters of the Pacific Ocean (station ALOHA, Taenzer et al., 2020). However, the MPn related CH_4 formation pathway might be less relevant for the experiments conducted in our study because of the following reasons. All of the investigated strains lack the C-P lyase gene (Bižić et al., 2020a) and the phosphate rich conditions of the culture medium would, if present, inhibit C-P lyase gene expression (Bižić et al., 2020a). Although Yao et al. (2022) showed for some freshwater bacterial cultures that C-P lyase gene expression was not completely inhibited by phosphorus, the addition of MPn was mandatory to induce C-P lyase gene expression. In addition, Sosa et al. (2021) showed that *Prochlorococcus* processes MPn to formate rather than to CH_4. Thus, in our experiments the cleavage of MPn is rather unlikely to explain the observed CH_4 formation. Consequently, there must be other mechanisms of CH_4 formation in addition to the C-P lyase pathway. According to Ernst et al. (2022), oxic CH_4 formation might occur in living organisms from all domains of life when sulfur or nitrogen-methylated compounds are converted to CH_4 by a Fenton-type reaction via formation of methyl radicals. This reaction might cause relatively small fractionations between biomass and CH_4, because radical-induced reactions are typically associated with small fractionations between precursors and reaction products (Morasch et al., 2004). Consequently, the ROS-driven pathway suggested by Ernst et al. (2022), might explain the small fractionations observed in our experiments for the three phytoplankton species *Chrysochromulina* sp., *Synechococcus* WH8102 and WH7803 (on average -1 ± 1 ‰, Figure 2). On the other hand, the larger calculated isotopic fractionations of -29.8 ± 1.7 ‰ to -17.9 ± 1.2 ‰ for *Prochlorococcus* MIT 9312, *E. huxleyi* and *P. globosa*, respectively, imply that different methyl precursor substrates and/or pathways were involved in the CH_4 formation by the three phytoplankton species.

Even though the reaction pathways and the specific circumstances leading to the observed fractionation patterns between POC and CH_4 of the six investigated species remain unclear, the results show, for the first time the range of $\varepsilon_{CH4/POC}$ values directly obtained from phytoplankton cultures. The fractionations between POC and CH_4 might help to trace back CH_4 formation in field studies, which will be discussed in greater detail in the section 2.3 below. To accomplish the presented dataset of marine algal and cyanobacteria species we provide further $\delta^{13}C\text{-}CH_{4\_source}$ values of freshwater and terrestrial cyanobacteria which were calculated from culture experiments performed in previous laboratory experiments (Bižić et al., 2020a). The data is provided in the Supporting Information (Figure S3; Text S6) and are considered in the discussion section below.

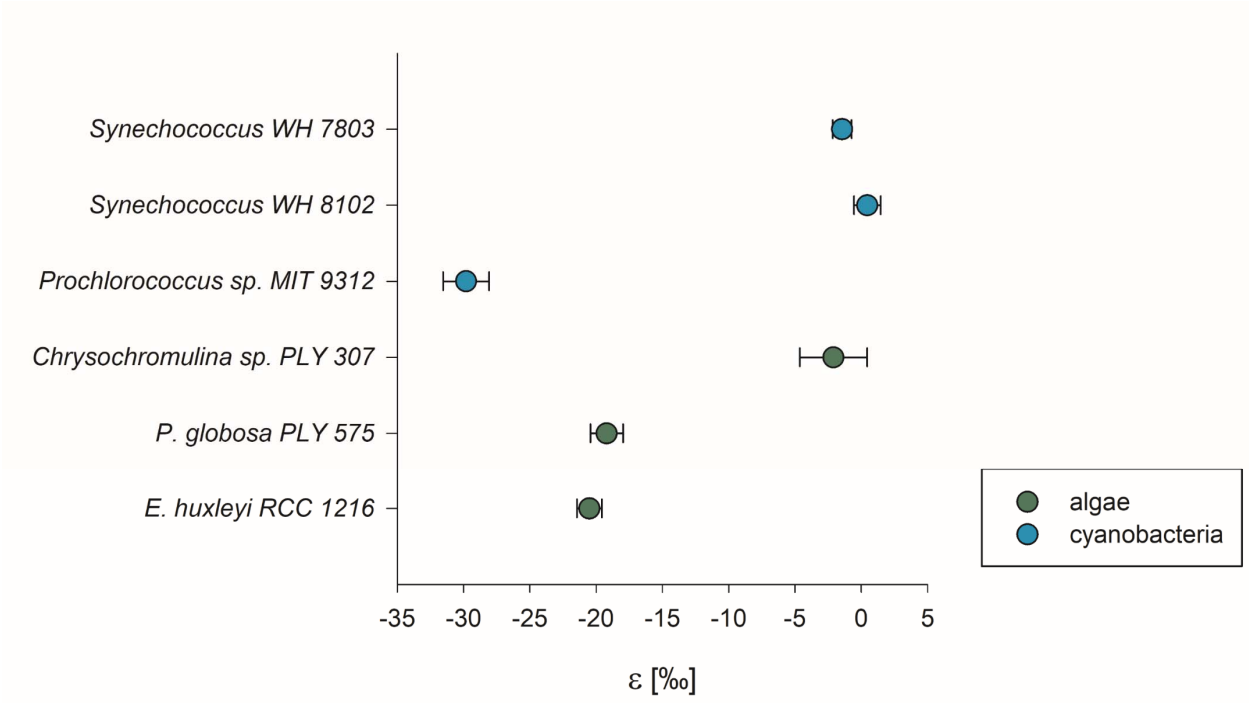

Figure 2. Apparent isotopic fractionation between phytoplanktonic POC and released CH_4. Values are the mean of replicated culture experiments. Error bars show the standard error.

2.2 The stable carbon isotope pattern of CH_4 released from phytoplankton compared with other well-known CH_4 sources

Global CH_4 monitoring is usually based on measurements of CH_4 mixing ratios, i.e., quantification of CH_4 emissions, while a growing number of studies include measurements of $\delta^{13}C$-CH_4 values in order to better constrain the strengths of different sources in context of total emissions (e.g., Allen, 2016; Dlugokencky et al., 2011; Fletcher & Schaefer, 2019; Houweling et al., 2017; Menoud et al., 2022; Nisbet & Weiss, 2010). Ranges of measured $\delta^{13}C$-CH_4 values have been reported for conventional sources which might be classified into thermogenic (from geological processes), pyrogenic (from biomass burning) and biogenic (from methanogenic archaea) origin (Saunois et al., 2020). Recently, $\delta^{13}C$-CH_4 values from eukaryotic sources including plants, fungi and humans have been reported (Keppler et al., 2006, 2016; Schroll et al., 2020; Vigano et al., 2009) which we categorize as "biogenic non-archaeal" CH_4 formation processes.

In Figure 3, we compare the already known $\delta^{13}C$-CH_{4_source} patterns from various sources with those observed from phytoplanktonic cultures obtained in our study. Pyrogenic CH_4, produced during biomass burning exhibits mean $\delta^{13}C$-CH_4 values of -26.2 ± 4.8 ‰ and thus is typically highly enriched in ^{13}C compared to atmospheric CH_4 (≈ -47 ‰). Thermogenic $\delta^{13}C$-CH_4 values, produced from buried biomass in the Earth's crust, shows median $\delta^{13}C$-CH_4 values of -49.8 ± 11.2 ‰, -42.5 ± 6.7 ‰ and -44.0 ± 10.7 ‰ for coal, shale gas and conventional oil and gas, respectively (Sherwood et al., 2017). These values are very similar to atmospheric values. Both source categories, pyrogenic and thermogenic, are often referred to as abiotic sources because a metabolic activity is not directly involved in their CH_4 formation process – although the

precursor compounds are derived from organic matter (Boros & Keppler, 2018). In contrast, biotic CH_4, including traditional pathways (from methanogens) and novel discovered non-archaeal sources, is directly linked to biological metabolic processes, and released CH_4 tends to be ^{13}C-depleted relative to atmospheric values (Figure 3). Biogenic CH_4, produced by methanogenic archaea in anoxic environments, typically ranges from -72 to -47 ‰ (Sherwood et al., 2017), depending on its individual source category. The $\delta^{13}C$-CH_4 values emitted from biogenic non-archaeal sources such as plants and fungi lie between -70 ‰ and -45 ‰ and thus are almost in the same range as those $\delta^{13}C$-CH_4 values reported for methanogenic archaea. $\delta^{13}C$-CH_4 values directly emitted from plants depend on the autotrophic carbon fixation pathway (Keppler et al., 2006; Vigano et al., 2009), as the C_3 and C_4 photosynthetic pathway controls the isotopic composition of biomass, which in turn influences the $\delta^{13}C$-CH_4 values from plants (see $\delta^{13}C$-CH_4 values of C_3 and C_4 plants in Figure 3). Similarly, $\delta^{13}C$-CH_4 values of CH_4 released by fungi is related to the $\delta^{13}C$ values of the growth substrate (Schroll et al., 2020). In human breath, a $\delta^{13}C$-CH_{4_source} values ranging from -90 ‰ to -49.3 ‰ were observed (Keppler et al., 2016). Traditionally, human CH_4 production was considered to exclusively arise from methanogenic archaea living in the gastrointestinal tract (Bond et al., 1971). However, recent investigations (Keppler et al., 2016; Polag & Keppler, 2018, 2022) suggest that CH_4 is also formed endogenously in human cells. Thus, $\delta^{13}C$-CH_4 values measured from human breath might include both pathways which are currently difficult to distinguish. The CH_4 production by marine algae and cyanobacteria investigated in this study is categorized into "biogenic non-archaeal CH_4", as the CH_4 is formed under oxic conditions by the metabolism of the members from the domain *Eukaryote* and *Procaryote*. The $\delta^{13}C$-CH_{4_source} values of marine phytoplankton, ranging from -54.5 ‰ to -19.3 ‰, showed mostly less negative $\delta^{13}C$-CH_4 values (median -33.7 ‰) when compared to both atmospheric values and previously described biogenic non-archaeal CH_4 sources (e.g., plants and fungi). The tendency of less negative values is in line with the $\delta^{13}C$-CH_{4_source} values of the two terrestrial and five limnic cyanobacteria (median -33.8 ‰) ranging between -61.4 ‰ to -5.4 ‰ (Figure S3).

The observed $\delta^{13}C$-CH_{4_source} values from phytoplankton considerably extend the range of biogenic non-archaeal CH_4 towards less negative $\delta^{13}C$-CH_4 values of up to -5.4 ‰. Therefore, biotic and abiotic CH_4 source categories are less clearly delimited due to their $\delta^{13}C$-CH_4 values isotopic signature when taking those of phytoplankton into account. Figure 3 shows that the range of measured $\delta^{13}C$-CH_4 values for methanogenic archaea has little overlap with $\delta^{13}C$-CH_{4_source} values of phytoplankton. Therefore, phytoplanktonic CH_4 might be clearly distinguished from CH_4 produced by methanogenic archaea based on their $\delta^{13}C$-CH_{4_source} values. However, at the ecosystem scale, even distinguishing between two different co-occurring methanogenic sources based on their $\delta^{13}C$-CH_4 values is complex, requiring knowledge of additional parameters as discussed in Conrad (2005). Furthermore, microbial CH_4 oxidation is a widespread feature in oxic and anoxic environments which might change the initial $\delta^{13}C$-CH_{4_source} value. The CH_4 oxidation reduces the ^{12}C content, resulting in an increase of the ^{13}C content in the remaining CH_4 pool (Barker & Fritz,1981). In recent field studies microbial CH_4 oxidation were considered for calculating $\delta^{13}C$-CH_{4_source} values of oxic CH_4 production by mass balance within the epilimnion of lakes (Hartmann et al., 2020; Thottathil et al., 2022). These researcher hypothesized the occurrence of oxic CH_4 production by phytoplankton because CH_4 formation was spatially associated with phytoplankton blooms and calculated $\delta^{13}C$-CH_4 values were less negative than would be expected from methanogenic archaea. In this context, it is important to note that the range of phytoplanktonic $\delta^{13}C$-CH_{4_source} values obtained in our

laboratory study largely overlaps with $\delta^{13}C$-CH_4 values previously calculated for aquatic oxic CH_4 production derived from field investigations of several lakes (Hartmann et al., 2020; Sasakawa et al., 2008; Thottathil et al., 2022). Therefore, our isotopic results support the hypothesis that in aquatic environments under certain conditions direct formation of CH_4 by phytoplankton might fully or partly explain the observed elevated CH_4 concentrations in oxic surface layers which often is described as the "methane paradox". In addition, the $\delta^{13}C$-CH_{4_source} values of phytoplankton complement our understanding of isotopic carbon source signatures of CH_4 in the environment. In the context of the aquatic CH_4 paradox, the results could help to differentiate between CH_4 produced by methanogenic archaea in anoxic microsites, the intestinal tract of zooplankton or sedimentary sources, and those produced from phytoplankton as for example recently applied by Einzmann et al. (2022) to constrain sources and sinks of CH_4 in a small lake in Southern Germany.

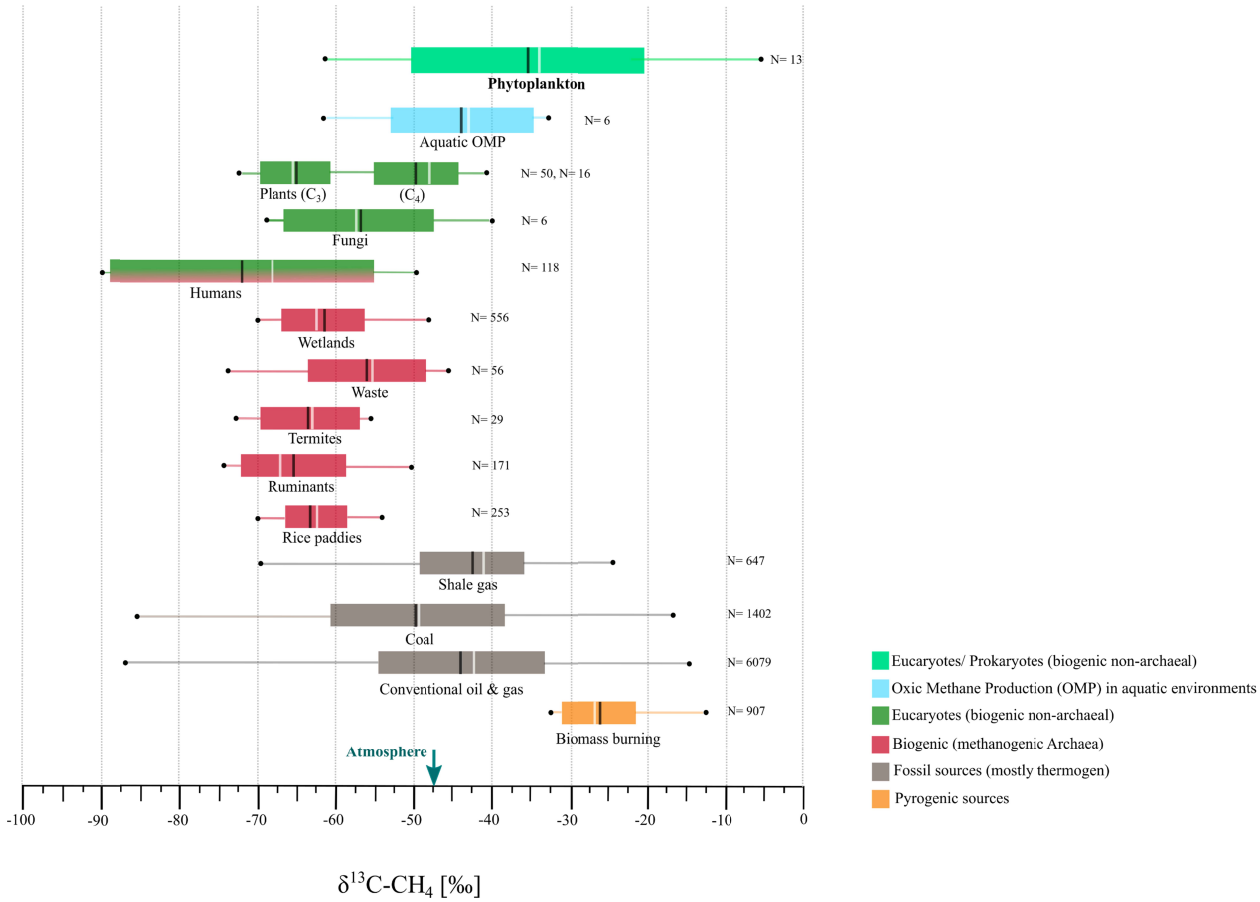

Figure 3. Typical range of $\delta^{13}C$-CH_{4_source} values of pyrogenic, fossil, biogenic and eukaryotic CH_4 sources. The box marks the SD and whiskers the min-max value. The mean and median are given by the black and white stripe within the box respectively. $\delta^{13}C$-CH_4 values of the thermogenic, pyrogenic and biogenic sources represent values from many individual studies summarized by Sherwood et al. (2017) which is currently the most comprehensive data set with respect to CH_4 source signature values. The $\delta^{13}C$-CH_4 value of plants were taken from Keppler et al. (2006) and Vigano et al. (2009) and the ones of fungi and humans from Keppler et al. (2016) and Schroll et al. (2020). $\delta^{13}C$-CH_4 values calculated for aquatic oxic CH_4 production (OMP) derived from lake and ocean field studies are taken from Thottathil et al. (2022), Holmes et al.

(2000) and Sasakawa et al. (2008). The $\delta^{13}C\text{-}CH_{4\_source}$ value of phytoplankton are summarized from both section 2.1 and Figure S3. Detailed information regarding classification of CH_4 can be found in Boros & Keppler (2018), Conrad (2009), Etiope & Sherwood Lollar (2013), Kirschke et al. (2013) and Saunois et al. (2016).

2.3 Potential contribution of phytoplankton to CH_4 supersaturated SML

To assess the potential environmental relevance of the isotope data of phytoplankton obtained by the laboratory experiments, we compiled the available isotope data for POC and $\delta^{13}C\text{-}CH_4$ values of CH_4 supersaturated SMLs reported from field studies of oceans and lakes (e.g., Forster et al., 2009; Grossart et al., 2011; Günthel et al., 2019; Hartmann et al., 2020; Scranton & Brewer, 1977; Weber et al., 2019).

We assume that $\delta^{13}C\text{-}CH_4$ values of phytoplankton depend on the $\delta^{13}C$-POC values according to equation 1

$$\delta^{13}C\text{-}CH_4 = \delta^{13}C\text{-}POC + \Delta^{13}C_{CH_4/POC}\,, \qquad (1)$$

where $\Delta^{13}C_{CH4/POC}$ is the isotopic difference associated with CH_4 release from POC ($\varepsilon_{CH4/POC} \approx \Delta^{13}C_{CH4/POC} = \delta^{13}C\text{-}CH_4 - \delta^{13}C\text{-}POC$). Therefore, $\delta^{13}C$-POC values and the isotope difference associated with the release of CH_4 from POC are fundamental for the evaluation of laboratory $\delta^{13}C\text{-}CH_4$ values with regard to their environmental relevance. A comprehensive compilation of $\delta^{13}C$-POC data of the world ocean has been provided by Goericke and Fry (1994). Most $\delta^{13}C$-POC values range from -28 ‰ to -18 ‰ with even lower values in the polar regions (see Goericke & Fry, 1994 and references inside). In this study, the $\delta^{13}C$-POC values of the investigated phytoplankton species range from ≈ -26 ‰ to -19 ‰ (Table S1) and thus reflect the range of $\delta^{13}C$-POC values typically found in marine environments. However, it should be noted, that the $\delta^{13}C$-POC values from oceanic POC samples are considered to reflect the carbon of the phytoplankton and are therefore often used as its proxy, but may also contain carbon from heterotrophic organisms or detritus, which may have distinct $\delta^{13}C$-POC values (Hansman & Sessions, 2016; Marty & Planas, 2008). An alternative biomarker and possibly better proxy for haptophytes in the ocean, are alkenone lipids synthesized by the haptophytes *E. huxleyi* and *Gephyrocapsa oceanica* (e.g., Bidigare et al., 1997; Popp et al., 1989). $\delta^{13}C$-POC values of haptophytes, estimated from alkenone lipids, globally range from -28.7 ± 1.2 ‰ to -21.5 ± 1.6 ‰ with the Santa Monica Basin and Peru Upwelling Zone showing the lowest and highest values, respectively (Table 3 in Bidigare et al., 1997). The reported range fits well with $\delta^{13}C$-POC data of the three haptophyte species investigated in our study (Table S1).

Based on the reported $\delta^{13}C$-POC values of natural haptophyte populations from the literature and $\Delta^{13}C_{CH4/POC}$ values established from our laboratory-grown haptophytes, using equation 1, natural haptophyte populations could generate $\delta^{13}C\text{-}CH_4$ values ranging from -49.2 ‰ to -23.6 ‰ within the SML. Analogously, by using the $\delta^{13}C$-POC values reported by Goericke & Fry (1994) for cyanobacterial populations and $\Delta^{13}C_{CH4/POC}$ values calculated from our experiments lead to $\delta^{13}C\text{-}CH_4$ values ranging from -56 ‰ to -22 ‰.

The next step is to compare the theoretical calculated data with field observations. Yet, only a few studies reporting $\delta^{13}C$-CH_4 values of CH_4 dissolved in the SML of seawater are available in the literature (Florez-Leiva et al., 2013; Holmes et al., 2000; Sasakawa et al., 2008; Yoshikawa et al., 2014), showing that the SML seawater is typically supersaturated with ^{13}C-enriched CH_4, relative to atmospheric values of around -47 ‰. It should be emphasized that $\delta^{13}C$-CH_4 values measured in the SML do not necessarily reflect their isotopic source value, since microbial CH_4 oxidation, input from lateral or sub-thermocline water masses and atmospheric release potentially modulate $\delta^{13}C$-CH_4 values (Reeburgh, 2007; Holmes et al., 2000; Sasakawa et al., 2008). For this reason, isotopic CH_4 source values need to be estimated by application of thorough mass balances. In this way, the $\delta^{13}C$-CH_{4_source} values maintaining CH_4 supersaturation were estimated to be -42.5 ‰ to -43 ‰ and -33 ‰ within the SML of the tropical and northwestern North Pacific respectively (Holmes et al., 2000; Sasakawa et al., 2008). These values are in good agreement with the above estimated range of $\delta^{13}C$-CH_4 source values for the six phytoplankton species investigated in our study. Thus, natural populations of phytoplankton are likely to be responsible for the ^{13}C-enriched CH_4 reported for the SML by Holmes et al. (2000) and Sasakawa et al. (2008).

Similar to the observation of oxic CH_4 production in the surface waters of oceans, there has been a controversial discussion about the occurrence of CH_4 formation in the epilimnion of lakes (Bižić et al., 2020b; Encinas Fernández et al., 2016; Grossart et al., 2011; Günthel et al., 2020; Hartmann et al., 2020; Tang et al., 2014, 2016; Peeters et al., 2019). A comprehensive data set of $\delta^{13}C$-CH_4 values of lake water has recently been provided for Lake Stechlin in Germany (Hartmann et al., 2020) and five lakes in Canada (Thottathil et al., 2022).

Based on the stable carbon isotope mass balance of CH_4 produced and the correlation between CH_4 and chlorophyll, the research teams suggested phytoplanktonic CH_4 production as the most likely source to explain the CH_4 oversaturation in the epilimnion during spring and summer. This hypothesis has recently been strongly supported by Perez-Coronel & Beman (2022) that associated aerobic CH_4 production with (bacterio)chlorophyll metabolism and photosynthesis. $\delta^{13}C$-CH_{4_source} values of oxic CH_4 production in surface water were distinct from the much more negative $\delta^{13}C$-CH_4 values measured in sediment pore water produced by methanogenic archaea (Thottathil et al., 2022; Hartmann et al., 2020). In the epilimnion of Lake Stechlin in Germany $\delta^{13}C$-CH_{4_source} values from oxic CH_4 formation during spring/summer were found to be less negative than -50 ‰ (Hartmann et al., 2020). A similar isotope pattern, i.e. an enrichment of ^{13}C in CH_4 relative to other sources, was also found by Thottathil et al. (2022). In four out of the five studied Canadian Shield lakes, $\delta^{13}C$-CH_{4_source} values of oxic CH_4 production, leading to CH_4 oversaturated surface waters during the summer period, ranged from -47 ‰ to -38 ‰. Therefore, a contribution of phytoplankton to the observed $\delta^{13}C$-CH_{4_source} values in the oversaturated oxic surface waters is greatly supported by our laboratory culture experiments as we found $\delta^{13}C$-CH_{4_source} values of the thirteen phytoplankton species ranging from -61.4 ‰ to -5.4 ‰ (median value -33.8 ‰). These data include five freshwater phytoplankton species (Figure S3) grown with $\delta^{13}C$-DIC values ≈ -4 ‰ (Text S7), which is within the natural various of $\delta^{13}C$-DIC values in lakes (Bade et al., 2004). Thus, based on the $\delta^{13}C$-DIC values, and assuming a dependence between the isotopic composition of the carbon precursor and the $\delta^{13}C$-CH_{4_source} values as described above, the $\delta^{13}C$-CH_{4_source} values of laboratory grown freshwater phytoplankton could be ecologically relevant. Although microbial consumption of CH_4 might be also involved in increasing $\delta^{13}C$-CH_4 values in the surface waters we strongly suggest that direct

formation of CH_4 by phytoplankton contributes substantially to the oxic CH_4 formation in the epilimnion of lakes during the growth period of these organisms.

5 Conclusions

Further insights into the CH_4 formation by phytoplankton were provided by determining stable carbon isotopic fractionation ($\varepsilon_{CH4/POC}$ values) and source signatures of CH_4 emitted by three marine haptophite algal and three cyanobacterial species. The observed isotopic fractionation suggests that different source substrates of CH_4 and/or pathways were involved in the CH_4 formation by the investigated species. The isotopic patterns suggest that in the absence of abiotic and thermogenic CH_4 sources, CH_4 released by phytoplankton can be clearly distinguished from CH_4 produced by methanogenic archaea, as phytoplankton exhibits significantly less negative $\delta^{13}C$-CH_4 values. Based on the comparison of stable isotope data from phytoplankton experiments with isotope data reported from field measurements in aquatic environments, we conclude that algal and cyanobacterial populations may indeed contribute to the CH_4 observed in the SML of oceans and lakes. However, more isotopic data than currently available is required to better distinguish between different CH_4 sources and sinks in aquatic systems. In this context, future applications of two-dimensional isotope studies including $\delta^{13}C$ and $\delta^{2}H$ values and even clumped isotope techniques but also in combination with metagenomic and metatranscriptomic data might be promising tools to allow for better differentiation between sources and sinks of CH_4.

Conflict of Interest

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

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Open Research

The data of this article will be made available after review but before publication via heiDATA, which is an institutional repository for research data of the Heidelberg University of the UFZ. A doi (digital object identifier) will be assigned and included in the last version of the manuscript.

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Supporting Information for

Stable Carbon Isotope Signature of Methane Released from Phytoplankton

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Figure S3 to Keeling plots of five limnic cyanobacteria (a, c, d, f, g) and two terrestrial cyanobacterial species (b, e).

Table S1 to δ^{13}C-POC [‰] values of phytoplankton species.

Introduction

The δ^{13}C-CH_{4_source} values from the three marine algae cultures (*E. huxleyi, Chrysochromulina* sp. and *P. globosa*) and three marine cyanobacterial cultures *(Prochlorococcus marinus* and two stains of *Synechococcus*) were determined by independent experiments using the Keeling plot technique. The stable carbon isotope composition of the phytoplankton POC (δ^{13}C-POC values) were recorded and the apparent isotope fractionation during POC and CH_4 formation was calculated. The experimental setup, measuring techniques and the calculation of the apparent fractionation are described in the following. In addition, δ^{13}C-CH_{4_source} values were determined using Keeling plots from five limnic and two terrestrial cyanobacteria incubation experiments previously published in Bižić et al. (2020). In addition, we determined the δ^{13}C-DIC values of the culture medium of these cultures. Keeling plots and a brief description of the experiments are included in these appendices.

Text S1 Culture and cultivation conditions.

The haptophyte algal species, *E. huxleyi* RCC 1216 was obtained from the Roscoff Culture Collection (http://roscoff-culture-collection.org/; last access: 2 December 2020) *P. globosa* PLY 575, and *Chrysochromulina* sp. PLY 307 were obtained from the Marine Biological Association of the United Kingdom (https://www.mba.ac.uk/facilities/culture-collection last access: 22 December 2022). *Prochlorococcus marinus* MIT 9313, *Synechococcus* WH 7803 and WH 8102 were obtained from Haifa University, Laboratory of Dr. Daniel Sher. All cultures grew in sterile, controlled laboratory conditions under a 16/8 h light-dark cycle and in sterile filtered (0.2 µm Ø pore size) natural North Sea seawater (sampled off Helgoland, Germany) enriched in nutrients according to F/2 medium (Guillard and Ryther, 1962). Cyanobacteria grew at22.5 °C with a light intensity of ≈ 100 µmol m^{-2} s^{-1} and alga cultures at 20 °C with ≈ 450 µmol m^{-2} s^{-1}.

Text S2 The experimental set-up

The experimental set-up for each algae and cyanobacteria species consisted of several cultivation groups that differed from each other only in their initial biomass density, resulting in a biomass dilution series. In this way, a continuous increase in headspace CH_4 mass, which is statistically ideal for the application of Keeling plots was

obtained. A culture-free control group (medium only) was included. Figure S1 shows the experimental approach, with the yellow box indicating the number of cell dilution steps and repetitions for the different algal and cyanobacteria species. All flasks of a dilution series were simultaneously sealed under ambient air and thus contained the same CH_4 background. The cultures grew in crimped serum bottles with a medium volume of 140 mL and 20 mL headspace. After one, two or six days (depending on the growth rates of the respective species) of incubation, the flasks of each species experiment were sampled simultaneously and the CH_4 mass (5 mL of headspace) and the $\delta^{13}C$-CH_4 values (15 mL of headspace) were analyzed. To maintain the headspace pressure while drawing the gas sample from the headspace, sample volume was displaced by seawater injected into the flasks with a syringe. The added volume was taken into account when determining the cell density. The obtained CH_4 mass and isotope data were then used to determine the $\delta^{13}C$-CH_4 values of the CH_4 source of each species by applying Keeling plots (Keeling, 1958). This technique is required for source identification, since the experimental set-up contained CH_4 background and the measured $\delta^{13}C$ values are a mixture of the CH_4 produced by the phytoplankton and background methane. For a detailed discussion regarding this subject, please refer to Pataki et al. (2003) and Keppler et al. (2016).

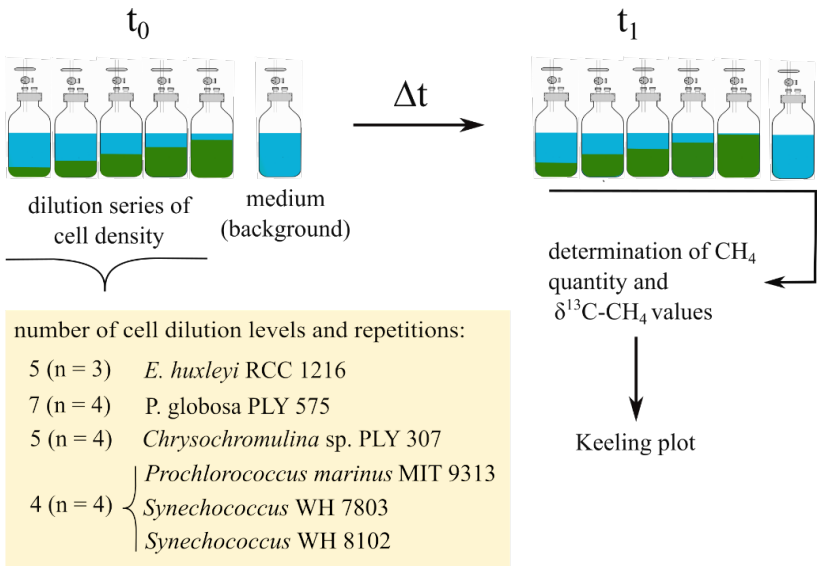

Figure S1. Experimental set up and the Keeling plot technique to determine $\delta^{13}C$-CH_{4_source} values of the CH_4 source of phytoplankton cultures. See the text of this section for further explanations.

Text S3 Determination of the stable isotope composition of the algae POC

For the determination of the stable isotope composition of phytoplankton POC (δ^{13}C-POC values), cultures were filtered at the end of the experiment on pre-combusted (500 °C, 5 h) glass fiber filters (Whatman, GF/F 25 mm Ø filters, 0.4–0.6 µm Ø pore size). Filter samples were dried for 24 h at 50 °C and fumed with saturated hydrochloric acid to remove all inorganic carbon afterwards. To prepare the samples for the measurements, they were encapsulated in tinplate. For practical reasons, we used two different measurement systems. For representative POC values, ≥ 45% of all culture flasks were determined.

The δ^{13}C-POC values of *E. huxleyi* RCC 1216, *P. globosa* PLY 575 and *Chrysochromulina* sp. PLY 307 were measured in duplicate with a mass spectrometer (ANCA-SL 20-20). Isoleucine with a δ^{13}C-POC of -12.6 ± 0.3 ‰ was used as working standard. (The mean and standard deviation is based on three measurements of working standard). All δ^{13}C-POC values were calibrated against standard material with δ^{13}C-POC of -26.4 ‰ (USGS40- standard, NIST, Gaithersburg, USA).

To determine the δ^{13}C-POC values of *P. marinus* MIT 9313, *Synechococcus* WH 7803 and WH 8102 the samples underwent total combustion at 920 °C under Helium atmosphere with additional oxygen (PyroCube, Elementar DE, Langenselbold, Germany). The CO_2 was trapped and purged from other elements oxidation products and its amount measured by thermal conductivity detection in the gas stream. $^{13}C/^{12}C$ ratios were determined in an isotope ratio mass spectrometer (Isoprime, Elementar UK, Stockport, UK) and calibrated against international standards (CH3, CH6) obtained from IAEA (Vienna, Austria). All isotope ratios were expressed as delta values ($\delta^{13}C_{VPDB}$) after Craig correction (Craig, 1957), i.e. as per mil difference in detected isotope ratios ($^{13}C/^{12}C$) against VPDB (Eq. S3).

The obtained δ^{13}C-POC and $\delta^{13}C\text{-}CH_{4\_source}$ values of the phytoplankton species were used to calculate the apparent isotopic fractionation (ε) of stable carbon isotopes between the different carbon species. The apparent isotopic fractionation during CH_4 formation ($\varepsilon_{CH4/POC}$) was calculated with regard to the algae POC due to equation S1.

$$\varepsilon_{CH_4/POC} = \frac{(\delta^{13}C\text{-}CH_4 + 1)}{(\delta^{13}C\text{-}POC + 1)} - 1 \qquad \text{Eq. S1}$$

The standard error of the isotopic fractionation was calculated using Gaussian error propagation by partial derivation of the individual error variables.

Text S4 Determination of CH_4 quantity using GC-FID

The CH_4 mass [ng] was determined for the entire incubation flask (i.e., CH_4 dissolved in the culture medium and CH_4 of the headspace volume). For this determination, a sample was taken from the headspace using a gas-tight syringe. Methane was analyzed using a gas chromatograph with FID detector (GC-FID, GC-14B, Shimadzu, Japan) and a 2 m column, (Ø = 3.175 mm inner diameter) packed with molecular sieve 5A 60/80 mesh (Supelco). The method was calibrated with two reference standards (2192 ppbv, 9837 ppbv CH_4 mixing ratio, average analytical standard deviation 5 ppbv and 53 ppbv, respectively, n = 3).

Prior to gas sampling, the pressure of the headspace was measured (GMSD 1.3 BA, Greisinger). The CH_4 mass was determined by its mixing ratio (x) and the ideal gas law (Equation S2)

$$m_{CH_4} = M_{CH_4} \times x_{CH_4} \frac{p \times V}{R \times T} , \qquad \text{Eq. S2}$$

where M is molar mass, p is pressure, T is temperature, R is the ideal gas constant, and V is volume. The concentration of dissolved CH_4 was calculated according to (Wiesenburg & Guinasso, 1979).

Text S5 Determination of stable carbon isotope values of CH_4 using GC-C-IRMS

Stable carbon isotope values of CH_4 in the headspace samples were analyzed by GC-C-IRMS. The GC-C-IRMS system consisted of a cryogenic preconcentration unit that was connected to a HP 6890N GC (Agilent Technologies, Santa Clara, USA) which is linked to the IRMS (Deltaplus XL, Thermo Finnigan, Bremen, Germany) by an oxidation reactor (ceramic tube, with oxygen activated Cu wire and /Ni/Pt wires serving as catalysts inside) and a GC Combustion III Interface (ThermoQuest Finnigan). For a detailed description of the $\delta^{13}C$-CH_4 measurements by GC-C-IRMS and technical details of the pre-concentration system, refer to previous studies by Althoff (2012), Comba et al. (2018) and Laukenmann et al. (2010). Ultra-pure carbon dioxide (carbon dioxide 4.5, Messer, Germany) was used as the monitoring gas. All $\delta^{13}C$-CH_4 values were normalized using two CH_4 standards (H-iso1 and B-iso1-standard, isometric instruments, Victoria, Canada) with values of -23.9 ± 0.2 ‰ and -54.5 ± 0.2 ‰ by two-scale anchor calibration according to Paul et al. (2007). The average standard deviation of the analytical measurements was in the range of 0.1 ‰ to 0.3 ‰ (based on three repeated measurements of CH_4 working standards). All $\delta^{13}C$-CH_4 values are expressed in the conventional δ notation, in permille (‰) *vs.* Vienna Pee Dee Belemnite (VPDB), using equation:

$$\delta^{13}C = \frac{\left(\frac{^{13}C}{^{12}C}\right)_{sample}}{\left(\frac{^{13}C}{^{12}C}\right)_{standard}} - 1 \qquad \text{Eq. S3}$$

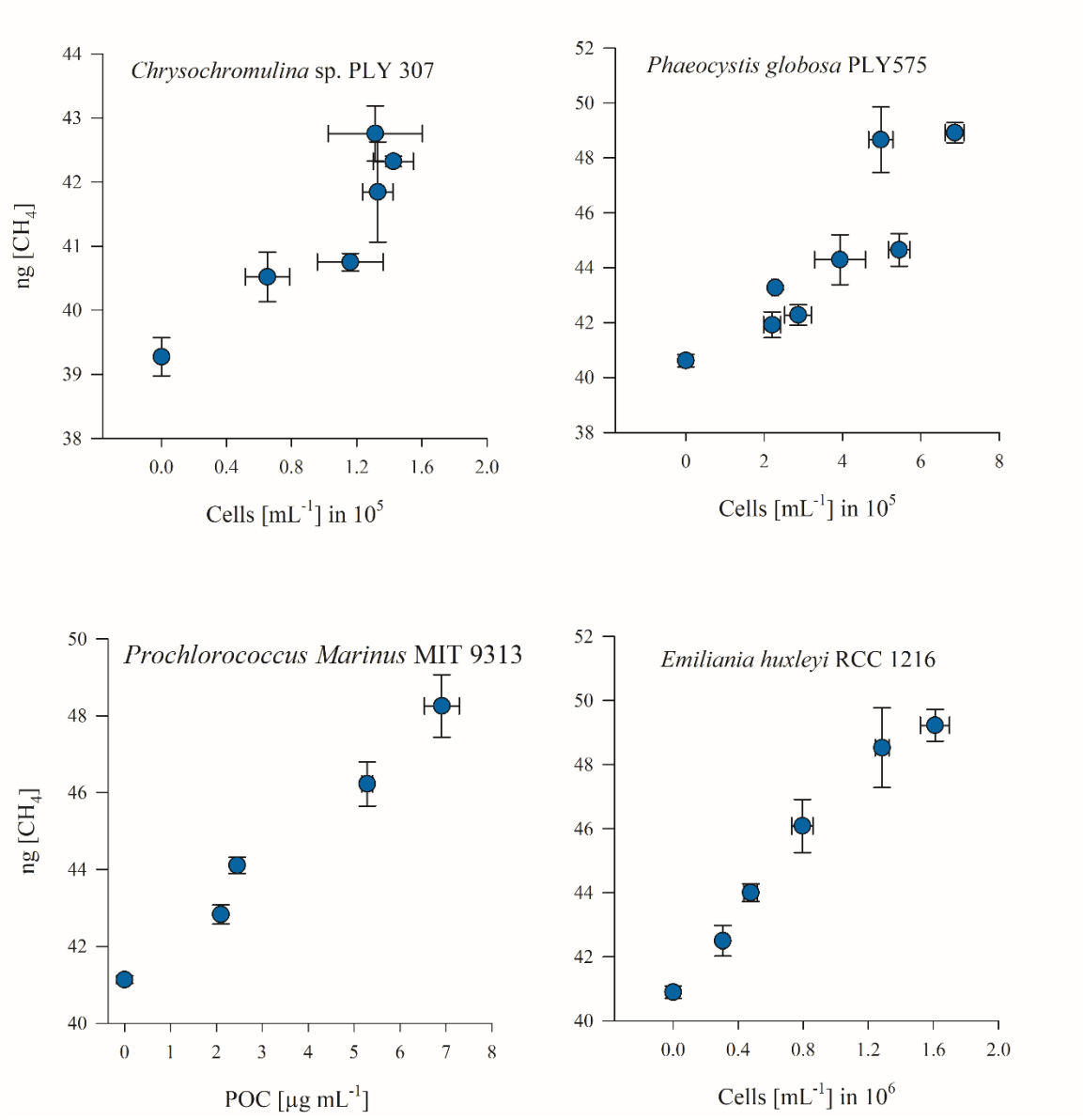

Figure S2. Correlation between CH_4 production and phytoplankton biomass. Please note that data for *Synechococcus* sp. are not shown. For these cultures, it was not possible to detach the biomass from the vessel wall without leaving any biomass residue.

Species	δ^{13}C-POC [‰]	n
Chrysochromulina sp.	-24.8 ± 1.5	9
E. huxleyi	-21.6 ± 0.6	9
P. globosa	-23.5 ± 0.4	11
Prochlorococcus marinus MIT 9313	-26.3 ± 0.3	10
Synechococcus WH 8102	-19.8 ± 0.4	10
Synechococcus WH 7803	-24.2 ± 0.7	10

Table S1. δ^{13}C-POC [‰] values of phytoplankton species.

Text S6 Determination of stable carbon isotope source values of CH_4 from previously published cyanobacterial incubation experiments.

We provide an additional dataset of calculated stable carbon isotope values of CH_4 emitted by cyanobacterial cultures. The experiments were performed in our laboratory and the δ^{13}C-CH_4 values were previously published in Figure 1 in Bižić et al. (2020), while the corresponding CH_4 mass values were not included in the mentioned publication and are presented here for the first time as reciprocal values. A detailed methodological description can be found in Bižić et al. (2020). In short, the authors incubated cyanobacteria in flasks containing medium and headspace with ambient background CH_4. The δ^{13}C-CH_4 values and CH_4 mass within the headspace were determined at the end of incubation. In the present study, we generated Keeling plots using δ^{13}C-CH_4 and CH_4 mass values of the treatments in which Bižić et al. (2020) cultured cyanobacteria with DIC corresponding to the natural abundance of ^{13}C (δ^{13}C-DIC = -4 ‰, see text below for methodical description of DIC determination). This corresponds to treatments "M": non-inoculated growth medium and "C": Growth medium with cyanobacteria culture, in Figure 1 in Bižić et al., 2020. The Keeling plots and the resulting δ^{13}C-CH_{4_source} values are shown in Figure S3.

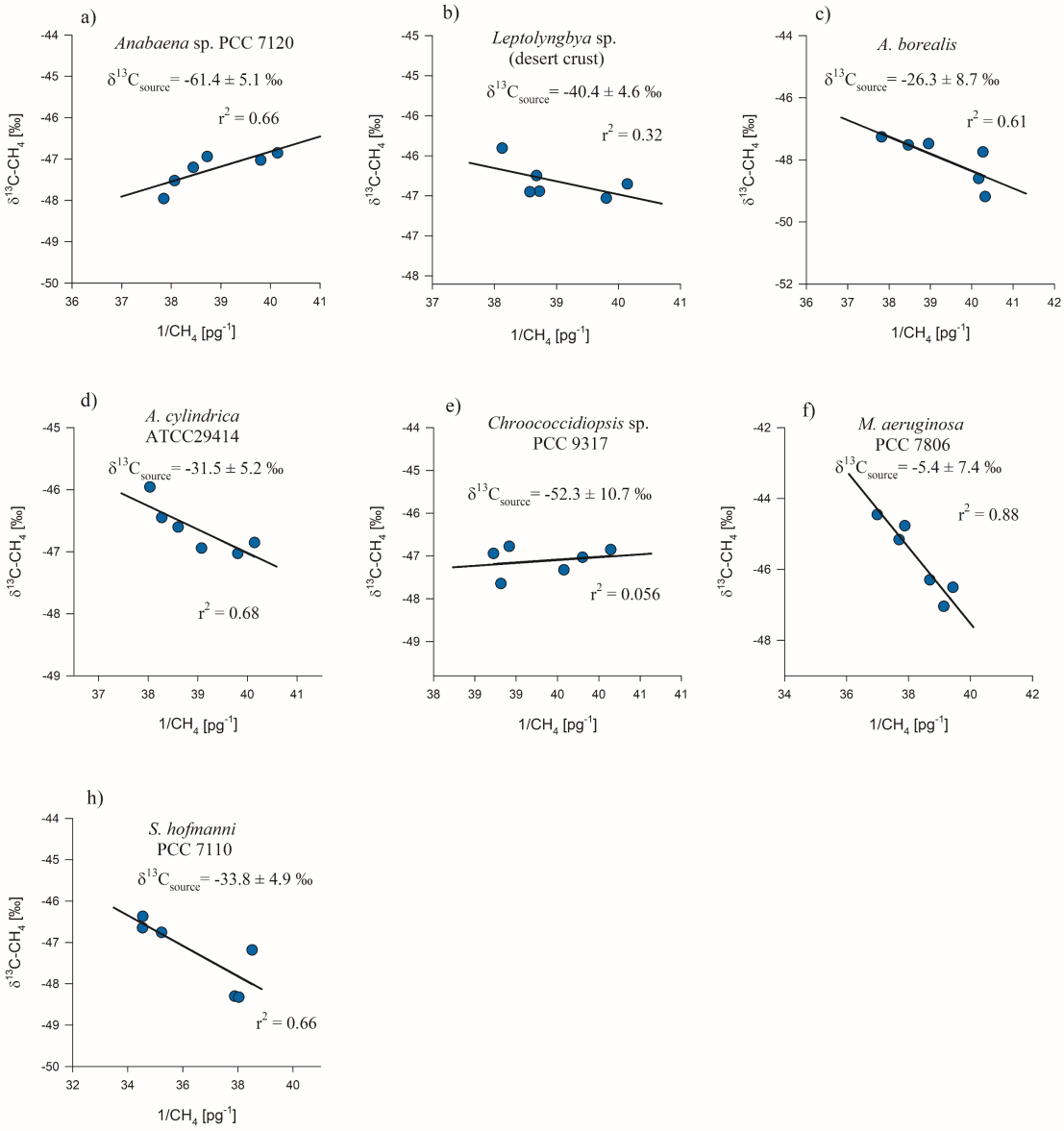

Figure S3. Keeling plots of five limnic cyanobacteria (a, c, d, f, g) and two terrestrial cyanobacterial species (b, e). $\delta^{13}C\text{-}CH_{4\_source}$ values used to generate the Keeling plots were obtained from Bižić et al. (2020). The calculated $\delta^{13}C\text{-}CH_{4\_source}$ values of each species are given by the extrapolated intercept with the y-axis CH_4 ($1/[CH_4] = 0$). The correlation between CH_4 mass (given as reciprocal) and the $\delta^{13}C\text{-}CH_4$ values of all incubations is shown in detail for each plot. The six data points are collected of each species are from independent incubation experiments.

Text S7 Determination of δ^{13}C-DIC values

We determined the δ^{13}C-DIC values of the culture medium (data were previously not shown in Bižić et al., 2020). To determine the isotopic composition of DIC, an aliquot of the medium (BG11 medium, Rippka et al. 1979, DIC = 0.4 mM, enriched by added $NaHCO_3$; pH 7.0) was transferred bubble-free into a 12 mL vial and sealed with a septum. The vial was inverted and a headspace of 8 mL N_2 was established using two syringe needles: N_2 gas flowed through one needle to introduce the headspace of the inverted vial, while displaced water exited the vial through the second needle. Afterwards, the entire DIC was converted into CO_2 by adding an excess of hydrochloric acid through the septum. To determinate δ^{13}C-DIC values, the δ^{13}C values of generated CO_2 were analyzed by transferring 2 mL headspace gas to the IRMS described above (Text S5). Deviating from this instrumental description, the sample was directly injected into the GC using an autosampler and was transferred to the IRMS under bypassing the oxidation reactor.

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