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Estimating Microbial Hydrogen Consumption in Hydrogen Storage in Porous Media as a Basis for Site Selection

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45 **ABSTRACT**

46 Subsurface storage of hydrogen, e.g. in depleted gas or oil fields (DOGF), is suggested
47 as a means to overcome imbalances between supply and demand in the renewable energy
48 sector. However, hydrogen is an electron donor for subsurface microbial processes,
49 which may have important implications for hydrogen recovery, gas injectivity and
50 corrosion. Here, we review the controls on the three major hydrogen consuming
51 processes in the subsurface, methanogenesis, homoacetogenesis, and sulfate reduction,
52 as a basis to develop a hydrogen storage site selection tool. Testing our tool on 42 DOGF
53 showed that seven of the fields may be considered sterile with respect to hydrogen-
54 consuming microbiota due to either temperatures >122 °C or salinities >5 M NaCl. Only
55 three fields can sustain all of the hydrogen consuming processes, due to either
56 temperature, salinity or pressure constraints in the remaining fields. We calculated a
57 potential microbial growth in the order of 1-17*10^7 cells ml^{-1} for these fields. The
58 associated hydrogen consumption is negligible to small (<0.01-3.2 % of the stored
59 hydrogen). Our results can help inform decisions about where hydrogen will be stored in
60 the future.

61 *Keywords*: Hydrogen, underground storage, microbial hydrogen consumption,
62 homoacetogens, methanogens, sulfate reducers

63

64 **Highlights**

65 • Review of the most important hydrogen-utilizing microorganisms in the
66 underground.
67 • Elucidation of the growth criteria for 480 strains of the mayor hydrogen-
68 utilizers.

- Development of a site selection tool for sterile hydrogen storage.
- Evaluation of the site selection tool on 42 depleted oil and gas fields (DOGF).
- Calculation of the microbial growth and hydrogen consumption in DOGF.

Abbreviations and units

SSR	Sulfur species reduction
SSRM	Sulfur species reducing microorganisms
DOGF	Depleted oil and gas fields
EPS	Extracellular polymeric substances
M	Molarity (mol L^{-1})
MPa	Megapascal

1. Introduction

Zero-carbon energy generation from renewable sources can help mitigate carbon emissions and abate climate change [1-3]. One of the most significant challenges for renewable energy is the imbalance between supply and demand [3, 4]. The generation of hydrogen (H_2) via electrolysis of water during periods of renewable energy oversupply and subsequent H_2 storage is one way of overcoming this imbalance, as H_2 can be recovered and used for electricity generation during periods of renewable energy shortage [1, 5]. Subsurface storage of H_2 in salt caverns, depleted gas or oil fields or saline aquifers is being considered as an alternative to expensive purpose-built storage containers [6]. However, the artificial elevation of the H_2 concentration in the subsurface may stimulate the growth of H_2-oxidizing (hydrogenotrophic) bacteria and archaea, here collectively referred to as microorganisms, with possible adverse implications for gas

injectivity and withdrawal via permeability reduction, H_2 volume loss and corrosion of metal infrastructure [4, 7]. Understanding the controls on microbial H_2 metabolism is therefore highly important.

Much of the subsurface is characterized by combinations of elevated temperature [7], high salt concentrations and high pressure [3], reduced void space [8], limited nutrient availability [9] and typically highly reducing conditions [9-11]. The evidence for microbial life at depth is plentiful (e.g. [12-16]). Most microorganisms in nature grow in biofilms attached to surfaces (communities of aggregated microbial cells embedded in a secreted matrix of extracellular polymeric substances (EPS)) [17, 18]. Even small amounts of biofilm can reduce pore throat sizes and increase the flow-path tortuosity, resulting in dramatic decreases in permeability [19]. It has been postulated that biofilms may not form in the nutrient-limited underground when the groundwater flow is low [19]. However, subsurface biofilms are commonly encountered during geoenergy activities such as fracturing, hydrocarbon recovery or in geothermal plants [20-25]. Biofilm formation may actually be enhanced under the harsh subsurface conditions as the EPS layer acts as a protective clothing which ensures the normal reproduction and metabolism of microorganisms [18].

Hydrogen plays a central role in the energy metabolism of subsurface life [9]. Yet, a quantitative assessment of the consumption of H_2 by deep microbial communities in the context of the global H_2 cycle is lacking [26]. In underground gas storage sites and oil reservoirs the most abundant H_2-oxidizers are hydrogenotrophic sulfate reducers, that couple H_2-oxidation to sulfate reduction to produce hydrogen sulfide (H_2S); hydrogenotrophic methanogens that reduce carbon dioxide (CO_2) to methane (CH_4) by oxidizing H_2; and homoacetogens that couple H_2 oxidation to carbon dioxide (CO_2) reduction producing acetate [7, 24, 27]. These

three groups of microorganisms are, amongst others, implicated in causing subsurface corrosion [7, 27, 28].

A recent review addressed the many possible abiotic and biotic H_2-producing and H_2-consuming processes in the subsurface [7]. However, it lacked a quantitative assessment of the processes of microbial growth and H_2 consumption relevant for H_2 storage. Strobel et al. [29] summarized the concept and potential of underground methanation using experimental data from the Sun Storage project. These authors highlighted controls on the growth of methanogens and changes in gas composition due to methanogenesis, but did not quantify microbial growth. Many studies report changes in gas composition, biofilm growth and clogging near injection wells but hardly any studies report quantitative figures on microbial growth or on permeability changes [30].

To date it remains unclear how subsurface microorganisms might react to elevated H_2 concentrations [7] and hence whether microbial growth is a concern for H_2 storage. Even in natural, non-engineered subsurface environments, there is little information on microbial H_2 turnover rates [31] and the behavior and population kinetics of microorganisms are not fully understood [29]. The majority of the available data on microbial H_2 turnover rates come from batch cultures at optimal growth conditions where the kinetics [31], the pace of life [32, 33], the physiological states and the prominent organisms may differ widely from the subsurface environment [7, 32]. A further complication arises from the fact that many microorganisms in the deep subsurface are not culturable with modern enrichment techniques [12, 34].

In this work, we review the state-of-the-art understanding of the controls of temperature, salinity, pH, pressure and nutrients and water on microbial growth on H_2 in the subsurface, with emphasis on the three major H_2-consuming processes methanogenesis, sulfate reduction and homoacetogenesis, to determine what reservoir conditions will be unfavorable to microbial

activity and as such more suitable sites for long term gas storage operations of 30 years or longer, such as the UK Rough gas storage site.

Physicochemical data from 42 depleted or close to depleted oil and gas fields (DOGF) of the British and Norwegian North Sea and the Irish Sea as well as five H_2 storage test sites provide the base for an evaluation of the number of sites where microbial growth of methanogens, sulfate reducers and homoacetogens can be expected. Using average nutrient contents of the microbial cells and site-specific dissolved ion concentrations, we calculate significant growth and a small H_2 consumption for growth-permitting DOGF.

2. State of the art understanding

2.1 Likely microbial hydrogen oxidation in hydrogen storage systems

Hydrogen oxidizing processes may be ranked according to the magnitude of their H_2 threshold and their standard free energy change ($\Delta G^{0'}$), two useful metrics to compare the likelihood of reactions to take place and the order at which they proceed (Table 1). The H_2 threshold defines the concentration of H_2 below which it is no longer consumed. Given all other factors are at optimum, the microbial population with the lowest H_2 threshold value is expected to be the most successful population in competing for H_2 [35].

The $\Delta G^{0'}$ marks the thermodynamic favorability of a reaction at ambient pressure and temperature, pH 7 and 1 M of all reactants. In oligotrophic (nutrient poor) high pressure and temperature environments, the order of the $\Delta G^{0'}$ may be used to determine which reaction is more energetically favorable. As can be seen from Table 1, more negative $\Delta G^{0'}$ values (more available free energy) are generally accompanied by lower H_2 thresholds. Not included in Table 1 are the kinetics which describe the rate of the electron transfer in the redox reaction.

Table 1. Biotic H_2-consuming processes ranked according to their free energy yield ($\Delta G^{0'}$) and measured H_2 threshold. Not included are Vanadium, Cobalt, Techneticum, Uranium and Selenium reduction, due their limited relevance for H_2 storage. NA= not available.

H_2- oxidizing process	Reaction (number)	H_2 threshold (nM)	$\Delta G^{0'}$ (KJ mol H_2^{-1})	Typical ambient $[H_2]$ (nmol L^{-1})	Relevance for H_2 storage
Chromate reduction	$\frac{1}{2}H_2 + \frac{1}{3}CrO_4^{2-} + \frac{5}{3}H^+ \rightarrow \frac{1}{3}Cr^{3+} + \frac{4}{3}H_2O$ **(1)**	<0.1[36]	NA	NA	low
Aerobic hydrogen oxidation (Knallgas)	$H_2 + \frac{1}{2}O_2 \rightarrow H_2O$ **(2)**	0.051[7]	-237[7, 36]	NA	low
Denitrification	$H_2 + \frac{2}{5}H^+ + \frac{2}{5}NO_3^- \rightarrow \frac{1}{5}N_2 + \frac{6}{5}H_2O$ **(3)**	<0.05-0.5[7]	-240.1[7, 36] -224[4, 37]	<0.05[4, 35, 36]	low
Halorespiration	$H_2 + halogenated\ compounds \rightarrow dehalogentated\ compounds + HCl$ **(4)**	0.05-0.27[36] <0.3 [38] 0.27-2[7]	-230 to -187[7]	NA	low
Iron (III) reduction	$H_2 + ferric(oxy)hydroxides \rightarrow ferrous\ iron + H_2O$ **(5)**	<0.11-0.8[36, 38]	-228.3[7, 38] -182.5[36] -114[4]	0.2[4, 35] 0.2-1[36]	intermediate
Manganese (IV) reduction	$2H_2 + MnO_2 \rightarrow Mn(OH)_2 + 2H_2O$ **(6)**	<0.05[35]	-163[4, 35]	<0.05[4, 35]	low
Arsenate reduction	$H_2 + HAsO_4^{2-} + 2H^+ \rightarrow H_3AsO_3 + H_2O$ **(7)**	0.03-0.09[36]	-162.4[36]	0.4-0.7[36]	low
Ammonification	$4H_2 + 2H^+ + NO_3^- \rightarrow NH_4^+ + 3H_2O$ **(8)**	0.015- 0.025[38, 39]	-150[4, 38]	<0.05[4, 35]	low
Fumarate reduction	$H_2 + fumarate \rightarrow succinate$ **(9)**	0.015[38, 39]	-86.2[38]	NA	low
Hydrogenotrophic sulfate reduction	$4H_2 + SO_4^{2-} + H^+ \rightarrow HS^- + 4H_2O$ **(10)**	1-15[38, 39]	-38[7, 38] -48[36] -57[4]	1-2[4, 35]	high
Hydrogenotrophic methanogenesis	$4H_2 + CO_2 \rightarrow CH_4 + 2H_2O$ **(11)**	0.4-95[38-40]	-34[4, 38] -43.9[36]	5-10[4, 35] 7-13[36]	high
Sulfur reduction	$H_2 + S \rightarrow HS^- + H^+$ **(12)**	2500[7]	-33.1[7]	NA	intermediate
Homoacetogenesis	$4H_2 + 2CO_2 \rightarrow CH_3COOH + 2H_2$ **(13)**	328-3640[38, 39]	-26[4, 38] -36.1[36]	100<[4], 117-150[36]	high

Abiotically, most of the H_2-oxidizing reactions are very slow but mediated by microbial enzymes the processes are catalyzed [37, 41].

The three main microbial processes with implications for H_2 storage, hydrogenotrophic sulfate reduction, hydrogenotrophic methanogenesis (for simplicity from now on just referred to as sulfate reduction, and methanogenesis unless otherwise specified) and homoacetogenesis, require the highest threshold [H_2] and are among the processes with lowest $\Delta G^{0'}$ (Table 1). Nevertheless, e.g. sulfate reduction is instantaneous in most geologic settings [42] possibly due to fast kinetics [37] and/or a relatively high availability of sulfate.

Because sulfate reducers may use the same substrates as sulfur reducers (i.e. sulfide and thiosulfate [43, 44]), they are here collectively referred to as sulfur species reducing microorganisms (SSRM) performing sulfur species reduction (SSR). Direct respiration of sulfur is limited by its low solubility ($1.6*10^{-7}$ M) and hence requires cell attachment to the sulfur particle [45]. However, sulfur readily reacts with sulfide formed during the reduction of sulfate to form easily metabolizable polysulphides [45, 46].

Iron (III) reduction relies on the availability of iron oxides and iron-bearing minerals such as smectite and chlorite [47, 48], as well as the availability of organic carbon, since dissimilatory iron reducing bacteria (DIRB) are strict heterotrophs, i.e. synthesize cell carbon from organic compounds [49]. Iron oxides are abundant in many sediments and aquifers [47] but are typically not available in the carbon-rich oil fields because they have been reduced over millions of years and are not replenished [24]. Meanwhile, bacteria capable of reducing iron are frequently isolated from hydrocarbon-contaminated or oil-associated sites (reviewed in [50]). However, the mere observation of iron reduction by bacteria, which are given a DIRB enrichment medium in the laboratory, does not imply that these bacteria will reduce iron in nature. In addition, cell counts are often low to intermediate (10–100 cells ml^{-1}) and may

include non-hydrogenotrophs (e.g. [51, 52]). In non-engineered environments rich in Fe oxides and organic carbon, IRB may have a great advantage over SSRM, methanogens and homoacetogens, due to a very high affinity for H_2 [47]. We evaluate this process as of intermediate relevance for H_2 storage in DOGF.

Many IRB and a few SSRM can also couple H_2 oxidation to reduction of a variety of other trace metal oxides, e.g. MnO_4^{2-}/MnO_2, CrO_4^{2-}, Co, SeO_4^{2-}, UO_2^{2}, TcO_4^{-}, AsO^{3-}, and VO_4^{-} [43, 53, 54]. After Fe, the most abundant metal in sedimentary environments is Mn (~10 % of Fe abundance) [47, 53]. Due to the trace content of these compounds in the environment, their reduction has low relevance for H_2 storage.

Oxygen and nitrate are scarce in the subsurface [11, 24, 55, 56] and aerobic hydrogen oxidation, denitrification and ammonification hence only become significant when contamination of the aquifer occurs, e.g. by drilling fluid [57-59].

Halogenated compounds are common in aquifers, and may arise from contamination or via natural processes in sediment [60, 61]. However, the concentrations of these compounds are extremely low: In aquifers of 167-1000 m depth, chloroflourocarbons reach maximum concentrations of $\leq$1.1 µg L^{-1} [61] and for pristine aquifers 0.003-0.007 µg L^{-1} of chlorinated hydrocarbons were measured [60]. We evaluate the relevance of this process to H_2 storage as negligible.

Literature on the importance of anaerobic fumarate respiration using H_2 is scarce. Fumarate may be used as an alternative electron acceptor by SSRM [43, 62] and homoacetogens [63-66]. In the non-engineered subsurface, readily metabolizable organic matter, like fumarate, is rare [67]. Oil fields being rich in organic C compounds may contain more fumarate. Payler et al. [12] confirmed the presence of fumarate reductase, the key enzyme in fumarate reduction, in three out of five metagenomes from subsurface brines within sandstone. However, the

metagenomes belonged primarily to non-H_2 utilizing bacteria (*Halorubrum*) and fumarate concentrations were not reported. Acknowledging the lack of data in this field, we evaluate this process as being of low relevance for H_2 storage.

2.2 Factors governing microbial growth

Microbial growth and H_2 consumption rates vary with nutrient availability and environmental variables (e.g. [17, 68].) Each strain is adapted to an optimum set of nutrients and environmental conditions where potentially the greatest growth rates occur. Beyond the optimum conditions, organisms may grow but at reduced rate or they become dormant. In this section, we discuss the requirements for nutrients and water, and the overall impact of temperature, salinity, pH and pressure on the growth of the major microbial H_2–oxidizers in DOGFs, in the ranges relevant to H_2 storage. The specific activity of microbial strains grown at optimum conditions varies as well (reviewed in [69]) but the elucidation of differences between strains is beyond the scope of this review.

2.2.1 Nutrients

Apart from water of sufficient thermodynamic activity (see Section 2.2.4), hydrogenotrophs require H_2 as a source of electrons (energy), an electron acceptor and a carbon source for cell division, together with a set of macro and trace elements as well as various organic nutrients [70]. Microorganisms can only access $H_{2(aq)}$ and hence the solubility of $H_{2(g)}$ is of direct relevance for all H_2-consuming reactions. Given a gas phase of ~100 % H_2 in an H_2 storage system, the equilibrium solubility of H_2 exceeds the highest threshold value of an H_2-consuming microorganism of 3.6 µM (Table 1) by ~3 orders of magnitude at ambient pressure and temperature and under static conditions (Fig. A.1a), with further increase at higher pressures (Fig. A.1b). While under non-static conditions hydrogenotrophs will consume part

236 of the H_2, these figures suggest no limitation by the H_2 solubility on microbial growth under
237 H_2 storage conditions.

238 Elemental requirements include the macro elements C, N, H, P, Ca, Mg, S and Fe (>95 % of
239 the microbial cell dry weight), and the trace elements Co, Mn, Ni, Mo, Cu, Zn, W as well as
240 Se for some metabolic groups [71, 72]. For optimum growth, many microorganisms
241 additionally require different vitamins (e.g. lipoic acid, biotin, riboflavin, folic acid, thiamine,
242 etc.), yeast extract, coenzyme M, aromatic acids and phospholipids or a combination of these
243 (e.g. [8, 65, 73-75]).

244 Nutrients may be assimilated from the solution or directly from minerals (e.g., [76-79]), the
245 latter being of particular importance in oligotrophic environments [77]. Carbon, sulfur,
246 phosphorous and iron are amongst the key elements released by mineral weathering [77]. The
247 extent to which subsurface microbial communities depend on mineral weathering is unknown
248 [77]. For soils, Huang et al. [80] analyzed that >50 % of the 1100 microbial strains were
249 capable of mineral weathering, as tested by their ability to mineralize biotite.

250 Microbial cell carbon may be assimilated from CO_2 alone (autotrophy) or from organic carbon
251 compounds (heterotrophy) [81]. Methanogens and homoacetogens can grow autotrophically or
252 heterotrophically, and several can grow mixotrophically (e.g. [66, 82, 83]). SSRM typically
253 grow heterotrophically but some grow autotrophically or mixotrophically [84, 85]. Nitrogen
254 may be assimilated from ammonia and nitrate or by nitrogen-fixation (diazotrophy).
255 Diazotrophy is common amongst SSRM, methanogens and homoacetogens [86-89], though
256 homoacetogens often inhabit ammonia-rich environments [88].

257 Little is known about the differences in the nutrient requirements on the level of functional
258 groups and the variation in nutrient requirement within a functional group. SSRM have a higher
259 requirement for iron ($1.8*10^{-6}$ M) than is usually observed for microorganisms [90] while

methanogens have a higher requirement for sulfur with optimal levels ranging from 0.03 to 0.79 mM (reviewed in [91]).

Literature on when nutrients become limiting is also scarce. Sulfate reducing SSRM require a minimum sulfate and phosphorus concentrations of ~3 mM and ~3.2-320*10^{-5} mM, respectively, for growth [92, 93]. Methanogens of the order *Methanosarcinae* require 29.6 mM Mg for optimum growth and growth ceases at 15.8 mM (reviewed in [91]). When grown under optimum conditions, the growth rate of autotrophs may be limited by the rate of transfer of H_2 and CO_2 from gas to liquid, as was shown for the methanogen *Methanobacterium thermoautotrophicum* [94] and for the sulfate reducers within *Desulfotomaculum sp* [95].

Carbon is unlikely to be limiting in the hydrocarbon-rich DOGF [56, 96, 97] but this is not a given in saline aquifers with no history of oil or gas. Sulfate is present in significant concentrations in most DOGF (Table 2) but H_2 injection can cause sulfate depletion due to accelerated growth of SSRM [98]. Nitrogen in the form of ammonia may be limiting in DOGF [51, 56, 90] but nitrate levels may be elevated [51], often due to contamination by drilling fluid [57-59].

2.2.2 Temperature

Temperatures of 22.5–80 °C or 20–100 °C have been suggested for H_2 storage based on a recommended depth range of 500- 2000 m for H_2 storage in DOGF and saline aquifers [99-101]. Microorganisms are classified according to their preferred growth temperature: psychrophiles grow optimally below 20 °C, psychotrophs grow optimally at or above 20 °C and may tolerate temperatures below 5 °C, mesophiles grow between 20 and 45 °C, thermophiles grow above 45-50 °C, and hyperthermophiles show optimal growth at temperatures of 80 °C or above [102, 103].

283 High temperatures alter the energetic properties (e.g., vibrational modes) of biomolecules in
284 their aqueous solvent, change the substrate solubility or viscosity and the ionization of the
285 aqueous medium [104]. Adverse effects of high temperature include DNA denaturing or
286 damage, decreased protein stability, hydrolysis of ATP and ADP, amongst others [104, 105].
287 The metabolic strategies of thermophiles are highly diverse. For a discussion, the reader is
288 referred to [106].

289 Thermophiles and hyperthermophiles are challenged by increased reaction rates at elevated
290 temperature which can imply that abiotic reaction rates are so fast that there is no benefit to the
291 microorganism if it catalyzes the reaction [41]. High-temperature-adapted microorganisms are
292 therefore thought to produce enzymes with faster reaction rates [107].

293 Most cultivated hydrogenotrophic methanogens are mesophiles but known optimal growth
294 temperatures for methanogens range from 15 to 98 °C (Fig. 1a). A considerable number of
295 methanogens favor temperatures above 60 °C (Fig. 1a). The highest temperature that a
296 methanogen was found to grow under is 122 °C (*Methanopyrus kandleri*) (Fig. 1b) [108].

297 Cultivated SSRM typically have optimum growth temperatures of 20-30 °C or 50-70 °C where
298 sulfur reducing archaea have higher optimum growth temperatures than sulfur and sulfate
299 reducing bacteria. The full range for optimum growth of SSRM spans 10-106 °C (Fig. 1i). The
300 critical temperature for growth of cultivated SSRM is 113 °C (*Pyrolobus fumarii*) [109].

301 Homoacetogens typically have optimum growth temperatures between 20-30 °C (85 % of the
302 here gathered cultivated strains; Fig. 1e). Thermophilic growth temperatures ≥60 °C have been
303 reported for eight strains, only (e.g. *Moorella mulderi*, *Thermoanaerobacter kivui*,
304 *Acetogenium kivui*) [110-112]. Corresponding upper limits for growth are 70-72 °C (Fig. 1f)
305 [110-112].

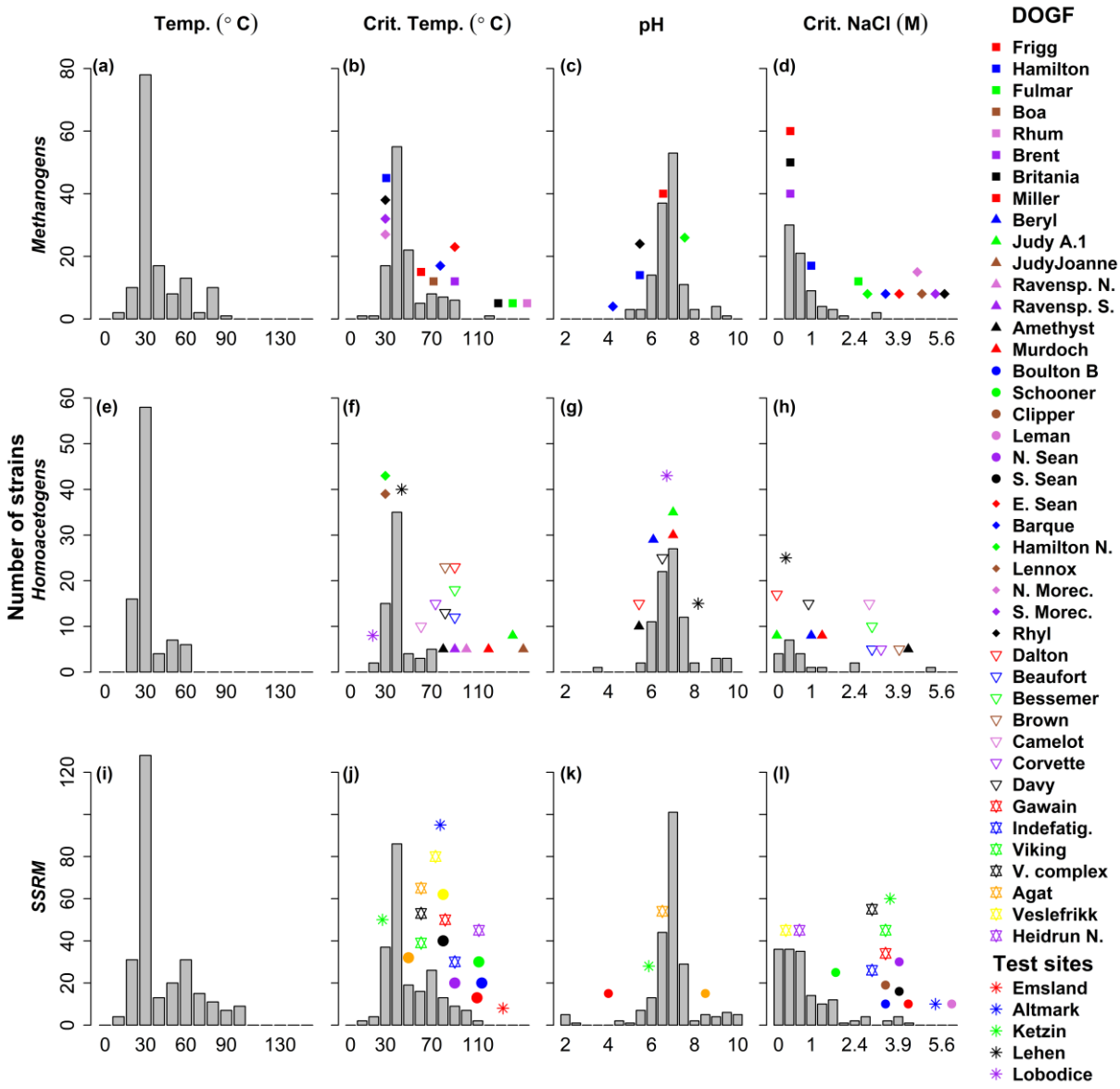

Figure. 1. Distribution of optimum growth temperature, critical growth temperature, optimum pH values and critical salinity for 123-140 methanogens (a-d), 21-91 homoacetogens (e-h) and 151-255 sulfur species reducing microorganisms (SSRM) (i-l). Distributed between the graphs for the different groups of H_2-oxidizers are the temperatures, pH values and salinities of 42 depleted oil and gas fields (DOGF) and five test sites for H_2 injection. Where ranges of a parameter were given (see Table A.4), the lower end value was plotted.

315 ***2.2.3 Salinity***

316 The relevant salt concentration range for H_2 storage is 0-5 M NaCl [100], at which highly
317 diverse prokaryote communities can be found [113]. Microorganisms are classified according
318 to their salt tolerance: Non-halophilic microorganisms grow up to 0.2 M NaCl, slight halophile
319 grow at 0.2–0.5 M NaCl, moderate halophile between 0.5–2.5 M NaCl, and extreme halophile
320 that grow best in hypersaline media containing 2.5–5.2 M NaCl [113].

321 High salt concentrations exert osmotic stress [114], requiring any microorganism living at high
322 salt concentrations to maintain its intracellular environment at least isosmotic with the
323 environment [113]. Commonly, salt tolerance/requirement is enhanced at increased
324 temperatures [113] but there are many examples of mesophilic halophiles.

325 Most hydrogenotrophic methanogens favor salt concentrations up to 0.77 M NaCl (the
326 approximate salinity for seawater) but 16 known strains survive under more halophilic
327 conditions. Two extremely halophilic mesophilic hydrogenotrophic methanogens, will tolerate
328 salt concentrations of ~3.3- 3.4 M, *Methanocalculus halotolerans FR1T* [115] and
329 *Methanocalculus natronophilus* [116] (Fig. 1d).

330 The large majority of SSRM grow optimally at low salinities between >0-0.4 M. However,
331 fourteen SSRM (all mesophiles) have upper salinity limits for growth of ≥ 1.7 M NaCl (Fig.
332 1h). *Desulfovibrio oxyclinae*, *Thiobacillus halophilus*, *Desulfohalobium utahense* and
333 *Desulfohalobium retbaense,* have the highest upper salinity limits for growth of 4.0 to 4.2 M
334 NaCl [117-120] (Fig. 1h).

335 The salt tolerance of homoacetogens is poorly investigated. The majority of homoacetogens
336 have low optimum salinities of >0-0.4 M NaCl. However, a few strains, i.e. *Natroincola*
337 *histidinovorans*, *Sporohalobacter lortii* and *Halanaaerobium praevalens*, grow optimally at
338 >1.4 M NaCl and will tolerate salinities up to 2.6-5.1 M (Fig. 1h) [121-123].

2.2.4 Brine complexity

Natural brines contain dissolved ions whose interaction is extremely complex and may cause physicochemical stressors to brine habitability such as low water activity (a_w), high ionic strength, chaotropy (ability to disrupt the network of H_2-bonds between water molecules) or a combination of these [12]. Most bacteria grow well at an a_w around 0.98 (the approx. a_w for sea water) but relatively few species can grow at a_w of 0.96 or lower [124]. Halophilic microorganisms, including halophilic methanogens are one exception; several can grow at a_w as low as 0.75 [125] in [124]; [126]. Steinle et al. [127] challenged these limits by detecting SSR in a nearly $MgCl_2$ saturated brine with a_w of ~0.4.

There are indications of a more important role of chaotropy over a_w in limiting microbial life [126]. Chaotropic agents include $MgCl_2$, $CaCl_2$, $FeCl_3$, KI, LiBr, LiCl while examples of kosmotropic agents are NaCl, KCl, Na_2SO_4, $MgSO_4$, K_2SO_4, $FeSO_4$ [128]. As such one may speculate that most subsurface brines due to their dominance of NaCl and richness in sulfate are kosmotropic and albeit also stress-inducing, more permissive of microbial growth [12, 126]. Meanwhile, the interactions between chao- or kosmotropic agents, a_w and other physicochemical properties of brines may be very complex and hitherto not understood [12]. The further elucidation of this topic is subject to more research and beyond the scope of this paper.

2.2.5 pH

The brine pH may affect the growth of microorganisms via 1) a direct effect on the growth metabolism, and 2) an effect on the redox reaction. With respect to the former, most methanogens, homoacetogens and SSRM are adopted to a pH of 6.5-7.5 (Fig. 1c, g, k). Most methanogens and SSRM cannot grow outside the pH range 4–9.5 [29, 129, 130] (Fig. 1c, k). Ten known methanogens can endure a critical pH-value of 10 (e.g. the *Methanosalsum*

363 *natronophilum* and *zhilinae*, and the *Methanocalculus natronophilus* and *alkaliphilus* [131].
364 At the other end of the spectrum, ten known methanogens can endure acidic conditions of pH
365 4, e.g. the *Methanoregula boonei*, the *Methanothermococcus okinawensis*, the *Methanosarcina*
366 *spelaei* and the *Methanocaldococcus bathoardescens* [132-135].

367 Eighteen known SSRM are adapted to highly alkaline environment >pH 10, e.g. the
368 *Desulfonatronovibrio hydrogenovorans,* the *Desulforispira natronophila and the*
369 *Desulfovibrio vietnamensis* [136-138]. Thirteen known SSRM grow down to a pH of 4. Nine
370 known SSRM, all of them sulfur reducers, grow down to a pH of 1, e.g. the *Thiobacillus caldus,*
371 the *Sulfolobus acidocaldarius*, the *Acidianus infernus* and *brierleyi*, and the *Stygiolobus*
372 *azoricus* [139-142].

373 Seven known homoacetogenic strains have high critical pH values up to 10.0-10.7, e.g.
374 *Clostridium ultunense*, *Natrionella acetigena, Fuchsiella alkaliacetigena and ferrireducens,*
375 *Natronoincola histidinovorans, Peptostreptococcus productus B-52* and *Moorella sp HUC22-*
376 *1* [121, 122, 143-146]. The *Clostridium drakai, ljundahlii*, *scatologenes*, *coccoides* and
377 *termoautrophicum* are the most acidophilic known strains; they can tolerate pH as low as 3.6-
378 4.5 [147-151].

379 ***2.2.6 Pressure***

380 Pressure ranges for H_2 storage of 5-20 MPa [99] or 1-50 MPa [100] have been reported. Life
381 at high pressure requires homeostatic changes [103]. The high pressures encountered in pore
382 spaces in the crust are generally less inhibitory to microbial cellular activity than the high
383 temperatures, partly because of the relatively high osmotic pressure of cytoplasm [102], in
384 particular in thermophiles and hyperthermophiles [41]. DNA synthesis and protein synthesis
385 are among the most pressure-sensitive cellular processes [103, 152]. Protection against pressure
386 includes biofilm [18] or spore formation [103].

At 30-50 MPa, the growth of various mesophilic, atmospheric-pressure-adapted microorganisms is inhibited [152] whereas pressure effects are generally favorable for the growth of hyperthermophiles; above 100 °C, elevated pressures are required to maintain a liquid environment [105]. Microorganisms that grow optimally at 10 MPa or above are obligate and facultative piezophiles, where the former do not tolerate ambient pressure and the latter do [103]. A recent publication listed all identified piezophiles and grouped them according to their growth temperature optimum [103]. The list of species is rather short (and as we find incomplete despite being published in 2020), possibly due to the fact that, to date, it has not been possible to isolate genes associated with piezophily, so the effects of pressure on any particular organism can only be determined empirically [103]. Empirical efforts however, do not commonly include pressure tolerance in the description of the environmental growth criteria of a microorganism. In addition, most mesophiles and thermophiles from habitats with pressures of <50 MPa will grow in enrichment cultures incubated at atmospheric pressure [34]. The large majority of identified cultivated piezophiles are psychrophiles (27 strains) [103], the relevance of which is low to our study. Only four mesophilic strains were reported, three of them hydrogenotrophic sulfate reducers (the *Desulfovibro profundus*, *piezophilus,* and *hydrothermalis*), growing optimally at 10-40 MPa [103]. Eight thermophiles were identified, including one hydrogenotrophic methanogen, *Methanococcus thermolithrophicus*, growing optimally at 50 MPa. The hyperthermophilic group hosts the hydrogenotrophic *Methanopyrus kandleri* and *Methanocaldococcus jannaschii* growing optimally at 20 to 75 MPa, respectively. Examples of hydrogenotrophic piezophiles that are not included in [103] are the mesophilic SSRM *Parococcus pantrophus* and *Pseudodesulfovibrio indicus* which growth optimally at 30 and 10 MPa, respectively [153, 154], and the thermophilic SSRM *Piezobacter thermophiles* and *Archaeoglobus fulgidus TF2* which grow optimally at 30 and 42 MPa, respectively [75, 155].

412 A temperature dependence of the pressure response was reported for the SSRM *Desulfovibrio*
413 *indonesiensis* which has similar growth rates at high and ambient pressure 45 °C but reduces
414 its growth rate at 20 °C and 30 MPa relative to at 0.1 MPa [156]. Elevated pressure may
415 increase the maximum growth temperature by 2-12 °C relative to lower pressure (0.1-3 MPa)
416 [105, 108, 157].

417 ***2.2.7 Inhibitors***

418 Exposure to hydrogen sulfide, H_2S, and its bisulfide ion, HS^-, causes damage to microbial
419 proteins and coenzymes [91, 158]. It remains unclear whether H_2S or HS^- is responsible for
420 the toxicity effect but there is general consensus that H_2S can penetrate the microbial cell
421 membrane more easily than HS^- [158]. Hydrogen sulfide dissociates with a pK_1 of 6.99 at 10
422 MPa and 25 °C to form >99 % HS^- at pH 8.5 [159].

423 Growth of SSRM and methanogens is adversely affected at concentrations of H_2S >3.8-4.0
424 mM [160-162]. At 5.0-6.3 mM H_2S growth is completely inhibited for SSRM [160, 162],
425 without however stopping all metabolic activity [160]. For methanogens and homoacetogens
426 3.8-7.5 mM H_2S and total sulfide concentrations of 3.3 mM, respectively, stop the growth [158,
427 162]. In systems with circumneutral pH and ferric ion concentrations above 1 mM, the
428 concentrations of H_2S are predicted to be kept below toxic levels due to its precipitation in
429 makinawite [46].

430 Carbon dioxide pressure above 1 bar can be toxic for microorganisms as shown for the SSRM
431 *Desulfotomaculum geothermicum* and the methanogen *Methanothermococcus*
432 *thermolithotrophicus* [163]. For many anaerobes like methanogens and homoacetogens,
433 oxygen is toxic too [64, 102].

434 Nitrate inhibits homoacetogenesis [164], and ammonium [165] and sulfate inhibit
435 methanogenesis (reviewed in [166]), with minimum inhibitory concentrations varying

436 depending on the environment [162, 165]. For instance, sulfate concentrations as low as $2*10^{-4}$ M were shown to inhibit methanogenesis for 10 hours in lake sediments, possibly by competition with SSRM for available H_2 and C-substrate [161] (see section 2.3.9). Under H_2 storage conditions however, sulfate is likely not to affect methanogenesis, because sulfate inhibition was shown to be reversed by addition of H_2 [161]. For a discussion of an inhibitory effect of H_2, see section 2.5.

2.2.8 Summary of environmental growth constraints

Acknowledging the lack of data for the pressure sensitivity of many microorganisms [103], and considering a general abundance of nutrients in DOGF (Table 2), we evaluate temperature and salinity as the most crucial environmental factors constraining the growth of homoacetogens, methanogens and SSRM in DOGF. Pressures encountered in the crust are documented to have less effect than temperature on microbial cellular activity, particularly in thermophiles and hyperthermophiles [41, 102]. The pH does not pose a similar constraint to the growth of homoacetogens, methanogens and SSRM because the pH ranges for growth typically span two to three pH units (not shown) and for most species they comprise the typical aquifer pH values of 6-7 [167] (Table A.4). Brine complexity and inhibitors were not included in this analysis due a lack of information on the brine composition of DOGF beyond a limited set of dissolved ions.

Figure 2 shows the critical temperature versus critical salinity for 269 cultivated strains and reveals that salt tolerances up to 1-1.7 M are widely distributed over the entire temperature range while salt tolerances >1.7 M are mainly found at a critical temperature tolerances of 40-50 °C. Hence, from the point of view of minimizing microbial impacts on H_2 storage, sites with temperatures >50 °C and salinities >1.7 M are preferred.

459 **Table 2.** Reservoir conditions for selected depleted, or soon to be depleted oil and gas fields. Except where otherwise indicated, the data are

460 from [168]. [S]= reference [167]. The salinity was calculated from the chloride concentration and the concentrations of dissolved N_2 was

461 estimated from the mol percentage in the gas phase, neglecting any effect of salinity. NA= not analyzed. See Table A.4 for extended data.

462

Field name	Area (Km^2)	P (MPa)	Temp (°C)	Salinity (M)	pH	HCO_3^- (mM)	N_2 (mM)	SO_4^{2-} (mM)	K^+ (mM)	Ca^{+2} (mM)	Mg^{+2} (mM)	P (mM)	Na^+ (mM)	Cl^- (mM)	Fe^{+2} (mM)	Organic acids (mM)
Frigg	100	19.5	61	0.07-0.53	6.5-7.4	16.3	0.4	NA	26.3-31.2	0.4-2.0	1.9-7.1	NA	75.2-534.8	58.7-490.3	0.04-0.27	NA
Hamilton	15	9.6	30	1.59-4.18	5.8	4.8	2.1	0.6-7.4	8.4-29.7	72.8-720.0	19.5-37.6	0.012-0.028	1354.8-2210.9	1453.3-3700.7	4.03	NA
Barque	36	26.0	79	4.83	4.7	0.3	0.8	3.5	42.2	535.0	156.8	NA	2920.4	4405.4	2.15	NA
Hamilton North	8	10.5	30	2.93	7.9	11.0	2.3	23.1	18.8	13.6	13.6	NA	2640.9	2662.9	NA	NA
Miller	45	49.3	121	1.61	7.2	NA	0.6	0.0	41.6	30.0	NA	NA	1358.7	1471.9	0.02	NA
Beryl	49	36.0	101	1.88	6.1	5.6	0.4	0.0	20.8	90.0	NA	NA	1469.6	1717.9	0.05	1.9
Judy (Andrew 1)	NA	46.9	137	0.14-0.15	6.8	8.4	0.6	6.4	2.9	4.5	NA	0.002	117.4	131.7	0.11	NA
Amethyst	97	27.9	88	4.45	5.6	1.0	1.6	3.7	33.2	521.5	148.5	0.452	2673.9	4064.6	2.51	NA
Rhyl	NA	14.9	36	5.80	5.5	13.5	2.8	14.0	62.4	147.0	21.2	0.031	4777.0	5297.9	0.81	>1.2
Dalton	NA	28.8	91	0.26	5	0.9	1.0	1.8		15.6	5.5	NA	189.1	237.0	0.00	NA
Davy	6	28.2	88	3.87	6.8	6.5	NA	7.0	219.2	15.6	10.7	0.155	818.3	1142.7	0.66	NA
Veslefrikk[S]	NA	29.8-35.0	67-114	0.29-0.72	6.5	8.4-17.2	NA	0.1-0.15	NA	NA	NA	NA	298.0-666.0	281.0-745.0	NA	2.2-8.1
Average						7.9	1.1	5.2	44.7	166.8	42.2	0.113	1473.7	1857.4	0.967	3.3

463 Growth of all investigated microbial groups occurs up to 72 °C (Fig. 1). Above 72°C, known
464 homoacetogens will not grow, and at 80-94°C sulfate reducers cease to grow. Thirty-six
465 cultivated SSRM and eleven methanogens have optimum growth temperature of ≥80 °C (Fig.
466 1a and g) and will still grow, albeit at reduced rate, beyond their optimum temperatures. The
467 maximum growth temperature for known methanogens and sulfur reducers is 122 °C and 113
468 °C, respectively. The upper salinity limit that allows growth of all the major groups of
469 investigated H_2-oxidizing microorganisms is 3 M NaCl. The upper pH limit is 9.5 and the upper
470 pressure limit for most mesophiles is 30-50 MPa.

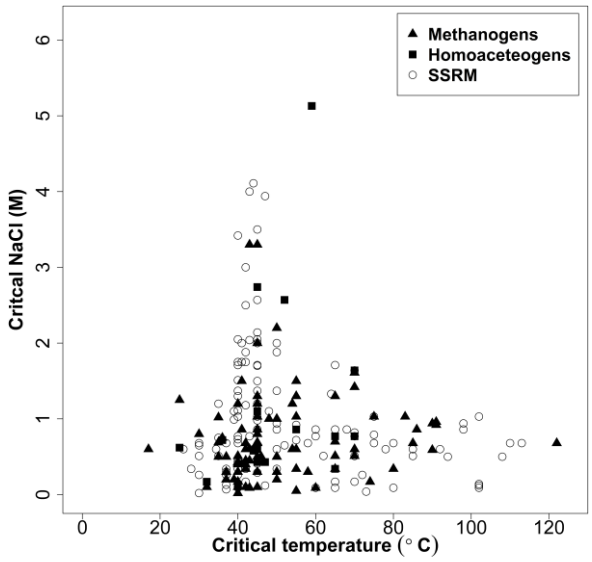

Figure. 2. Critical temperature (without salinity stress) versus critical salinity (without temperature stress) for methanogens, homoacetogens and SSRM.

471

472 **2.3 Microbial growth regulation by competition and syntrophy**

473 Homoacetogenic bacteria are ubiquitous in anaerobic sediments [65, 169] and often co-exist
474 with SSRM and methanogens [15, 170], as revealed by a combination of molecular (16S RNA

475 gene sequences) and culturing (e.g. metabolites, radiotracer) techniques. Few habitats have
476 been identified in which homoacetogens compete with other H_2-consumers (culturing studies)
477 [169, 171]. Exceptions include a low-temperature and low-salinity petroleum reservoir where
478 homoacetogens dominated over methanogens and SSRM (molecular study) [62], a granite
479 groundwater at 400 m depth where cell numbers of methanogens and homoacetogens were
480 balanced (molecular study) [83], and subsurface marine sediments where mixotrophic
481 homoacetogenesis outperformed methanogenesis (culturing study) [82].

482 Kinetic advantages of SSRM and methanogens (i.e. a higher affinity for H_2, expressed as a
483 low Michaelis-Menten constant, K_M, or Monod half saturation constant, K_S (H_2 concentration
484 at which growth rate reaches half maximum growth rate), and a higher maximum
485 growth/reaction rate, V_{max} or μ_{max} for Michaelis-Menten kinetics and Monod kinetics,
486 respectively) were proposed as the underlying cause for the few examples of the poor
487 competitiveness of homoacetogens [172]. Very limited information on the H_2 consumption
488 kinetics of homoacetogenic bacteria is available in literature [173]. The available data show
489 that μ_{max} differs by one order of magnitude between strains (0.02-0.5 h^{-1}) [4, 173]. This may or
490 may not be lower than the μ_{max} for SSRM 0.057-5.5 h^{-1} [4, 40, 174] and methanogens 0.032-
491 1.4 h^{-1} [40, 174]. Krumholz et al. [172] showed that homoacetogens were not able to compete
492 effectively for H_2 in the presence of SSRM in a subsurface sandstone ecosystem at 30 °C
493 regardless of pH_2, and despite significant homoacetogenesis at excess H_2. Findings by Berta et
494 al. [4] for a groundwater sediment held under excess pH_2 and 20 °C contrasts this as
495 homoacetogenesis rates were up to 21 times higher than SSR.

496 Environmental conditions may be a crucial determinant for the competitiveness of
497 homoacetogens, as low temperatures (~15 °C) [175, 176] and low pH values [64, 93] favor
498 their growth over methanogens. Under excess pH_2, homoacetogenic strains with high μ_{max} such

499 as *Acetobacterium bakii* will outcompete methanogens [176]. The outstanding metabolic
500 flexibility of homoacetogens for utilizing a vast variety of substrates may additionally explain
501 why homoacetogens can compete with more specialized microorganisms like SSRM or
502 methanogens [65, 176, 177].

503 As for the competitiveness of methanogens and SSRM, the H_2 thresholds of methanogens
504 may be comparable (1-15 nM) or higher (>15-95) than for sulfate reducers and significantly
505 lower than for sulfur reducers (≪2500 nM; Table 1), indicating an advantage of sulfate
506 reducers over methanogens and sulfur reducers in most non-engineered, low pH_2
507 environments. In line with this, Lackner [178] recently reviewed that sulfate reducers
508 outcompete methanogens for H_2 in most studies. However, at excess H_2, methanogens and
509 sulfate reducers would be expected to process equal shares of the in situ H_2 pool [174]. Also,
510 since concentrations of sulfate are much lower than bicarbonate in non-marine natural
511 environments [40] (Table 2), the growth of sulfate reducers at excess H_2 will be limited by
512 availability of their electron acceptor, making it possible for methanogens to compete [40]. As
513 a general rule pH values below 7 favor the growth of methanogens over sulfate reducers [130].
514 Above pH 7.5, sulfate reducers grow faster than methanogens and would be expected to
515 outcompete them [130].

516 Syntrophic relationships between different functional groups have been documented frequently
517 (whereby the metabolic products of one group serve as substrates for the other). For example,
518 SSRM and homoacetogens were shown to participate cooperatively in microbial induced
519 corrosion of steel where SSRM grew on acetate produced by homoacetogenesis [70]. Substrate
520 provision by the co-culturing *Desulfovibrio vulgaris* enhanced growth of the dehalogen
521 *Dehalococcoides ethenogenes 195* by 24 % and caused three times higher dechlorination rates
522 [179]. Syntrophy may also explain the detection of a combination of the SSRMs *Desulfovibrio*

523 and the homoacetogens *Acetobacterium* in petroleum and subsurface CO_2 reservoirs [62, 180],
524 and the presence of H_2-producing heterotrophs along with methanogens in petroleum reservoirs
525 where the latter rely on H_2-transfer by the former [181].

526 **2.4 Microbial ecology in natural gas and petroleum reservoirs**

527 Recent years have seen a considerable effort in describing deep subsurface microbial
528 communities, including those from gas and petroleum reservoirs. Isolated hydrogenotrophic
529 microbes from these habitats are from the SSRM families *Archaeoglobaceae [182],*
530 *Desulfomicrobiaceae*, *Desulfobulbaceae, Peptococcaceae, Desulfobacteracceae*,
531 *Desulfovibrionaceae, Desulforobacteriaceae, Sulfurospirillaceae*, *Rhodobacteraceae*,
532 *Ectothiorhodospiraceae, Hydrogenothermaceae [27, 56, 97, 98, 183-187],* the
533 *Eubacteriaceae* and *Sporomusaceae* families which host homoacetogenic strains [97, 186,
534 188], and the methanogen families *Methanosarcinaceae*, *Methanobacteriaceae*,
535 *Methanomicrobiaceae*, *Methanopyraceae*, *Methanococcaceae*, *Methanocalculaceae* and
536 *Methanosaetaceae* [98, 115, 186] in addition to uncultured microbial taxa [56, 184, 185, 189].
537 Our collection of hydrogenotrophs (Fig. 1) lists many examples of the above microbial
538 families, including the strain that holds the highest critical temperature for a methanogen,
539 *Methanopyrus kandleri*. Sulphur reducing families that define the upper temperature limits for
540 SSRM like *Thermoproteaceae* and *Pyrodictiaceae* were not reported. The cause for their
541 absence may be a predominance of mesophilic and thermophilic sites but may also reflect a
542 generally stronger growth of sulfate reducers over sulfur reducers in oil and gas reservoirs.
543 Ranchou-Peyrouse et al. [98] showed that the microbial community in 35 out of 36 subsurface
544 wells from seven natural gas storage sites was dominated by sulfate reducers.

545 **2.5 Effect of high hydrogen concentrations on the microbial metabolism and community**
546 **structure**

547 A range of studies investigated the metabolism of methanogens at excess H_2 and ambient
548 pressure, with unambiguous results. Conrad et al. [190] demonstrated that excess H_2 stimulated
549 methanogenesis and growth rates in a paddy soil (species not specified). Opposed to this,
550 results by Topcuoglu et al. [181] and Stewart et al. [191] suggest an inhibitory effect of high
551 partial pressures of H_2, pH_2, expressed as a ~10-fold drop in the growth yield (cells per mole
552 CH_4) of *Methanocaldococcus jannaschii* and a slight drop of ~0.1-0.7 h^{-1} in the growth rate.
553 Similar observations were made for *Methanothermobacter thermoautotrophicus* [192].
554 However, within the excess H_2 experiment, higher H_2 concentrations stimulated growth [181],
555 suggesting a complex influence of pH_2. Methanogens seem to express a pH_2-dependent change
556 in their ecological strategy, i.e. maximum growth rate vs. maximum growth yield, as a means
557 to cope with different environmental conditions [181]. Indeed, *M. jannaschii* is capable of
558 sensing subtle changes in dissolved H_2 concentration and restraining the energy-intensive
559 growth of flagella to H_2-limiting conditions whereas at excess H_2 cells are mostly flagella
560 devoid [193].

561 Only few studies investigated microbial H_2 turnover at high pH_2 of up to 1.5-24.8 MPa [4, 194,
562 195]. Methanogens (*M. jannaschii*) showed a strong inhibitory effect at high pH_2 [194].
563 However, the authors added CO_2 at a pressure of at least 0.2 MPa to the hydrogen gas mixture
564 which at pCO_2 >0.1 MPa can be toxic methanogens [163]. Hence it is not clear whether H_2 or
565 CO_2 performed the toxic action. For homoacetogens and SSRM, the H_2 consumption was
566 shown not to change in response to different pH_2 of 0.1-3.5 MPa [4, 195], indicating neither
567 stimulation nor toxicity at different levels of excess H_2. The comparison to limiting H_2
568 conditions was not made.

569 Apart from microbial metabolism, the microbial community may also change in response to
570 high pH_2. Given a pertubation by H_2 injection it can be anticipated that other types of

571 microorganisms, e.g. the in hydrocarbon reservoirs, common fermenters [24, 96, 98, 183] will
572 decrease in abundance while hydrogenotrophs will increase [7], in line with the Baas Becking
573 principle [196]. An increase in hydrogenotrophs in response to H_2 addition was recently
574 confirmed for soils, however H_2 consumption increased in only one of the investigated soils,
575 suggesting a pronounced influence of the indigenous microbial community [197]. Bioreactor
576 experiments support a decrease in microbial diversity in response to high pH_2 as well [198,
577 199]. Puente-Sanchez et al. [200] were the first to report differences in the subsurface H_2-
578 consuming community in response to varying pH_2 within the Iberian Pyrite Belt. Ranchou-
579 Peyruse et al. [98] showed that town gas storage with more than 50 % H_2 changed the microbial
580 community from a predominantly sulfate reducing community to a dominance of methanogens,
581 and this balance was active even decades after injection stopped, possibly via H_2 trapping in
582 the microporous system [98]. It was suspected that all sulfate was initially used up by SSRM
583 following increased growth of methanogens [98].

584 # 3. Evaluating the potential hydrogen consumption in DOGFs

585 ## 3.1 Calculation of the microbial growth

586 We screened 42 DOGF in the North Sea and the Irish Sea and five H_2 storage test sites for
587 temperature, salinity, pH and pressure data (Fig. 1, Table A.4). We discovered significant
588 differences in the salinity for the DOGF reported by sources [201] and [168]. Because we relied
589 on the solution compositions for the calculation of the potential microbial growth in the fields,
590 which are available from [168], we chose to use the salinity data from the same source.

591 The environmental data from the DOGF and H_2 storage test sites were aligned with the
592 constraints for growth of methanogens, homoacetogens and SSRM (Fig. 1-2) to select in which
593 fields growth can be expected. For the few fields that fulfil the growth constraints of all

investigated microorganisms, we calculated a first-order estimate of the microbial growth using the elemental cell composition as a proxy for the nutrient requirement [202, 203] (Text A.1).

Our calculations assumed that the supply of N and C are covered by diazotrophic and autotrophic growth, respectively. Requirements for trace elements were neglected in the calculation due to a lack of information on the relevant trace element contents in the reservoirs. Where a nutrient for a specific field was not available we used the average value from the fields given in Table 2. Any effect of the pH_2 on microbial growth was neglected. We assumed that cells neither die nor are removed, and that nutrients are not replenished by inflow, re-mineralization from decaying biomass or mineral dissolution. Simultaneous growth by different microorganisms was not considered.

Percentages of nutrients in the cells (Text A.1) were converted to mass using a wet cell mass of $1.77*10^{-12}$ g for methanogens [204], $3.2\text{-}6.2*10^{-13}$ g for homoacetogens and $7.81*10^{-13}$ g for SSRM. The cell wet weight of homoacetogens was calculated by dividing the cell volume of 1.62-3.14 μm^3 for the subsurface mixotrophic homoacetogen *Acetobacterium psammolithicum* [172] with an assumed bacterial density of $1*10^{-12}$ g μm^{-3} [205]. The cell wet weight of SSRMs was calculated using a cell dry weight of $3.125*10^{-13}$ g for *Desulfovibrio desulfuricans* [206] and dividing this with a general bacterial dry weight to wet weight ratio of 0.4 [207]. Subsequently, the concentrations of C, H, O, Ca, K, Na, S, Mg, P and Fe in the DOGF (Table 2) were divided by the mass of the respective cell nutrients per microbial cell calculated above. This resulted in the maximum cell count within each microbial group, *G*, that could potentially be created based on a single nutrient, where the lowest *G* indicated the limiting nutrient for cell growth. For an example of those calculations, see Text A.1.

3.2 Estimation of the cell-specific hydrogen consumption

Hydrogen may be consumed at rates of 0.02-5.0*10^5 nM h^{-1} for homoacetogens, 0.02-5.8*10^5 nM h^{-1} for methanogens and 0.005-130*10^5 nM h^{-1} for SSRM (Tables A.1-A.3), the latter considering sulfate concentrations in the range of 0-2.3*10^{-2} M in the DOGF (Table 2). In a few studies, the microbial H_2 consumption was related to growth (Tables A.1-A.3), enabling the calculation of the H_2 consumption per synthesized cell and the time for when the microbial cell count *G* would be reached (Text A.2).

3.3 Calculation of the hydrogen consumption in a hydrogen storage system

We calculated the minimum H_2 consumption for the DOGF Frigg and Hamilton by dividing the H_2 consumption per synthesized cell with the microbial cell count. The calculation of the moles of H_2 the in aquifer anticipated equal volumes of H_2 and water and used the ideal gas law and the field size, temperature and pressure data in Table 2 and Table A.3. The percentage of H_2 that was consumed as a function of growing and resting microbial cells was calculated by dividing the potential H_2 consumption with the H_2 concentration in the reservoir. Text A.3 shows our calculations for the Frigg reservoir and methanogens.

4. Results and discussion

4.1 Characterization of the likelihood for growth in 42 DOGF

Using the environmental limits constraining microbial growth on H_2, we analyzed the physicochemical parameters for 42 DOGF in the British and Norwegian North Sea and the Irish Sea and five H_2 storage test sites (Fig. 1, Table A.4). Of the 47 fields, five fields have a temperature of 122 °C or higher and may be considered sterile with respect to H_2-consuming microorganisms. Thirty-two fields have a temperature >72 °C, implying that homoacetogenesis cannot take place. Twenty fields have a temperature ≥90 °C implying that homoacetogenesis and sulfate reduction cannot take place. Fourteen DOGF have a temperature >90 °C and <122 °C and pressures of 18.2-44 MPa where (piezophile) methanogens and SSRM will grow.

Of the fifteen sites with temperatures <72 °C where all investigated groups of microorganisms will grow, only six fields (Frigg, Hamilton, Veslefrikk, Ketzin, Lehen and Lobodice) fulfill the remaining pressure and salinity requirements for growth. Two fields, Leman and Rhyl, have salinities ≥5.8 M where no significant microbial growth can be expected. This finding is supported by stable gas compositions at the similarly saline H_2-storage test sites of the H2STORE project, Emsland and Altmark (Fig. 1, Table A.4), though a low microbial population of ~10^2 cells ml^{-1} was present [208]. Lennox, North Morecambe and South Morecambe with temperatures of 30-33 °C and salinities of 4.6-5.1 M, could permit the growth of the halophile homoacetogenic strain *Halanaerobium praevalens*, only. Hamilton North, Camelot and The V gas field complex with salinities of 2.9-5.0 M may permit the growth of sulfate reducers and *Halanaerobium praevalens*. The Viking field has temperature of 65-80 °C and a salinity of 3.8 M and so is likely to host only mesophilic SSRM, although pressures >30 MPa that could become growth inhibiting. The H_2-storage test site Ketzin has similar salinity to the Viking field but a lower pressure (4.0 M NaCl, 35 °C, 6 MPa). Here SSRM were suspected to cause a 2-4 % decrease in H_2 and a reduction in the concentration of sulfate from 22 to $8*10^{-3}$ M [208].

4.2 Microbial growth estimates for three low-temperature and low-salinity DOGF

Our first order approach for calculating microbial growth in the Veslefrikk reservoir yielded a maximum $1*10^8$ methanogenic cells mL^{-1}, $2*10^8$ SSRM cells mL^{-1} or $5*10^8$ homoacetogenic cells mL^{-1}. The Frigg reservoir a maximum of $1*10^8$ methanogenic cells mL^{-1}, $1*10^8$ SSRM cells mL^{-1} or $2*10^8$ homoacetogenic cells mL^{-1}. The Hamilton reservoir could host a maximum of $1*10^7$ methanogenic cells mL^{-1}, $2*10^7$ SRCM cells mL^{-1} or $6*10^7$ homoacetogenic cells mL^{-1}. These cell counts describe a maximum cell growth for each hydrogenotrophic group because simultaneous growth of hydrogenotrophs was not considered. The higher growth of homoacetogens over SSRM and methanogens results from a lower wet cell mass that causes a

lower nutrient demand per cell (see Text A.1). Our calculations are in line with total cell concentrations of 10^5-10^{15} cells/ mL^{-1} in oil reservoirs [209], and equal to or up to four order of magnitudes higher than cell counts from gas reservoirs (0.001-1.2*10^7 cells mL^{-1})[51, 97, 185]. The range of the literature data reflects that our simple methodology to calculate microbial numbers may serve as a first approximation to estimating microbial growth in the subsurface, only.

Acknowledging that trace elements were not accounted for in our calculation, N and P are the first limiting nutrients in the reservoirs Frigg, Hamilton and Veslefrikk. However, this does not imply that microbial growth is N and P limited, as many microorganisms may use of ammonium (not measured) as N-source, and in the Hamilton reservoir the C:P ratio was between 59:1 and 158:1, whereas the limiting C:P ratio for microbial growth is in the range of 400:1 to 800:1 (reported for the SSRM *D. desulfuricans*) [92]. At moderately acidic pH values such as the pH of 5.8 in the Hamilton reservoir, P may further be continuously replenished by mineral buffering with apatite.

4.3 Hydrogen consumption in three low-temperature and low-salinity DOGF

The H_2 consumption in the Frigg reservoir by homoacetogens constitutes <0.01- 3.2 % of the H_2 in the aquifer, <0.01- 1.3 % for methanogens and <0.01- 1.3 % for SSRM. In the Hamilton reservoir, the rates are <0.01- 2.0 %, <0.01- 2.3 % and <0.01- 0.5 % for homoacetogens, methanogens and SSRM, respectively. For actively growing cells these consumption rates may be reached after only 0.1-19.1 days, which is the time it takes for the microorganisms to grow up to their maximum cell counts, based on the dissolved nutrient concentrations. Resting cells, i.e. cells that undergo no or only very little cell division, need 2.5-3.5 months (SSRM) or up to 3.6-6.6 years (methanogens) to reach the maximum cell count and consume the given percentage H_2.

690 In a real aquifer system, nutrients are likely to at least partly be replenished by decaying cells,
691 mineral weathering and inflowing brine, and cells will continue to consume H_2 beyond the time
692 it takes to reach the maximum cell count (maintenance). As such our H_2 consumption estimates
693 may be regarded as minima. On the other hand, considering that, with the exception of one
694 study (Berta et al. [4]), our calculations employ laboratory H_2 consumption rates at optimal
695 nutrient supply and optimal physicochemical conditions (Tables A.1-A.3), the H_2 consumption
696 in the oligotrophic subsurface is likely overpredicted. Comparing the employed laboratory H_2
697 consumption rates to H_2 consumption rates by SSR and methanogenesis in oil and natural gas
698 reservoirs of ~0.4-330 nM h^{-1} and 0.02-1205 nM h^{-1}, respectively (SO_4^{2-}: 8.3-805*10^{-5} M;
699 HCO_3^-: 3.5-246*10^{-4} M) [51, 183], shows that the field H_2 consumption by SSR is 1.5 times to
700 five orders of magnitude lower, and 1.4 times to 7 orders of magnitude lower for
701 methanogenesis. Within the operation and injection wells of a natural gas reservoir, H_2
702 consumption rates by SSR and methanogenesis were 2393 and 4475 nM h^{-1}, respectively, [51],
703 which falls within the lower range of the values reported from laboratory studies.
704 Acknowledging the unknown but presumably low pH_2 in above experiments, and that
705 maintenance requirements were not included in our H_2-consumption calculations, we expect
706 the actual H_2 consumption in a H_2 storage system to lie within the higher range of our calculated
707 values.

708 Our lower-end results are in agreement with no H_2 consumption during storage operations of
709 H_2 -rich town gas in Beynes, France [210]. Our upper end results are in agreement with a loss
710 of ~3 %, presumably by methanogenesis, at the H_2 storage (SunStorage) test site in Lehen,
711 Austria [211]. A H_2 consumption of 17 % by methanogens at the Lobodice town gas storage
712 site over a time span of seven months [210, 212] seems exceptional in the light of our
713 calculations and the reported SSR and methanogenesis rates from the field. With a very low
714 salinity of 0.03 M, temperatures of 20-45 °C, a pH of 6.7 and 4 MPa pressure, Lobodice is

among the few sites which has highly favorable conditions for microbial growth considering *all* of these parameters (Table A.4). The high H_2 consumption at Lobodice highlights the importance of our site selection tool, as H_2 storage may face serious economical and technical problems if a site with growth-favoring conditions is selected.

As mentioned, Berta et al. [4] measured high H_2 consumption rates under excess H_2 and oligotrophic conditions (P< $9.7*10^{-7}$ M; $SO_4^{2-} \leq 9.5*10^{-4}$ M; DOC= $2.6*10^{-4}$ M), indicating that nutrient scarcity does not imply low H_2 consumption. A comparison to the nutrient concentrations in the DOGF reveals that many of them have a higher nutrient status (P= 0.002-$0.452*10^{-3}$ M; SO_4^{2-}= up to $23.1*10^{-3}$ M; organic acids= 1.2-$8.1*10^{-3}$ M, Table 2), implying that H_2 consumption in DOGF under excess H_2 conditions may be even higher than reported in [4]. The experiment by Berta et al. [4] is further highly relevant because cells were at steady state, i.e. at the predominant growth stage in nature, but still consumed vast amounts of H_2. Indeed the H_2 consumption of cells at steady state or resting may be just as high or higher than for growing cells but growth is low or absent (Tables A.1-A.3).

4.4 Knowledge gaps and future research

More work is needed to predict the magnitude of microbial growth, H_2 consumption rates, and (not least) the mutual interaction of the microbial processes in DOGFs. The list of unknowns and uncertainties is long. To begin with are the poorly elucidated nutrient requirements of the microorganisms, especially in mixed cultures (e.g., [71]). Adding to this are the missing or incomplete datasets on the physical environment of certain reservoirs along with their gas phase and brine compositions, including chaotropy and kosmotropy characteristics. A better elucidation of the latter would allow the calculation of the dominating microbial processes via their free energies of the reaction. Combined with an analysis of the microbial community and

738 metabolism this could give new insights into whether or not we can theoretically predict which
739 microbial processes occur in DOGF and to which extend.

740 A further complication is the non-cultivability of many microorganisms in the deep subsurface,
741 including DOGF [12, 34, 56, 98, 183]. Considering tiny culturabilities of ≤0.1% of the total
742 viable cell count in many subsurface environments [34], any attempts to assign sterile habitats
743 or quantify microbial H_2 consumption via cultivated microorganisms may seem in vain. In gas
744 reservoirs, the percentage of cultured bacteria may be higher, ranging between 86-95% within
745 each phylum [98]. Field-based metabolic activity measurements could circumvent any non-
746 cultivability issues observed in laboratory experiments. Field studies should also be prioritized
747 considering that microbial cell sizes and masses in nature are only 4-21 % of the laboratorial
748 cell masses [213] which reduces the nutrient requirement per cell, thereby allowing more cells
749 to proliferate on any given amount of nutrients.

750 The lack of knowledge about the changes in microbial ecology as a response to increased H_2
751 concentrations beyond the level of functional groups is one of the major hurdles in our attempt
752 to understand of the effect of high H_2 concentrations on the subsurface microbiology. Emerging
753 evidence on the subject highlights species-specific responses to high pH_2 [98, 198, 200], and
754 that H_2 injection may leave its fingerprint on the subsurface microbial community for decades
755 [98]. Knowledge about the initial effect of a drastic increase in pH_2 in the subsurface is lacking.
756 One possibility is that more EPS will be produced as a response to the perturbation with
757 increased H_2, as has been shown for other types of perturbation [18, 92, 214], and considering
758 the toxicity of high pH_2 on methanogens [181, 192, 194], with possible adverse effects on gas
759 injectivity and withdrawal.

760 Future research should address the effect of high pH_2 on the metabolisms of different functional
761 groups and the EPS production in different geological settings and under changing nutritional

762 supply and physicochemical conditions. Mixed culture studies at low and high pH_2 can give
763 insight into competitive and syntrophic relations under these conditions and reveal changes in
764 the microbial community structure due to the pertubation with elevated H_2. Protocols for the
765 careful cultivation of nutrient-deprived deep subsurface cells need to be developed. More base-
766 line research includes determinations of the critical salinities and pressure tolerances that to
767 date are missing for many cultivated strains, as well as the study of the brine compositional
768 effects on the microbial community and metabolism. Research employing already cultivated
769 species can make use of the fact that the large majority of the cultivated species isolated from
770 subsurface environments can be found in other near-surface marine and terrestrial geothermal
771 environments [9, 183], and should employ chemostat studies that mimic the natural
772 environment.

773 5. Conclusion

774 Here we presented a novel site selection tool for H_2 storage and demonstrated its application
775 for 42 DOGF in the British and Norwegian North Sea and the Irish Sea and five H_2 storage test
776 sites. Our results highlight the hard limits to the cultivable microbial life on H_2 and can –with
777 some certainty- exclude life in several high-salinity or high-temperature, i.e. deeper reservoirs.
778 For low-salinity and low-temperature reservoirs our calculations indicate significant microbial
779 growth and a small but not insignificant H_2 consumption, both of which may further increase
780 during repeated storage cycles, giving replenishment of nutrients by mineral weathering,
781 decaying microbial cells and inflowing water. Hence, from the point of view of minimizing H_2
782 loss, clogging and corrosion, sites with more extreme conditions may be chosen over low-
783 temperature and low-salinity reservoirs where the majority of microorganisms can proliferate.
784 Yet, any storage operation will have to consider increased operational difficulties and costs

785 with increased depth. Additional investigation on subsurface life on H_2 is encouraged to help
786 manifest whether H_2 consumption in low-temperature aquifers is a threat to H_2 storage.

787

788 ASSOCIATED CONTENT

789 **Appendix.** Figure A.1 shows the solubility of hydrogen as a function of temperature and
790 pressure. Laboratories studies investigating homoacetogenesis, methanogenesis and SSR are
791 listed in Tables A.1, A.2 and A.3, respectively. Table A.4 provides the reservoir conditions
792 for 42 DOGF and five H_2 storage test sites. Text A.1 holds a discussion of the importance of
793 other hydrogen oxidizing processes for hydrogen storage. A detailed calculation of the
794 number SSRM cells that could grow based on the N content in the Frigg reservoir can be
795 found in Text A.1. Text A.2 and A.3 hold an example calculation of the hydrogen
796 consumption per synthesized cell and the calculation of the potential hydrogen consumption
797 in a hydrogen storage system, respectively.

798 **Author Contributions**

799 The manuscript was written through contributions of all authors. All authors have given
800 approval to the final version of the manuscript.

801 **Declaration of interest**

802 The authors declare no competing financial interest.

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