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1	Low apparent $\Delta^{12}CH_2D_2$ in microbialgenic methane
2	result from combinatorial isotope effects
3 4	Lina Taenzer ^a , Jabrane Labidi ^b , Andrew L. Masterson ^c , Xiahong Feng ^d , Douglas Rumble III ^e , Edward D. Young ^f , William D. Leavitt ^g
5	$correspondence:\ william.d.leavitt@dartmouth.edu,\ eyoung@epss.ucla.edu$
6 7 9 10 11 12 13	^a Department of Earth Sciences, Dartmouth College; Present Address: MIT-WHOI ^b Department of Earth, Planetary, and Space Sciences, UCLA; Present Address: Institut de Physique du Globe de Paris ^c Department of Earth & Planetary Sciences, Northwestern University ^d Department of Earth Sciences, Dartmouth College ^e The Geophysical Lab, Carnegie Institution for Science ^f Department of Earth, Planetary, and Space Sciences, UCLA ^g Department of Earth Sciences, Department of Biological Sciences, Department of Chemistry, Dartmouth College
11 12 13 14	^c The Geophysical Lab, Carnegie Institution for Science ^f Department of Earth, Planetary, and Space Sciences, UCLA ^g Department of Earth Sciences, Department of Biological Sciences, Department of Chemistry, Dartmouth College

15 Abstract

Methane generated by microorganisms is most often depleted in the doubly substituted isotopologue ${}^{12}CH_2D_2$ relative to the stochastic reference distribution. To constrain the controls on depleted $\Delta^{12}CH_2D_2$ values, we experimentally isolated the root cause with microorganisms that produce methane from methylphosphonate via the C-P lyase pathway. This mechanism of methane production preserves the three hydrogens from methylphosphonate and adds one hydrogen from water. When maintaining the same methylphosphonate source, but varying the D/H composition of growth medium water, we observed significant shifts in methane $\Delta^{12}CH_2D_2$ values, but little to no change in Δ^{13} CH₃D values. We reproduced these observations with a model that considers only the combinatorial isotope effect. The variation in Δ^{12} CH₂D₂ values of product methane resulted from the differences in D/H between reactants water and methylphosphonate. This work validates the hypothesis that combinatorial effects can strongly influence methane $\Delta^{12}CH_2D_2$ values, and must be considered for low temperature, abiotic or biotic systems where methane hydrogen is derived from multiple reservoirs.

¹⁶ Keywords: methane, clumped isotopes, methanogenesis, C-P lyase

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17 1. Introduction

Multiply-substituted ("clumped") isotopologues are powerful tracers of 18 molecular formation reactions (Eiler and Schauble, 2004; Stolper et al., 2014; 19 Wang et al., 2015; Yeung et al., 2015; Young et al., 2017; Yeung et al., 2017; 20 Popa et al., 2019). Exploring variations in the relative abundance of the two 21 doubly-substituted mass-18 isotopologues of methane, ¹²CH₂D₂ and ¹³CH₃D, 22 have provided promising constraints on provenance, even where bulk C and 23 H isotopic ratios $({}^{13}C/{}^{12}C, D/H)$ yielded ambiguous information as to source 24 and process (Young et al., 2017; Haghnegahdar et al., 2017; Young, 2019; 25 Giunta et al., 2019; Ash et al., 2019). The relative abundance of the two 26 mass-18 clumped isotopologues in a given population of methane molecules 27 formed at high temperature (> 1000 K) in thermodynamic equilibrium, are 28 approximated by a random distribution of all possible isotopologue combi-29 nations. This apportioning of isotopes is referred to as a "stochastic distri-30 bution," and provides the reference frame for reporting the relative abun-31 dances of clumped isotopologues (Eiler and Schauble, 2004). The abundance 32 of a given multiply-substituted isotopologue relative to the most abundant 33 isotopologue (e.g. ${}^{13}CH_3D/{}^{12}CH_4$) is reported as a fractional difference from 34 the stochastic relative abundances, Δ_i , where subscript *i* refers to the specific 35 clumped species, and Δ_i are reported in permil (%). This stochastic refer-36 ence frame highlights whether a process has favored or discriminated against 37 the formation of molecules with bonds containing multiple heavy isotopes 38 (e.g., ${}^{13}CH_3D$), rather than only differences in bulk isotope ratios. Under 39 equilibrium conditions at low temperatures (< 300 K), the stability associ-40 ated with bonds between heavy isotopes in a molecule increases, promoting 41 the formation of the isotopically clumped molecular species. As tempera-42 ture approaches infinity, this effect diminishes and the relative abundance of 43 multiply-substituted molecules decreases, approaching $\Delta_i = 0$. Under non-44 equilibrium conditions at low temperatures, departures from the stochastic 45 distribution may provide insights into the kinetics and reaction(s) of forma-46 tion for a given methane population's natural history. 47

⁴⁸ Methane produced by microorganisms is characterized by significant de-⁴⁹ pletion or "anti-clumping" in the Δ^{12} CH₂D₂ values by more than 20 to 50‰, ⁵⁰ relative to thermodynamic equilibrium (Young et al., 2017). These Δ^{12} CH₂D₂ deficits ⁵¹ are accompanied by negligible depletion in Δ^{13} CH₃D values (Figure 1). Sev-⁵² eral hypotheses have been put forward to explain these observed departures ⁵³ from thermodynamic equilibrium. The two hypotheses in the literature thus

far are: i) contributions from distinct pools of hydrogen with disparate D/H 54 ratios and/or differentially fractionated H sites during formation, and ii) 55 quantum tunneling of hydrogen during methane formation (Young et al., 56 2017; Yeung, 2016; Röckmann et al., 2016; Young, 2019; Cao et al., 2019). 57 The former refers to the so-called "combinatorial effect." The importance of 58 the combinatorial effect as a source of anti-clumping, wherein the measured 59 clumped isotopologue abundance is less than predicted by theory, was first 60 hypothesized during the study of molecular oxygen clumped isotopologues 61 (Yeung et al., 2015; Yeung, 2016; Röckmann et al., 2016) and was suggested 62 as relevant to microbially produced (microbialgenic) methane (Young et al., 63 2017). However, the combinatorial effect has not been directly tested or 64 demonstrated in any experimental study. While this effect can arise from 65 drawing on two or more reservoirs, it is not simply mixing in the general sense. 66 To interpret the significance of depleted (anti-clumped) Δ^{12} CH₂D₂ values re-67 quires a thorough understanding of if, when and how the combinatorial effect 68 is expressed. This understanding is essential to the application of clumped 69 isotope signatures as tracers of methane provenance, and extends to other 70 gasses that could hypothetically experience combinatorics in altering the rela-71 tive abundance of multiply substituted isotopologue ratios, such as molecular 72 oxygen ($\Delta^{18}O^{18}O$) or dinitrogen ($\Delta^{15}N^{15}N$). 73

To experimentally test for the combinatorial effect and quantify its in-74 fluence on $\Delta^{12}CH_2D_2$ values, we examined the bulk and clumped methane 75 isotopologue abundances produced by bacteria operating the C-P lyase path-76 way. This microbialgenic methane production pathway is related to phospho-77 rous acquisition and not core energy metabolism (White and Metcalf, 2004; 78 Sosa et al., 2019), the canonical anaerobic microbial methanogens (Valen-79 tine, 2011). This metabolism provides a unique opportunity to study the 80 combinatorial effect because this pathway incorporates hydrogen from two 81 distinct reservoirs during methane formation: three from the methyl group 82 of methylphosphonate and one from water (Kamat et al., 2011, 2013). More-83 over, this methane is generated by rapidly growing bacteria where the bulk 84 isotopic fractionations are independent of energy metabolism and growth 85 rate (Taenzer et al., 2020). By varying the D/H composition of the water in 86 which the bacteria grew and generated methane, we observed dramatic shifts 87 in $\Delta^{12}CH_2D_2$ with minimal effect on $\Delta^{13}CH_3D$. Our experimental and model 88 results together indicate that shifts in methane $\Delta^{12}CH_2D_2$ produced by the 89 C-P lyase pathway were primarily due to the relative differences in D/H 90 between water and methylphosphonate methyl hydrogens. The consistency 91



Figure 1: The distribution of laboratory axenic cultures (circles with crosses) and naturally-produced methane (open circles) by microbial methanogenesis in Δ^{12} CH₂D₂ vs. Δ^{13} CH₃D space. The curve representing thermodynamic equilibrium is shown for reference, annotated with temperatures. Calculations and values are from Young (2019) and references therein.

⁹² between model predicted and experimentally generated isotopologue abun ⁹³ dances demonstrates that the combinatorial effect can yield markedly nega-

⁹⁴ tive Δ^{12} CH₂D₂ values (below < -50%) with little influence on Δ^{13} CH₃D values

 $_{95}$ (<1%). Implications for the interpretation of experimental and natural methane

⁹⁶ clumped isotopologue studies are discussed.

97 2. Principles of the Combinatorial Effect

The stochastic distribution is the reference frame for reporting multiply 98 substituted (clumped) isotopologue abundances. It is defined by the most 99 probable abundance of the multiply-substituted isotopologue of interest as-100 suming that the isotopes comprising the molecules were randomly distributed 101 among all possible isotopologues. The stochastic reference is calculated by 102 equating fractional isotopic abundances with probabilities. To illustrate the 103 essence of the combinatorial effect and for simplicity we examine cases for the 104 formation of two diatomic molecules, carbon monoxide (CO) and molecular 105 oxygen (O_2) . 106

¹⁰⁷ The stochastic distribution for the relative abundance of the multiply-¹⁰⁸ substituted isotopologue ¹³C¹⁸O in a sample of carbon monoxide gas is cal-¹⁰⁹ culated as

$$x({}^{13}C{}^{18}O) = x({}^{13}C)x({}^{18}O)$$
(1)

where x^{13} C is the fractional abundance of 13 C relative to all carbon iso-110 topes by number (i.e., ${}^{13}C/({}^{12}C + {}^{13}C)$), $x^{18}O$ is the fractional abundance 111 of ¹⁸O relative to all oxygen isotopes (i.e., ${}^{18}O/({}^{16}O + {}^{17}O + {}^{18}O))$, and 112 $x(^{13}C^{18}O)$ is the fractional abundance of the $^{13}C^{18}O$ isotopologue relative 113 to all CO molecules. The ratio of this multiply-substituted isotopologue 114 to the most abundant isotopic species is therefore $x({}^{13}C{}^{18}O)/x({}^{12}C{}^{16}O)$. It 115 is common to express ratios of relative isotopologue fractions in terms of 116 the isotope ratios of their constituent elements. In this case, $x({}^{13}C{}^{18}O)/$ 117 $x({}^{12}C{}^{16}O) = ({}^{13}C/{}^{12}C)({}^{18}O/{}^{16}O) = {}^{13}R{}^{18}R$. Similarly, the stochastic frac-118 tional abundance of the multiply-substituted isotopologue of molecular oxy-119 gen (O_2) composed of two ¹⁸O atoms is 120

$$x({}^{18}O{}^{18}O) = x({}^{18}O)x({}^{18}O)$$
(2)

where the symbols are analogous to those in Equation 1. In this case $x({}^{18}O{}^{18}O) = ({}^{18}O{}^{16}O) = ({}^{18}O{}^{16}O) = {}^{18}R^2$.

For both ¹⁸O¹⁸O and ¹³C¹⁸O, the accuracy of the estimated stochas-123 tic distribution is dictated by the fidelity of the bulk isotope ratios (e.g., 124 ${}^{13}R = {}^{13}C/{}^{12}C$ and ${}^{18}R = {}^{18}O/{}^{16}O$ relative to these ratios at the time the 125 molecules formed, and the degree to which the sample separation chemistry 126 and mass-spectrometry can capture these ratios, free of subsequent fraction-127 ation effects. The cases of CO and O_2 represent contrasting examples of the 128 ability to reconstruct the actual isotope ratios of the constituent atoms dur-129 ing assembly of the molecules. In the case of CO, the isotopic compositions 130 of C and O unambiguously represent the isotope ratios of the constituent 131 atoms since carbon and oxygen are distinguishable; the analysis of carbon 132 monoxide yields ${}^{13}C/{}^{12}C$ and ${}^{18}O/{}^{16}O$ bulk ratios that faithfully record the 133 actual isotopic compositions of the two constituent atoms (there is no confus-134 ing C and O, see Figure 2). In contrast, in the case of O_2 , the isotopologue of 135 interest is composed of two atoms of the same element and so the molecular 136 positions can not be distinguished from one another. Therefore, despite the 137 fact that the two atoms comprising the O_2 molecule may have originated 138 from different reservoirs with distinct ${}^{18}O/{}^{16}O$ ratios (Yeung et al., 2015), 139 the stochastic abundance of the ${}^{18}O{}^{18}O$ molecule is calculated on the basis 140 of the average ${}^{18}O/{}^{16}O$ ratio. That is, the ${}^{18}O/{}^{16}O$ of the O₂ sample reflects 141 an average of the two individual molecular sites and their source reservoirs. 142 By necessity the $x({}^{18}O{}^{18}O) / x({}^{16}O{}^{16}O) = {}^{18}R^2$ value for the stochastic iso-143 topologue ratio calculation assumes that the two molecular positions were 144 formed from identical oxygen isotope ratios of ${}^{18}R$. In reality, the oxygen 145 isotope ratio is the average of two potentially distinct ratios, ${}^{18}R_1$ and ${}^{18}R_2$, 146 which individually contributed to the O_2 molecule, such that: 147

$$[x(^{18}O^{18}O)/x(^{16}O^{16}O)]_{\text{stochastic}} = \left(\frac{(^{18}R_1 + ^{18}R_2)}{2}\right)^2 \tag{3}$$

where subscripts 1 and 2 refer to two distinct oxygen reservoirs. The difference between using the actual constituent ratios ${}^{18}R_1{}^{18}R_2$ and using the average ratio $({}^{18}R_1 + {}^{18}R_2)/2$ (by necessity) to calculate the stochastic ratio for the calculation of $\Delta^{18}O^{18}O$ is a manifestation of the mathematical truism that

$$({}^{18}R_1)({}^{18}R_2) \le \left(\frac{({}^{18}R_1) + ({}^{18}R_2)}{2}\right)^2.$$
 (4)

¹⁵³ In particular, we have for the true value for the fractional departure in



Figure 2: Schematic illustrations showing the pairing of oxygen-oxygen or oxygen-carbon isotopes when molecules of O_2 or CO are formed, respectively. The potential for two separate reactant reservoirs to contribute atoms from pools of distinct isotopic composition is illustrated for each case. For CO, the oxygen and carbon reservoirs are always distinguishable by virtue of their different elemental identities. The composition of the C and O sources are reflected in the isotopic ratios of the product CO, offset by any fractionation, which can be individually traced. On the contrary, in the case of two oxygen reservoirs contributing to O_2 , only a single average isotopic composition can be determined for the product O_2 which obscures contributions from two separate, and potentially distinct oxygen sources and any fractionation between product and either of the sources.

 $x^{(18}O^{18}O)/x^{(16}O^{16}O)$ from stochastic

$$\Delta^{18} \mathcal{O}^{18} \mathcal{O} = \frac{[x(^{18}\mathcal{O}^{18}\mathcal{O})/x(^{16}\mathcal{O}^{16}\mathcal{O})]_{\text{sample}}}{(^{18}R_1)(^{18}R_2)} - 1$$
(5)

where "sample" refers to the measured isotopologue ratio. The $\Delta^{18}O^{18}O$ value from Equation 5 cannot be reconstructed *a priori*. Rather, the estimate obtained from the measured, average bulk isotopic composition of the O₂ gas itself is actually

$$\Delta^{18} \mathcal{O}^{18} \mathcal{O} = \frac{4[x(^{18}\mathcal{O}^{18}\mathcal{O})/x(^{16}\mathcal{O}^{16}\mathcal{O})]_{\text{sample}}}{\left(\left(^{18}R_1\right) + \left(^{18}R_2\right)\right)^2} - 1.$$
(6)

Only when ${}^{18}R_1 = {}^{18}R_2$ will the two estimates be equal. Since the left-hand 159 side of Equation 4 is the square of the geometric mean and the right-hand side 160 is the square of the arithmetic mean, the inequality in this simple example is 161 an expression of the well-known inequality of the geometric and arithmetic 162 means, and is a general result (Yeung, 2016). Comparing Equations 4, 5, 163 and 6 illustrates the general principle that when molecular positions are in-164 distinguishable, and the average isotope ratios rather than the site-specific 165 isotope ratios are all that is available for calculating the stochastic distri-166 bution of a multiply-substituted isotopologue, the stochastic abundance of 167 the isotopologue *i* is overestimated, resulting in a spuriously low Δ_i value. 168 The spuriously low and even negative Δ_i values are the result of the refer-169 ence frame (Figure 3). Yeung and colleagues showed that for the case of 170 multiply-substituted oxygen isotopologue in molecular oxygen that the mea-171 sured $\Delta^{18}O^{18}O$ diverged drastically from the stochastic prediction (Yeung 172 et al., 2015), and predicted that this is potentially due to two contributing 173 sources (reservoirs) of isotopically distinct oxygen – that is, the combinatorial 174 effect (Yeung, 2016). To date, however, no study has tested this experimen-175 tally for any other multiply substituted isotope system, be it oxygen, methane 176 or another. 177

Given these examples above, we predict the combinatorial effect is possible whenever a molecule composed of multiple isotopes of the same element is constructed from more than one isotopic pool. The source of the different pools may result from different isotope effects for each step involved in constructing the molecule, or from drawing on isotopically distinct reservoirs. Candidates include, but are not limited to, multiply substituted isotopologues of N₂, O₂, H₂, CH₄, and N₂O. Despite the established theoretical



Figure 3: An illustration of the combinatorial effect seen when plotting $\Delta^{18}O^{18}O$ as a function of the ratio of the isotopic compositions, R_1 and R_2 , of the distinct contributing oxygen reservoirs.

¹⁸⁵ impact of combinatorics in influencing clumped isotopologue Δ_i values, it ¹⁸⁶ has yet to be demonstrated unambiguously in the laboratory. Substantiat-¹⁸⁷ ing the existence of the combinatorial effect and quantifying its magnitude ¹⁸⁸ are prerequisites to interpreting existing and future clumped isotopologue ¹⁸⁹ signatures in molecules composed of multiple atoms of the same element.

¹⁹⁰ 3. Methods

¹⁹¹ 3.1. Microbial cultivation and gas production

The model microorganism *Pseudomonas stutzeri* strain HI00D01 (here-192 after, strain HI00D01) was cultivated following the protocols in our recent 193 study (Taenzer et al., 2020), with modifications to generate large enough 194 quantities of methane for clumped isotope analyses. For methane generation 195 experiments all sources of P were removed and the medium was amended 196 with methylphosphonic acid (aka MPn; Sigma-Aldrich, CAS Number 993-197 13-5) to a concentration of 2mM, with glucose (electron donor and carbon 198 source) to a concentration of 3g/L, and sodium nitrate (NaNO₃) used as 199 the terminal electron acceptor to a final concentration of 40mM. The growth 200 medium was filter-sterilized then transferred to 160mL, 1 or 5L borosilicate 201 bottles and vigorously degassed with ultra-high purity helium (UHP-He) for 202 one hour per liter. Cell pellets from aerobic cultures were re-suspended and 203 incubated on amended MPn and NaNO₃ media in 160mL butyl stoppered 204 serum bottles. After reaching exponential phase on the MPn-amended media 205 and positive head-space methane detection (via GC-FID), 1 or 5L cultures 206 were inoculated to an optical density (OD600) of 0.001 and incubated at 207 30°C in the dark. Medium for D-enriched water experiments was prepared 208 following the approach of Zhang and colleagues (Zhang et al., 2009), where 209 it was enriched by adding a calculated quantity of D_2O (Sigma-Aldrich, CAS) 210 Number 7789-20-0) to the stock media prior to UHP-Helium flushing and 211 sterilization. 212

The gaseous methane, dinitrogen, and carbon dioxide produced by strain 213 HI00D01 were captured into gas-impermeable 0.25, 1, or 4L Tedlar bags, 214 along with trace water vapor. The gas bags were built with straight thru 215 1/4 inch stainless steel tubing (GSB-P-1 Calibrated Instruments) to which 216 we fitted with a 1/4 inch stainless steel needle value by compression fitting 217 to seal the gas bags before and after sample collection. To allow sample 218 into the bag, we attached to the needle valve another 1/4" stub of stainless 219 tubing, followed by a tube-to-pipe adapter 1/4" compression to 1/8" NPT, 220

followed by an 1/8" NPT to 1/4-28 adapter to then a luer lock and finally 221 a threaded 18-G stainless steel dispensing needle (all plumbing parts from 222 McMaster-Carr or Swagelok). The needle was inserted through black butyl 223 stopper (GlasgerA€tebau Ochs GmbH) into the top of the bags through 224 plastic funnels that were added for stability. At the end of the incubations, 225 UHP-He sparged water was used to displace all remaining headspace into 226 the Tedlar bags, allowed to equilibrate, then sealed by the needle valves 227 and removed from experiment bottles, and the values plugged with metal 228 compression septa until preparation on the vacuum line. 220

230 3.2. Bulk isotope ratio measurements

Bulk carbon (δ^{13} C) and hydrogen (δ D) isotope compositions of methylphos-231 phonic acid (Sigma-Aldrich, CAS Number 993-13-5) were determined at the 232 Northwestern University Stable Isotope Laboratory. Briefly, the δ^{13} C value 233 of MPn was determined via EA-IRMS on a Costech 4010 Elemental An-234 alyzer, coupled to a Delta V Plus isotope ratio mass spectrometer via a 235 Conflo IV interface. Analyses were done in triplicate, and placed on the 236 VPDB-LSVEC scale via analysis of organic standards supplied by Indiana 237 University (acetanilide #1, urea #2a, and D-glucose) (Schimmelmann, 1991; 238 Qi and Coplen, 2011). The bulk hydrogen (δD) isotope composition of MPn 239 was determined via TC/EA-IRMS, operated at 1420°C, and coupled to a 240 Delta V Plus isotope ratio mass spectrometer via a Conflo IV. Analyses 241 were done in triplicate, and cross-referenced to the Ag-tube water isotope 242 standards supplied by the USGS (GISP2, VSMOW, and UC03). The aver-243 age composition of the non-exchangeable hydrogens on MPn (i.e., $R-CH_3$) 244 was determined by equilibration with D-enriched waters (2mL) in a custom-245 designed vacuum chamber modified from a Costech zero-blank auto-sampler. 246 Incubations were done at room temperature $(25^{\circ}C)$ for 6 days. At the end 247 of the equilibration, water vapor was pumped to <50 mTorr for 2 hours, 248 followed by subsequent TC/EA analyses with Ag-tube USGS standards as 249 above, following published methods (Qi and Coplen, 2011). 250

Isotopic analysis of the medium water was conducted at the Stable Isotope Laboratory at Dartmouth College following published procedures (Kopec et al., 2019). Briefly, water hydrogen isotopic ratios (δ D) were measured using the H-Device, in which water was reduced by hot chromium (850°C) and the resulting hydrogen gas was measured by an isotope ratio mass spectrometer (IRMS, Thermo Delta Plus XL). Isotopic ratios (D/H) are reported in

delta notation in permil (%) deviation from the international standard VS-257 MOW on the VSMOW-SLAP (Vienna Standard Mean Ocean Water, Stan-258 dard Light Antarctic Precipitation) scale. The measurement 1σ uncertainty 259 is 0.5% for δD , and the measured value was converted to the water isotope 260 equivalent by calibration with known standards. When samples were pre-261 sumed to be outside the range of the standards (e.g. for the enrichment 262 experiments), samples were first diluted gravimetrically with a water stan-263 dard of known composition. Uncertainty's due to dilution are accounted for 264 and reported in Table 1 as the propagated 1se. 265

The stable isotopic compositions of methane samples generated by the C-P lyase in cultures of strain HI00D01 were measured on an ultra-high mass resolution isotope ratio mass spectrometer (Panorama, Nu Instruments) as part of the measurements to determine Δ^{12} CH₂D₂ and Δ^{13} CH₃D.

270 3.3. Multiply-substituted isotopologue measurements

The abundance of the two multiply-substituted mass-18 isotopologues 271 of methane gas samples were measured on a Panorama (Nu Instruments) 272 ultra-high-resolution gas-source isotope ratio mass spectrometer housed in 273 the Department of Earth, Planetary, and Space Sciences at the University 274 of California Los Angeles. Detailed descriptions of the mass spectrometry 275 method were given by Young and colleagues (Young et al., 2016), and applied 276 in recent studies (Young et al., 2017; Haghnegahdar et al., 2017; Giunta et al., 277 2019; Ash et al., 2019; Young, 2019). 278

Methane sample gases were purified on a vacuum line interfaced with a gas 279 chromatograph (SRI GC-FID 8610) prior to isotopic analysis. This method 280 was previously described in Young et. al (2016). Modification to the pub-281 lished procedures were as follows. The Tedlar gas bag holding the C-P lyase 282 generated methane gas (mixed with UHP He, water vapor, and the other 283 metabolic products N_2 and CO_2) was connected to the line with compression 284 fittings and PTFE ferrules. Prior to gas introduction, the hydrocarbon-free 285 vacuum line was evacuated to at least 4.0×10^{-7} mbar. Sample gas was in-286 troduced from the bag to the line in aliquots of 1000 mbar into a calibrated 287 50cc volume. Water vapor was trapped in a U-trap by ethanol-liquid nitro-288 gen (LN_2) slurry at -80°C. The rest of the sample gas was then trapped on 289 silica gel in a U-trap at LN_2 temperature for 10min, after which the non-290 condensable He was slowly pumped away. The methane aliquot was then 291 cryofocused to remove the N_2 and CO_2 via GC and re-trapping on silica 292

gel as previously described (Young et al., 2017). Due to the significant par-293 tial pressure of N_2 relative to methane, and because complete separation of 294 methane from N_2 was not achieved on the first pass through the GC, mul-295 tiple aliquots were first passed though the GC, cryofocused, and co-trapped 296 onto the same silica gel in a single glass cold-finger (6 to 7 GC-passes per 297 sample bag). Once the requisite sample size of methane was captured (> 40) 298 micromoles), the combined sample was once again cryofocused and passed 299 through the GC a final time to remove trace N_2 . The purified methane was 300 then transferred to the Panorama inlet system for the bulk and clumped 301 isotope ratio analyses following published protocols (Young et al., 2017). 302

303 3.4. Isotope notation

The isotopic compositions of carbon and hydrogen are reported as deviations from the carbon and hydrogen reference materials Vienna Peedee Belemnite and Vienna Standard Mean Ocean Water (VPDB and VSMOW, respectively). Standard delta notation is used to express the fractional differences:

$$\delta^{13}C = 10^3 \left(\frac{({}^{13}C/{}^{12}C)_{\text{sample}}}{({}^{13}C/{}^{12}C)_{\text{VPDB}}} - 1 \right)$$
(7)

309 and

$$\delta \mathbf{D} = 10^3 \left(\frac{(\mathrm{D/H})_{\mathrm{sample}}}{(\mathrm{D/H})_{\mathrm{VSMOW}}} - 1 \right)$$
(8)

where all values are given in permil (‰), as shown. The relative abundances of the two multiply-substituted mass-18 isotopologues of methane are reported relative to the stochastic reference frame using the Δ_i notation, also in permil, where Δ^{13} CH₃D and Δ^{12} CH₂D₂ are (Young et al., 2016):

$$\Delta^{13} \text{CH}_3 \text{D} = 10^3 \left(\frac{x(^{13} \text{CH}_3 \text{D})_{\text{sample}}}{x(^{13} \text{CH}_3 \text{D})_{\text{stochastic}}} - 1 \right)$$
(9)

314 and

$$\Delta^{12} \text{CH}_2 \text{D}_2 = 10^3 \left(\frac{x ({}^{12} \text{CH}_2 \text{D}_2)_{\text{sample}}}{x ({}^{12} \text{CH}_2 \text{D}_2)_{\text{stochastic}}} - 1 \right), \tag{10}$$

respectively (Young et al., 2016). The stochastic fractional abundances of the
mass-18 isotopologues are obtained from the measured bulk isotope fractional
abundances of atoms in the sample such that

$$x({}^{13}CH_{3}D)_{\text{stochastic}} = 4\left(x({}^{13}C)x(H){}^{3}x(D)\right)$$
 (11)

318 and

$$x({}^{12}CH_2D_2)_{\text{stochastic}} = 6\left(x({}^{12}C)x(H){}^2x(D){}^2\right),$$
 (12)

and where the coefficients of 4 and 6 account for the number of permutations for the positions of the D and H isotopes (Young et al., 2016).

321 4. Results

The isotopic compositions of methane produced from the degradation of 322 MPn by strain HI00D01 in waters with different δD values in the range from 323 -376 to +6800% are given in Table 1. The δD of product methane correlates 324 closely with the δD of water (Figure 4). The methane $\delta^{13}C$ values vary little 325 between -97 to -101% (mean = $-99.9\pm1.2\%$, 1σ), closely tracking the 326 δ^{13} C of the source MPn of near -100% relative to VPDB (Taenzer et al., 327 2020). The three non-exchangeable H-sites on the MPn methyl-group have 328 a δD of $-138 \pm 5\%$ relative to VSMOW for all of the experiments except 329 those that utilized normal house water (-60%), both B1 and B2). In the 330 latter two experiments a different batch of MPn was used with the measured 331 MPn methyl-group δD being $-132 \pm 5\%$ relative to VSMOW. These results 332 show that the final hydrogen added to the methyl-group derives from medium 333 water during methane formation, and supports the recent finding that neg-334 ligible carbon-isotope fractionation occurs during methane production from 335 MPn via the C-P lyase pathway (Taenzer et al., 2020). 336

The measured Δ^{13} CH₃D values of C-P lyase generated methane ranged 337 between -0.29 and 0.934%, with an average of $0.35 \pm 0.401\sigma$ (Figure 5, 338 Table 1). The variation in Δ^{13} CH₃D values was only marginally greater 339 than measurement uncertainties, and did not vary systematically with water 340 δD , despite the significant contribution of water sourced from the medium 341 with a range of δD values from -376 to +6800%. In sharp contrast, the 342 Δ^{12} CH₂D₂ values varied from -69.2 to +7.1‰, a spread much greater than 343 measurement uncertainty of < 1% (Figure 5). The methane $\Delta^{12}CH_2D_2$ 344 values correlated closely with the medium water δD in a non-linear, semi-345 parabolic relationship (Figure 5). 346



Figure 4: The D/H ratios of product methane vs. the D/H of medium water expressed in per mil deviations from VSMOW. Linear regression yields $\delta D_{CH_4} = 0.05 \ \delta D_{H_2O} -301.5$, with an R² of 0.999. The strong correlation between the isotopic ratios demonstrates addition of a consistent fraction of reactant water to product methane, and allows for the calculation of the fractionation factor between water D/H and the D/H of the single hydrogen added to the MPn CH₃ to form methane (see text).



Figure 5: The measured (left) Δ^{13} CH₃D and (right) Δ^{12} CH₂D₂ of microbialgenic methane produced in experiments with water of varying δ D water for methane produced in various D-spiked experiments. Errors are smaller than the symbols.

water			Methane							
Sample ID	δD	1se	$\delta^{13}C$	1se	δD	1se	$\Delta^{13}CH_3D$	1se	$\Delta^{12} CH_2 D_2$	1se
-400 B1	-376	0.5	-100.388	0.012	-319.26	0.04	0.93	0.35	-69.18	1.15
-400 B2	-376	0.5	-98.950	0.013	-319.22	0.04	0.85	0.44	-69.10	0.83
-60 B1	-63	0.5	-99.993	0.006	-299.49	0.04	0.02	0.13	-52.28	0.83
-60 B2	-63	0.5	-100.15	0.010	-300.22	0.03	0.50	0.24	-51.11	0.88
750 B1	1013	1.7	-97.047	0.006	-249.08	0.05	0.28	0.31	-14.90	1.32
750 B2	1022	7.3	-100.297	0.024	-250.12	0.05	0.77	0.42	-13.82	1.17
1500 B1	2007	5.1	-100.745	0.010	-194.72	0.04	0.26	0.18	-0.01	0.96
1500 B2	2188	5	-100.846	0.007	-190.06	0.04	0.54	0.27	0.79	1.11
3000 B1	3797	3.1	-100.213	0.009	-106.08	0.05	0.72	0.38	5.2	1.14
3000 B2	3868	2.3	-100.606	0.071	-104.59	0.06	-0.29	0.71	7.06	1.10
3900 B1+2	4871	7.9	-97.949	0.019	-46.43	0.03	0.24	0.36	0.12	0.72
5500 B1	6800	11.1	-100.480	0.006	42.39	0.04	-0.03	0.25	-25.46	0.85

Table 1: The isotopic compositions of medium waters and product methane.

347 5. Discussion

348 5.1. D/H fractionation between MPn and water

³⁴⁹ Understanding the sources of hydrogen used in methane formation by ³⁵⁰ the C-P lyase enzyme is central to understanding the results of these exper-³⁵¹ iments. The main substrate MPn is an organophosphonate synthesized by ³⁵² certain microbes in nature when faced with inorganic phosphate limitation ³⁵³ (Metcalf et al., 2012; Yu et al., 2013). The methyl-group hydrogens on MPn

are ultimately derived from the water in which MPn is biosynthesized, offset 354 by an unknown isotope effect. The hydrogen isotope fractionation between 355 methyl-group hydrogens and water in more thoroughly studied processes, 356 such as acetogenesis, show offsets from bulk water δD of hundreds of per-357 mil (Hattori et al., 2010). Here we utilized synthetic MPn with an average 358 δD value distinct from all medium waters utilized (see Results). Phosphorus-359 starved microbes that encode the C-P lyase enzyme are able to grow on MPn 360 as their sole source of phosphorus by breaking down MPn (Repeta et al., 2016; 361 Sosa et al., 2019; Carini et al., 2014), and as a by-product, release methane 362 (Kamat et al., 2011). The carbon-phosphorus bond in the methyl phos-363 phonate intermediate, ribose-1-methylphosphonate 5-phosphate (PRPn), is 364 attacked by the C-P lyase enzyme subunit PhnJ, producing ribose-1,2-cyclic-365 phosphate-5-phosphate (PRcP), and releasing the methyl group used to form 366 methane. This reaction breaks the methyl group from the rest of the phospho-367 nate compound. In vitro experiments with PhnJ showed that the hydrogen 368 added to the methyl group originates from the bulk solvent (water) via a sol-369 vent exchangeable site on an amino acid in PhnJ (Kamat et al., 2011). The 370 medium-derived hydrogen is delivered to form methane either by abstraction 371 from the 5'-deoxyadenosine or the PhnJ amino acids. A representation of 372 the overall reaction that underscores the sources of hydrogen from medium 373 water and the MPn methyl group is 374

$$H_{2}O + [PO_{4}-C_{5}O_{3}H_{8}-PO_{3}-CH_{3}] + C_{15}H_{23}^{SAM}O_{5}S \xrightarrow{PhnJ} \\ \stackrel{5'-deoxyadenosine}{C_{10}H_{13}N_{5}O_{3}} + OH + [PO_{4}-C_{5}O_{2}H_{7}-PO_{4}] + C_{5}H_{11}NO_{2}S + CH_{4}$$
(13)

In our labelled water experiments, the methane δD increased with the water 375 δD (Figure 4). Moreover, because we used the same lot of MPn for all 376 reactions, with one exception that was isotopically similar (see *Results*), the 377 methyl-group D/H was the same for all our experiments, and the increase 378 in the D/H of product methane solely reflects the addition of water derived 379 hydrogen with different D/H ratios. The tight correlation between bulk water 380 and methane δD is described by the linear regression with an \mathbb{R}^2 value of 0.999 381 (Figure 4). The regression equation is 382

$$\delta D_{CH_4} = 0.05 \,\delta D_{H_2O} - 301.5. \tag{14}$$

The good correlation is consistent with the conclusion that methane is formed by transfer of a hydrogen from the medium water to the methyl group of MPn, and indicates that the transfer of hydrogen from water to the methyl group was consistent for all incubations in medium waters of different δD values. The slope in Equation 14 is the product of the fractionation factor between water and the hydrogen transferred to methane and the fraction of hydrogen in the methane derived from the water.

The good correlation described by Equation 14 is best explained as the result of constant fractions of hydrogen coming from the methyl group in MPn and water to produce methane. The most likely reason for this is that methane inherits 3/4 of its hydrogen directly from CH₃, and that water contributes the last hydrogen. The hydrogen isotope conservation equation for the formation of methane is therefore

$$0.75({}^{\mathrm{D}}R_{\mathrm{Methyl}}) + 0.25 {}^{D}\alpha_{\mathrm{CH}_4/\mathrm{H}_2\mathrm{O}}({}^{\mathrm{D}}R_{\mathrm{H}_2\mathrm{O}}) = {}^{\mathrm{D}}R_{\mathrm{CH}_4}$$
(15)

where ${}^{\mathrm{D}}R_i$ is the D/H ratio for species *i*. Using the known $\delta \mathrm{D}$ values for the product methane, medium water, and MPn methyl group from each experiment, the fractionation factor between methane and water, ${}^{\mathrm{D}}\alpha_{\mathrm{CH}_4/\mathrm{H}_2\mathrm{O}}$, for the one hydrogen transferred from water to make methane was determined by rearranging Equation 15, yielding:

$${}^{\mathrm{D}}\alpha_{\mathrm{CH}_4/\mathrm{H}_2\mathrm{O}} = \frac{4({}^{\mathrm{D}}R_{\mathrm{CH}_4} - (0.75 \, {}^{\mathrm{D}}R_{\mathrm{Methyl}}))}{{}^{\mathrm{D}}R_{\mathrm{H}_2\mathrm{O}}}.$$
 (16)

The D/H fractionation factor between water and methane calculated from 401 Equation 16 for the experiments with differing water δD values vary from 402 0.203 to 0.219 with an average value of $0.209 \pm 0.005 \ 1\sigma$. The consistency is 403 a reflection of the good correlation between δD values for CH₄ and H₂O (Fig-404 ure 4). This fractionation factor corresponds to ${}^{\rm D}\varepsilon_{\rm methane/water} = -790 \pm 5$ 405 ∞ . The magnitude of fractionation between water and methane is relatively 406 large, though not uncommon for processes involving hydrogen (Valentine 407 et al., 2004; Kawagucci et al., 2014). However, the fractionation is not a pri-408 ori outside the range for classical effects given the likelihood that it reflects 409 a convolution of steps (i.e., product of fractination factors) involving D/H 410 exchange on amino acids that accommodate the transfer of the last hydrogen 411 that forms methane from water (Kamat et al., 2011). For this reason we do 412 not attribute the magnitude of our derived fractionation factor to quantum 413 tunneling. We note that because we know the D/H of the methyl group (ex-414

changable hydrogen in MPn) and we can calculate the D/H of the hydrogen donated from water, we have characterized the D/H for the two sources of hydrogen drawn upon to construct the CH_4 molecules in each experiment.

The large isotope fractionation during the transfer of water hydrogen to 418 the methyl group ensures that two compositionally distinct hydrogen reser-419 voirs with distinct δD values contribute to product methane, one ultimately 420 from medium water and the other from the methyl group in the MPn. Other 421 mechanisms of methane formation that are analogous to the C-P lyase, such 422 as microbial methylotrophic and acetotrophic methanogenesis (Penger et al.. 423 2012), are likely influenced similarly. These metabolisms have been the target 424 of recent investigations into their variance in Δ^{13} CH₃D in response to labelled 425 substrate or water (Gruen et al., 2018), although $\Delta^{12}CH_2D_2$ values were not 426 determined. In addition to these biogenic methane formation pathways, abi-427 otic methane formation pathways where hydrogenated sites on end-product 428 methane derive from two or more different reservoirs or with different frac-429 tionations from the source reservoir may be similarly influenced, as has been 430 suggested (Yeung, 2016; Young et al., 2017; Young, 2019). Evidence of ei-431 ther quantum tunneling or the combinatorial effect were captured in methane 432 generated at low-temperature via the abiotic Sabatier reaction, where a clear 433 anti-clumped signal was observed in the $\Delta^{12}CH_2D_2$ with minimal variance in 434 Δ^{13} CH₃D (Young et al., 2017). To determine if this was the combinatorial 435 effect, future experiments with isotopically enriched molecular hydrogen are 436 needed. 437

⁴³⁸ 5.2. Effect of multiple D/H reservoirs on $\Delta^{12}CH_2D_2$

The combination of multiple reservoirs with distinct D/H ratios has a 439 clear influence on the $\Delta^{12}CH_2D_2$ value of product methane. There was no 440 corresponding effect on Δ^{13} CH₃D values. The negative Δ^{12} CH₂D₂ values re-441 sult from the nature of the clumped isotope reference frame. In general, 442 when the stochastic distribution is calculated from a sample gas that av-443 erages different isotopic pools, negative Δ_i values result. By altering the 444 isotopic composition of one of the two pools of hydrogen in the C-P lyase 445 pathway, the medium water, we have apparently isolated this combinatorial 44F effect on $\Delta^{12}CH_2D_2$. 447

In Figure 6, we illustrate the expected combinatorial effect on product methane for experiments like those reported here. When calculated Δ^{12} CH₂D₂ values are plotted against the D/H isotopic composition of the water hydrogen isotopic composition where the methyl D/H is unchanged,

a parabolic trend emerges with an $\Delta^{12}CH_2D_2$ value near zero at the apex, 452 whereas the Δ^{13} CH₃D is unchanged. This topology is predicted by the in-453 equality in Equation 4 and has been demonstrated mathematically (Yeung 454 et al., 2015; Yeung, 2016; Röckmann et al., 2016). As the isotopic com-455 position of the hydrogens originating from the water and the methyl group 456 diverge, the $\Delta^{12}CH_2D_2$ values become exponentially more negative. Negative 457 values for Δ^{13} CH₃D do not emerge because of the unambiguous distinction 458 between the ${}^{13}C/{}^{12}C$ and D/H ratios, yielding no ambiguity in the stochastic 459 distribution (Figure 6). 460

⁴⁶¹ 5.3. Model for the observed $\Delta^{12}CH_2D_2$ effect

Our results resemble those expected for the combinatorial effect (com-462 pare Figures 5 and 6) and suggest that a combinatorial effect in $\Delta^{12}CH_2D_2$ is 463 indeed manifest in at least one pathway for microbialgenic methane for-464 mation. In order to determine the extent to which the range of observed 465 Δ^{12} CH₂D₂ values is explained solely by the combinatorial effect we applied a 466 model in which we calculate methane isotopologue abundances produced by 467 a network of bi-molecular reactions between the isotopologues of the MPn 468 methyl group and water, including the fractionation factor derived from 469 Equation 16. The relative rates of the reactions were taken to be the product 470 of the reactant relative concentrations. The eleven reactions comprising the 471 model are 472

$\mathrm{H}_{2}\mathrm{O} + {}^{12}\mathrm{CH}_{3} \to {}^{12}\mathrm{CH}_{4} + \mathrm{OH} $ (17)	7))
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$$H_2O + {}^{12}CH_2D \rightarrow {}^{12}CH_3D + OH$$
(18)

$$H_2O + {}^{12}CHD_2 \rightarrow {}^{12}CH_2D_2 + OH$$
(19)

$$HDO + {}^{12}CH_3 \rightarrow {}^{12}CH_4 + OD \tag{20}$$

$$HDO + {}^{12}CH_3 \rightarrow {}^{12}CH_3D + OH \tag{21}$$

$$HDO + {}^{12}CH_2D \rightarrow {}^{12}CH_3D + OD$$
(22)

$$HDO + {}^{12}CH_2D \rightarrow {}^{12}CH_2D_2 + OH$$
(23)

$$HDO + {}^{12}CHD_2 \rightarrow {}^{12}CH_2D_2 + OD$$
(24)

$$HDO + {}^{-2}CHD_2 \rightarrow {}^{-2}CHD_3 + OH$$
(25)

$$D_2 O + {}^{2} CH_3 \rightarrow {}^{2} CH_3 D + OD$$
(26)

$$D_2O + {}^{12}CH_2D \rightarrow {}^{12}CH_2D_2 + OD.$$
(27)



Figure 6: An illustration of the difference between the stochastic abundances of Δ^{12} CH₂D₂ and Δ^{13} CH₃D predicted when using average isotopic compositions of the sample gas versus the isotopic compositions of the specific reactants. The abundance of the clumped isotopologues that results from the δ D and δ^{13} C in any given methane population is shown by the white bars, whereas, the abundance of the clumped isotopologues predicted from using the isotopic composition of the specific reservoirs, water and MPn, is given in the black bars, and correspond to the left Y-axes. The clumped isotope values are depicted by the blue dashed line, and correspond to the right Y-axes. If the isotopic composition of the source reservoirs that contribute to product methane have the same δ D values, then the clumped values will not vary, shown by the horizontal blue bar at zero in each panel. In reality, the clumped isotopic compositions are negative across most water δ D values (assuming an invariant methyl-group), because the stochastic isotopologue abundance using the average C and H isotopic composition of the sample gas is greater than that given by the isotopic composition of the methyl group and water. All points in this plot are illustrative and not real data.

We also used an analogous set of reactions in which the ¹³C-bearing isotopologues of the methyl group were included. The rate of reaction was modified by the fractionation factor from Equation 16 where a D in CH₄ comes from water. We performed the calculations for values of ${}^{\rm D}\alpha_{\rm CH_4/H_2O}$ ranging from 0.19 to 0.23 in order to allow for uncertainties in the precise value.

We performed the calculations in two ways. In the first calculation, we assumed that the reactants had stochastic relative abundances of isotopologues calculated from their measured bulk δ^{13} C and δ D values. From the relative rates of reaction we calculate the resulting abundances of the methane isotopologues and the Δ^{12} CH₂D₂ and Δ^{13} CH₃D values expected for each incubation experiment.

⁴⁸⁴ The fit of the model curves obtained using purely stochastic reactant ⁴⁸⁵ isotopologue abundances is sufficiently good (Figure 7) that we conclude ⁴⁸⁶ that the combinatorial effect is the dominant process governing the values ⁴⁸⁷ for Δ^{12} CH₂D₂ in the product methane. However, there is a marked offset ⁴⁸⁸ between the model curves and the measured values at higher water δ D values. ⁴⁸⁹ As expected, the calculations, produce Δ^{13} CH₃D within < 0.2‰, signifying ⁴⁹⁰ no effect on Δ^{13} CH₃D, as observed in our experiments.

In our second calculation method, we obtained an improved fit to the data 491 by considering that the reactant methyl group did not have a purely stochas-492 tic distribution of isotopologues. Specifically, we allowed for a higher concen-493 tration of CHD₂ relative to stochastic. In order to determine a best-fit value 494 for the reactant methyl clumping, we adjusted the ratio $CHD_2/(CHD_2)_{stochastic}$ 495 to minimize the chi-square calculated from the deviation in $\Delta^{12}CH_2D_2$ values 496 between the data and the model. For this minimization we adopted the mean 497 ${}^{\rm D}\alpha_{\rm CH_4/H_2O}$ value of 0.209. The results yield a best-fit $\rm CHD_2/(\rm CHD_2)_{\rm stochastic}$ 498 ratio of 1.0114 that can be expressed as a Δ^{12} CHD₂ value of 11.4‰ (Figure 499 7). For a nominal reproducibility of $\pm 2\%$ for $\Delta^{12}CH_2D_2$ values implied by 500 some of the replicate experimental results in Table 1, the reduced chi-square 501 value for the fit of this model is 2.5 (for n = 12 experiments). This value is 502 sufficiently close to unity to suggest that the vast majority of the variation 503 exhibited by our data is due to the combinatorial effect that includes inher-504 itance of a modest amount of DD clumping from the reactant methyl group 505 in MPn. 506

⁵⁰⁷ In order to assess the importance of the analytical uncertainties in the ⁵⁰⁸ two input parameters for our calculations, we performed Monte Carlo (MC) ⁵⁰⁹ simulations of the experiments by randomly varying the MPn methyl-group ⁵¹⁰ δD values and the ${}^{D}\alpha_{CH_4/H_2O}$ values in our model calculations at the water



Figure 7: Plots of Δ^{12} CH₂D₂ vs. water δ D showing our experimental results (triangles) and the two model calculations described in the text (curves). The model curves in panel A assume stochastic distributions for all of the reactant isotopologues. The model curves in panel B are obtained using a best-fit Δ^{12} CHD₂ value of 11.4% for the reactant methyl group (see text). Curves for a range of ${}^{\rm D}\alpha_{\rm CH_4/H_2O}$ values from 0.19 to 0.23 are shown for reference. Monte Carlo simulations of the effects of uncertainties in MPn methyl δ D and our derived ${}^{\rm D}\alpha_{\rm CH_4/H_2O}$ values are shown by the circles. Means and standard deviations for the Monte Carlo simulations are shown by the filled circle and 1 σ vertical error bars.

 δD values corresponding to the experiments. We drew 100 random instances 511 of these values from parent Gaussian distributions based on the measured 512 means and standard deviations for these parameters and used these as inputs 513 to the calculations. The resulting MC estimates for the uncertainties in the 514 models are shown in both panels in Figure 7. For the 7 groups of experiments 515 representing 7 distinct δD water values, 6 have measured $\Delta^{12}CH_2D_2$ values 516 that are within the 4σ uncertainty in our best-fit model with Δ^{12} CHD₂ = 517 11.4% (panel B, Figure 7). 518

⁵¹⁹ Our best-fit model allows us to not only simulate the combinatorial effect ⁵²⁰ on the product methane, but it also affords an estimate of the DD clumping in ⁵²¹ the MPn methyl group that produced the methane. The value for Δ^{12} CHD₂ ⁵²² in this instance reflects the process of forming reagent MPn. Experiments ⁵²³ similar to these might be useful in exploring the DD ordering in naturally ⁵²⁴ occurring MPn methyl groups.

525 5.4. Implications for applications of $\Delta^{12}CH_2D_2$

Negative Δ^{12} CH₂D₂ values have been attributed to either combinatorial 526 effects or quantum tunneling effects (Young et al., 2017; Young, 2019). The 527 results of this study lend support to the interpretation that combinatorial 528 effects dominate. These effects may arise from enzymatically-mediated ki-529 netic steps within a cell or surface catalyzed steps during abiotic synthesis. 530 In both cases we refer to these as endogenous combinatorial effects because 531 they are the result of distinct pools of hydrogen created by the kinetic steps 532 leading to methane formation. In the present study, the pools of contrasting 533 D/H ratios arise in part because of the isotopic composition of the growth 534 medium, comprising what we refer to as an example of exogenous combi-535 natorial effects to emphasize that the pools of hydrogen with distinct D/H 536 ratios include an external reservoir. Endogenous combinatorial effects may 537 explain the very low $\Delta^{12}CH_2D_2$ values seen in microbial methanogenesis and 538 in abiotic Sabatier reaction products (Young et al., 2017; Young, 2019). 539

A critical advantage of using Δ^{12} CH₂D₂ and Δ^{13} CH₃D values to charac-540 terize the provenance of methane molecules is their relative insensitivity to 541 substrate bulk isotopic compositions (Young et al., 2017; Young, 2019). For 542 example, the very negative $\Delta^{12}CH_2D_2$ values that are characteristic of, or 543 even diagnostic of, microbialgenic methane appear to be insensitive to the 544 δD of the local aqueous environs (Young et al., 2017; Young, 2019; Ash et al., 545 2019). However, the strong response of $\Delta^{12}CH_2D_2$ values to the isotopic com-546 position of water in these experiments raises the specter of substrate bulk 547

isotope effects on methane $\Delta^{12}CH_2D_2$ values. Though some of the experi-548 mental water values were not representative of natural systems (e.g. δD_{H_2O} 549 > 0%), both the Hanover, NH, USA (house) and South Pole, Antarctica 550 waters represent values for reservoirs in nature that can contribute hydrogen 551 to methane. We note that the more than 300% difference in the δD of the 552 two waters resulted in a more than 15% shift in methane $\Delta^{12}CH_2D_2$ values 553 at a fixed substrate MPn isotopic composition (Figure 5). The likelihood 554 for such effects in nature depends on the variability of D/H in natural wa-555 ters and variability in fractionation factors between water and the natural 556 methyl-type substrates used in methanogenesis. For the step-wise addition 557 of hydrogen to carbon during hydrogenotrophic $(H_2 + CO_2)$ methanogene-558 sis, where all of the hydrogen for the product methane ultimately originates 559 from water, endogenous combinatorial effects likely dominate due to the dif-560 ferent D/H fractionation factors associated with each hydrogen addition step 561 (Young, 2019). This said, if some of the hydrogens on methane come from 562 molecular hydrogen (Valentine et al., 2004; Kawagucci et al., 2014), the op-563 portunity for combinational influence arises. Indeed, the other canonical 564 microbial pathways of methane formation, methylotrophic or acetotrophic, 565 are clear analogs to the C-P lyase pathway, in that different D/H pools are 566 accessed in the form of water and preexisting methyl groups, suggesting that 567 exogenous combinatorial effects are at play. This is especially true given 568 the likelihood for large D/H fractionations between water and C-H bearing 569 organic sources of H in nature (Hattori et al., 2010), without which reser-570 voir (exogenous) combinatorial effects are unlikely. More work is required to 571 understand whether or not differences in $\Delta^{12}CH_2D_2$ values among different 572 methanogenesis pathways (Giunta et al., 2019; Young et al., 2017) could in 573 part reflect the different magnitudes of endogenous and exogenous combina-574 torial effects. 575

576 6. Conclusions

The source of depleted Δ^{12} CH₂D₂ values in methane produced by microbes is evidenced in the aerobic C-P lyase pathway. This metabolism for methane production incorporates hydrogen from two distinct reservoirs: a methyl group, contributing three hydrogenated sites, and water that donates a single hydrogen. By varying the D/H composition of the water medium in which the bacteria generate methane, we observed the effect of combinatorics on Δ^{12} CH₂D₂ values. Our results indicate that variations in the Δ^{12} CH₂D₂ of

methane produced by C-P lyase is primarily the result of the difference in 584 D/H between the water and the reactant methyl group. The consistency be-585 tween predictions for the purely combinatorial reservoir effect and the mea-586 sured isotopologue abundances demonstrates that in this case, combinatorics 587 are the main cause of the negative $\Delta^{12}CH_2D_2$ values with no resolvable effect 588 on Δ^{13} CH₃D values for the product methane. These results lend credence to 589 the interpretation that combinatorial effects dominate the depleted micro-590 bialgenic methane Δ^{12} CH₂D₂ values as well as those those arising from some 591 surface catalyzed abiotic methane production pathways. This work raises 592 the prospect that differential water H-isotopic compositions or fractionations 593 in nature may induce the combinatorial effect in some microbial methane 594 production pathways. 595

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601 Research Data

All code for model and figures is posted in a permanent archive FigShare DOI: 10.6084/m9.figshare.11676357

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