

13th International Conference on Greenhouse Gas Control Technologies, GHGT-13, 14-18
November 2016, Lausanne, Switzerland

The effect of variable oxygen impurities on microbial activity in conditions resembling geological storage sites

Hayden Morgan^{ab}, David Large^b, Keith Bateman^a, David Hanstock^c and Simon Gregory^a

^aBritish Geological Survey, Nicker Hill, Keyworth, Nottingham, NG12 5GG, UK

^bUniversity of Nottingham, Nottingham Road, Nottingham, NG7 2QL, UK

^cProgressive Energy, Bonds Mill, Stonehouse, Gloucestershire, GL10 3RF, UK

Abstract

Current specifications on carbon dioxide (CO₂) storage do not take into account the effect of oxygen (O₂) present as an impurity, on storage site microbiology. Some microbiology related impacts related to the CCS process include the potential blockage of injection well, corrosion of pipes, oil souring and oil degradation. To investigate this, microcosm experiments were set up using the O₂ concentrations of 0 ppm, 10 ppm, 100 ppm and atmospheric. Artificial groundwater and sandstone microcosms were inoculated with a mixed microbial community, incubated for 29 days and regularly sampled for gases produced and sampled at the end of the experiment to analyse the microbiology. Gas chromatography analysis of these microcosms showed no hydrogen sulphide (H₂S) production and a variable amount of CO₂ production. Microbial analysis of the microcosms show that the microbial inoculum (including sulphate reducing bacteria) was able to survive/grow better in the microcosms with 10 ppm and below compared to the higher levels of O₂. The levels of CO₂ for 100 ppm and atmospheric levels of O₂ were similar indicating the introduction of 100 ppm of O₂ could promote aerobic processes. This experiment has shown that small differences in O₂ concentrations affects microbial communities relevant to geological storage sites which could cause operational issues. Further investigation is required to properly assess the effect of small O₂ changes on H₂S production.

© 2017 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Peer-review under responsibility of the organizing committee of GHGT-13.

Keywords: CCS; Sulphate Reducing Bacteria; Saline Aquifers; Oxygen; Hydrogen Sulphide; Impurities.

1. Introduction

The storage of carbon dioxide (CO₂) in geological storage sites introduces a new range of gases to native microbial communities. In addition to CO₂, impurities are present within the injected gas such as oxygen (O₂). The presence and concentration of these impurities depends on the source of CO₂ and the type of capture used. It is predicted that the amount of O₂ could be as high as 6% [1]. Recommendations on the amount of O₂ impurities allowed within gas streams are mainly focused on the transport of the gas and not on the impacts upon storage.

Transport specifications of O₂ vary on the operator, some of which are 10 - 100 ppm [2]. Microbes can still survive in deep geological storage sites for CO₂, at depths 800 - 2000 m beneath the surface [3]. The introduction of low levels of O₂ is likely to affect microbial communities within the geological storage sites, which could lead to operational issues. Undesirable microbial impacts have been linked to such carbon capture and storage (CCS) operational issues such as injection blockages [4], pipeline corrosion [5], oil souring [6] and oil degradation [7]. These issues have been connected to hydrogen sulphide (H₂S) production by sulphate reducing bacteria (SRB). Sulphate reduction to H₂S is a process which occurs when there is no O₂ and the presence of O₂ should reduce the production of H₂S. However, the presence of O₂ encourages the activity of microorganisms capable of using O₂. Some microbes can survive without O₂ but can preferentially use O₂ when it is available. These O₂ utilising microorganisms can interact with SRB potentially stimulating the production of H₂S [8]. An experimental programme was conducted in order to investigate the effects of 0 ppm, 10 ppm, 100 ppm and atmospheric levels of O₂ to observe any changes in microbial communities and gases produced. The production of different gases, related to microbial activity, such as increase CO₂ could be because of increased respiration. Increases in H₂S from increased SRB activity could cause CCS operational issues. The analysis of microbial communities would indicate which conditions are more favourable for microbial growth and survival. This paper looks at the preliminary data from the variable O₂ microcosms.

2. Methods

2.1 Rock sample and preparation

The sandstone used in the experiments was a section of a core from the Cleethorpes borehole in North East Lincolnshire, England. The samples used were from approximately 900 m below the surface. The sandstone was crushed to particle sizes smaller than 500 µm. Sterilisation of the sandstone was performed by gamma irradiation using Gammacell[®] 1000 Elite with a total dose of 30 kGy from Cesium¹³⁷.

2.2 Artificial groundwater (AGW)

Using water chemistry data from Sherwood sandstone saline aquifer [9], the Welton borehole in the Sherwood sandstone saline aquifer, artificial ground water (AGW) was formulated as follows: MgCl₂·6H₂O (0.24 g), Na₂SO₄ (2.22 g), CaCl₂·2H₂O (4.40 g), NaCl (3.25 g), KCl (0.007 g), NaHCO₃ (1.00 g) and yeast extract (0.05 g), made up to a litre with deionised water and autoclaved to sterilise. Yeast extract was added to the AGW to represent the introduction of potential nutrients associated from drilling fluids aquifer. Prior to addition to the microcosms AGW measured pH 8.18.

2.3 Microbial inoculum

The inoculum added to the experiments was an enrichment culture of sandstone samples in Postgate's Medium B [10]. Attempts to obtain a sulphate reducing enrichment culture from sandstone obtained from Cleethorpes borehole were used in the microcosms, but they did not show positive growth for SRB. Instead, the sandstones samples from Godstone and Marden from the Upper Cretaceous Greensands formation in Kent were used for enrichment cultures. These were obtained at an approximate depth of 100-200 m below the surface in an underground cave network. Positive identification of the growth of SRB was indicated by a black precipitate of iron sulphate. The enrichment community was pelleted and washed three times with the AGW to remove the enrichment media. Some of the dominant bacteria within the enrichment culture were identified using Sanger DNA sequencing [11]. These were identified as being most closely related to a *Pseudomonas* species (KT991031), *Desulfotomaculum* species (KM494501), uncultured Firmicute (AB874517) and *Halomonas* species (KP241932). This demonstrates that the inoculum contained not only the key organisms of interest (SRB), but also a range of other bacteria likely to be encountered within a CO₂ storage site and which may have ecological interactions with the SRB in a storage site [12,13,14].

2.4 Experimental set up

Microcosms were set up containing 5 g crushed sandstone, 30 ml AGW and 1 ml microbial inoculum in 250 ml glass bottles. A control was set up without microbial inoculum. Both the experimental and the control microcosms were set up in triplicate. The microcosms were set up under 4 conditions to investigate the role of O₂ contaminants with CO₂ storage sites (atmospheric concentrations - approximately 209,500 ppm O₂), 100 ppm, 10 ppm and 0 ppm O₂. The atmospheric concentration microcosm experiments were set up in a laminar flow hood. The 0 ppm O₂ was achieved by putting the equipment into an anaerobic chamber, with an atmosphere of 95% nitrogen (N₂) and 5% hydrogen (H₂). The 10 ppm and 100 ppm levels of O₂ were achieved by bubbling gas of appropriate composition for 5 minutes to remove excess O₂ from the microcosms (10 ppm O₂ with N₂ balance and 100 ppm O₂ with N₂ balance, Calgaz Ltd) and sealing immediately. These were set up in an anaerobic chamber of N₂ and 200 ppm O₂ to reduce any contamination with atmospheric O₂ and to reduce starting levels of H₂ in the experiments. The microcosms were then sealed with a butyl rubber stopper and aluminium seal crimp tops. The microcosms were incubated at 37°C for 29 days.

2.5 Gas, pH and Eh measurements

Gas samples were taken from each microcosm every 5 days using a gas syringe. 2 ml samples were taken and analysed using Agilent Technologies 7820A GC for gas chromatography (GC). The carrier gas used for GC was helium. The program for GC analysis was held at 23°C for 3 minutes followed by a 3°C/min increase to 40°C and finally a 5°C/min increase to 90°C with a hold at 90°C for 2 minutes. Gases detected by GC analysis were H₂, N₂ and CO₂. Further gas analysis was performed using a Dräger gas monitor X-am 2000 used for the detection of H₂S and H₂/methane (CH₄). 2 ml gas samples were taken for Dräger gas analysis.

Groundwater samples were taken from the microcosms at the end of the experiment. pH and redox potential (Eh) were measured immediately after the experiment.

2.6 Microbial analysis

After 29 days, the microcosms were disassembled and samples were taken for microbial analysis. 1 ml mix of sandstone and groundwater from each microcosm was placed in 9 ml 1% glutaraldehyde fixative for epifluorescence cell counts. Epifluorescence cell counts will be completed later using an Acridine orange stain, which fluoresces between 500-526 for DNA, and visualised with a Zeiss III RS epifluorescence head filter. 1 ml mix of sandstone and groundwater was also taken for DNA extraction using a FastDNA™ SPIN kit for soil (MP Bio) according to the manufacturer's instructions. The extracted DNA was tested for the presence of bacterial and SRB DNA sequences by performing polymerase chain reaction (PCR) with the primers BAC341F-GC and BAC534R [15], which are specific for the bacterial 16S rRNA gene, and DSRp2060F and DSR4R, which are specific of the gene *dsrB* which is found in SRB [16][17]. This technique amplifies the targeted gene, if it is present within the extracted DNA, to detectable levels. The DNA was used to create community profiles to observe differences between the microcosms through denaturing gradient gel electrophoresis (DGGE). DGGE separates DNA by a denaturing gradient which creates a fingerprint of a microbial community [18]. Gene fingerprints for the gene 16S rRNA were obtained using a DGGE of 40-70% denaturing gradient. Range-weighted richness is one way to interpret data from a DGGE to give a value to the number and range of bands in a given sample. It is calculated by squaring the number of bands and multiplying it by the percentage of denaturing gradient between the first and last band. A range-weighted richness value above 30 is considered a highly habitable environment, 10-30 is considered moderately habitable and below 10 is considered show restricted colonisation [19].

3. Results

3.1 Gas analysis

Table 1. Mean Dräger gas readings for 0 ppm O₂ microcosms with standard deviation.

Days Incubated	Mean H ₂ /CH ₄ (LEL%)			
	Control	Standard Deviation	Inoculated	Standard Deviation
5	41	5.69	49	4.93
8	53	2.08	48	10.41
12	31	1.53	25	2.52
20	43	2.08	33	5.13
25	36	2.08	29	6.66

No H₂S was detected during the experiments in any microcosm. H₂/CH₄ was only detected in the 0 ppm O₂ microcosms (Table 1). The H₂/CH₄ levels detected using the Dräger were measured in terms of the lower explosive limit (%). The uninoculated control showed higher levels of H₂/CH₄ compared to the inoculated microcosm.

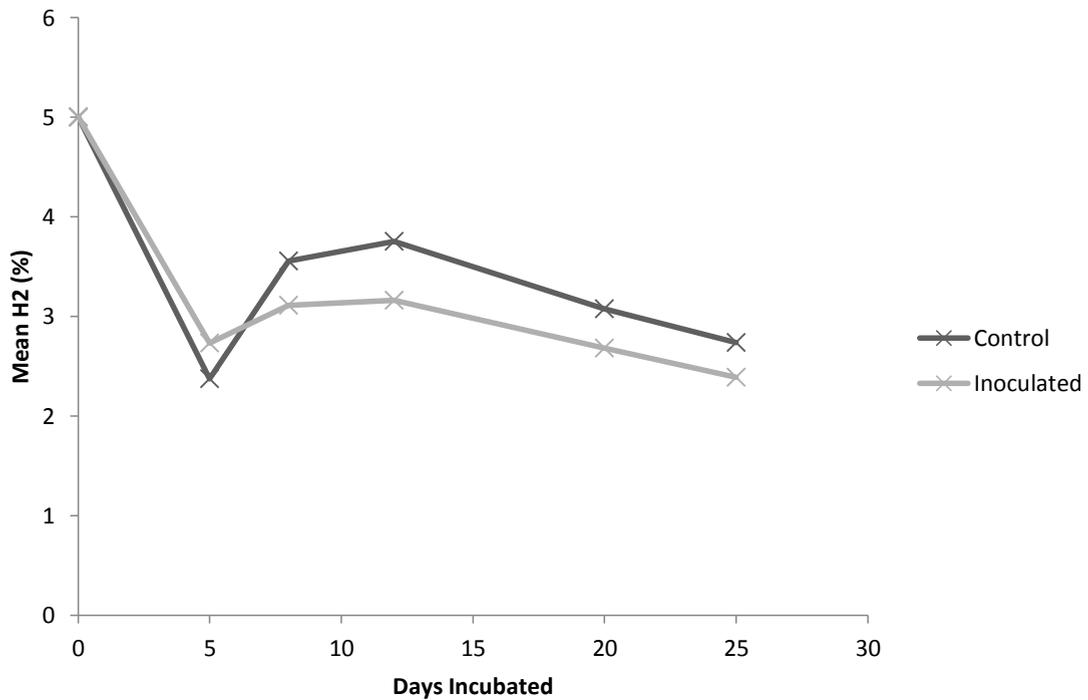


Figure 1. Mean H₂ (%) in 0 ppm O₂ microcosms.

Table 2. Standard deviations for mean H₂ (%) in 0 ppm O₂ microcosms.

Days Incubated	Standard deviations for mean H ₂ (%) in 0 ppm O ₂ microcosm	
	Control	Inoculated
5	0.04	0.08
8	0.02	0.02
12	0.08	0.06
20	0.27	0.43
25	0.52	0.29

Figure 1 shows hydrogen concentration in the microcosms throughout the experiment measured by GC. A decrease from the starting 5% H₂ after 5 days was observed for both the uninoculated control and inoculated microcosm. Readings peaked at 12 days with 3.2% and 3.8% for inoculated and uninoculated microcosms. There was then a drop on 20 and 25 days. The control microcosms showed a higher mean level of H₂ than the inoculated microcosm.

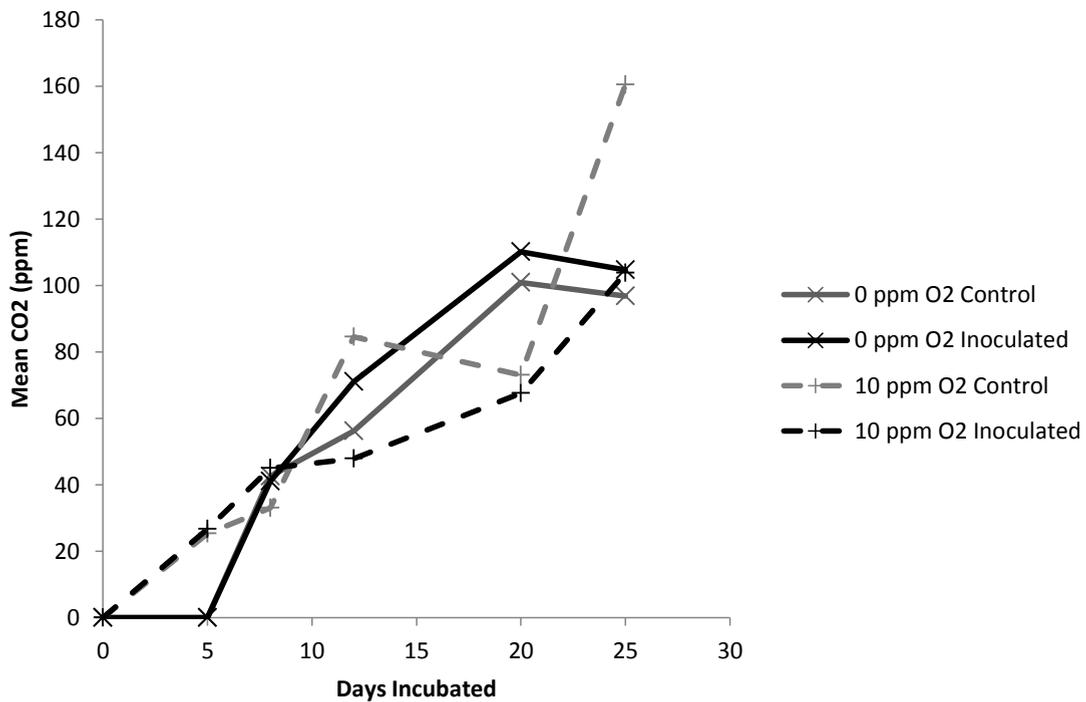


Figure 2. Mean CO₂ (ppm) in 0 ppm and 10 ppm O₂ microcosms.

Table 3. Standard deviations for mean CO₂ (ppm) in 0 ppm and 10 ppm O₂ microcosms.

Days Incubated	Standard deviations for mean CO ₂ (ppm) in 0 ppm O ₂ microcosms		Standard deviations for mean CO ₂ (ppm) in 10 ppm O ₂ microcosms	
	Control	Inoculated	Control	Inoculated
	5	-	-	11.08
8	4.88	6.60	9.35	12.24
12	3.83	6.57	5.36	9.59
20	8.01	10.54	3.39	2.84
25	16.14	8.67	84.25	34.43

Figure 2 shows the average CO₂ production from the 0 ppm and 10 ppm O₂ microcosms from GC measurement. CO₂ was not detected after 5 days in the either 0 ppm O₂ microcosm. The readings at 8 and 12 days showed an increase in CO₂ levels in the 0 ppm O₂ microcosms and the CO₂ levels showed a small drop after 20 and

25 days. The inoculated microcosm at 0 ppm O₂ had higher levels of CO₂ production than the control. Highest CO₂ readings of around 100 ppm were seen at the final reading.

In the 10 ppm O₂ microcosms the CO₂ was detected in all GC readings. The levels of CO₂ in the 10 ppm O₂ microcosm were generally higher in the control than the inoculated microcosm. The inoculated microcosm reached a CO₂ peak of 104 ppm (day 25) with the control microcosm producing levels greater than 160 ppm CO₂. The results for day 25 of 10 ppm O₂ microcosms had high standard deviations values (Table 3).

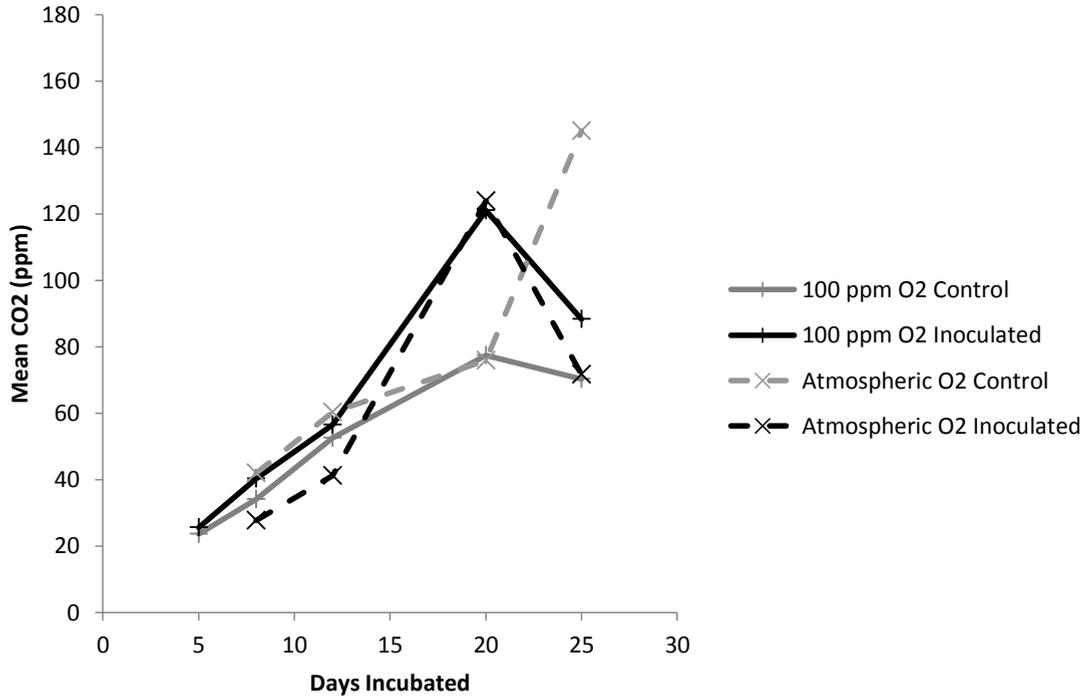


Figure 3. Mean CO₂ (ppm) in 100 ppm O₂ and atmospheric microcosms.

Table 4. Standard deviations for mean CO₂ (ppm) in 100 ppm and atmospheric O₂ microcosms.

Days Incubated	Standard deviations for mean CO ₂ (ppm) in 100 ppm O ₂ microcosms		Standard deviations for mean CO ₂ (ppm) in atmospheric O ₂ microcosms	
	Control	Inoculated	Control	Inoculated
5	7.52	6.76	-	-
8	7.52	7.91	27.13	8.80
12	2.71	10.86	24.94	0.45
20	11.46	66.91	13.56	58.47
25	4.65	5.22	118.66	12.22

CO₂ was detected in all readings for the 100 ppm O₂ microcosm (Figure 3). An increase in CO₂ was detected in both microcosms peaking on day 20 before dropping in the final reading. The inoculated microcosm showed higher levels of CO₂ than the uninoculated control. A high standard deviation (Table 4) for the 100 ppm microcosm can be seen for the inoculated microcosms on day 20.

In the microcosms with atmospheric conditions (Figure 3), CO₂ was not detected in the first reading. The control microcosm for atmospheric conditions showed higher levels of CO₂ in the experiment apart from the reading on day 20 where the inoculated microcosm produced higher levels of CO₂. Standard deviations are highest for atmospheric microcosms on day 25 for the control and day 20 for the inoculated microcosms.

3.2 Microbial analysis

PCR using the primers DSRp2060F and DSR4R were able to detect the presence of *dsrB* gene in one out of three of the atmospheric, one out of three of the 100 ppm O₂, two out of three of the 10 ppm O₂ and two out of three of the 0 ppm O₂ microcosms. No positive results for the *dsrB* gene were seen in the control microcosm.

Bands for the 16S rRNA gene were seen in all microcosms. The control microcosms showed 1-3 bands per lane and the inoculated microcosms showed 1-7 bands per lane. The inoculated microcosms had more bands of a greater intensity compared to the control microcosms which all had weak band intensity. The highest number of bands per group is 10 ppm O₂ with 19 bands in total. The lowest number of bands for an inoculated microcosm group is 100 ppm with 7 bands. The atmospheric inoculated microcosms had 13 bands and the 0 ppm O₂ had 16. All of the range-weighted richness values were below 10 which means that all of the microcosms would be considered to only allow restricted colonisation.

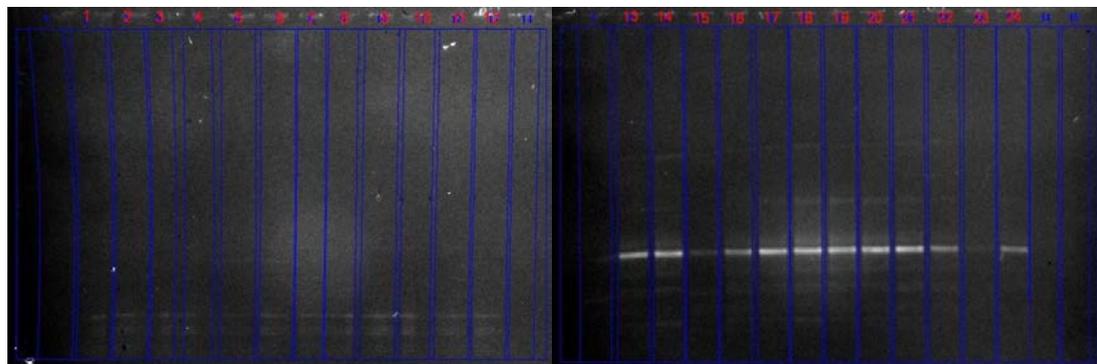


Figure 4. DGGE analysis of *16S rRNA* genes from variable O₂ microcosms. (1-3) Atmospheric controls, (4-6) 0 ppm O₂ control, (7-9) 10 ppm O₂ control, (10-12) 100 ppm O₂ control, (13-15) atmospheric inoculated, (16-18) 0 ppm O₂ inoculated, (19-21) 10 ppm O₂ inoculated and (22-24) 100 ppm O₂ inoculated.

Table 5. Range-weighted richness of each lane of DGGE.

Microcosm	Range-Weighted Richness
Atmospheric Control 1	0
Atmospheric Control 2	0.115
Atmospheric Control 3	0.044
0 ppm Control 1	0.044
0 ppm Control 2	0.425
0 ppm Control 3	0.425
10 ppm Control 1	0.044
10 ppm Control 2	0.051
10 ppm Control 3	0.115
100 ppm Control 1	0.115
100 ppm Control 2	0.044
100 ppm Control 3	0.044
Atmospheric Inoculated 1	2.716
Atmospheric Inoculated 2	2.716
Atmospheric Inoculated 3	0.256
0 ppm Inoculated 1	0.256
0 ppm Inoculated 2	5.323
0 ppm Inoculated 3	5.323
10 ppm Inoculated 1	5.323
10 ppm Inoculated 2	5.323
10 ppm Inoculated 3	2.183
100 ppm Inoculated 1	1.397
100 ppm Inoculated 2	0
100 ppm Inoculated 3	0.256

3.3 pH and Eh measurements

Table 6. pH and Eh measurements for the microcosms at the end of the experiment.

Microcosm	pH	Eh (mV)
Artificial Groundwater	10.50	162.6
0 ppm Control 1	10.33	38.5
0 ppm Control 2	10.17	-32.0
0 ppm Control 3	9.94	-0.3
0 ppm Inoculated 1	10.07	-29.4
0 ppm Inoculated 2	9.97	-6.1
0 ppm Inoculated 3	10.02	-23.5
10 ppm Control 1	10.22	164.0
10 ppm Control 2	10.16	132.6
10 ppm Control 3	10.43	141.4
10 ppm Inoculated 1	9.72	170.5
10 ppm Inoculated 2	10.12	204.1
10 ppm Inoculated 3	10.30	149.2
100 ppm Control 1	10.36	155.2
100 ppm Control 2	10.20	164.9
100 ppm Control 3	10.38	171.0
100 ppm Inoculated 1	10.25	189.1
100 ppm Inoculated 2	10.16	184.6
100 ppm Inoculated 3	10.18	189.9
Atmospheric Control 1	9.65	205.1
Atmospheric Control 2	10.07	78.0
Atmospheric Control 3	9.95	133.0
Atmospheric Inoculated 1	9.91	122.9
Atmospheric Inoculated 2	9.94	140.0
Atmospheric Inoculated 3	9.89	134.4

ZoBell's solution standard value for atmospheric and 0 ppm 0 ppm was 261.0 mV and for 10 ppm and 100 ppm O₂ was 262.8 mV.

pH and Eh values can be found in Table 6. They can influence microbial and chemical reactions within an environment. The pH of the ground water had evolved over the course of the experiment from 8.18 to 10.5 making the environment more alkaline than was originally planned. This can be seen in all the microcosms, with pH ranging from 9.65 to 10.43. The lowest average pH readings are seen in the atmospheric microcosms. Microcosms set up with 0 ppm O₂ have the lowest average Eh.

4. Discussion

H₂S was not detected in any microcosm which was unexpected since because of the identification of SRB in the enrichment cultures used as inoculum (as detected by the presence of a black precipitate in the culture media and the retrieval of SRB DNA sequence from the same) and the amplification of the *dsrB* gene in inoculated, but not control microcosms. The *dsrB* gene was detected in the microcosms with lower O₂ (0 ppm and 10 ppm O₂) than the microcosms with higher levels of O₂ (100 ppm and atmospheric). This is consistent with literature on O₂ conditions tolerances of SRB as they have been observed to have reduced activity in increasing O₂ concentrations but can still grow in O₂ concentrations up to 144ppm [20]. If a balance was achieved where the O₂ could suppress microorganisms which need O₂ and those that have reduced activity in its presence this could be a way to prevent any undesirable microbial impacts. Quantitative PCR (a method for quantifying DNA) has not been carried out but the low intensity of positive PCR bands suggests that only low levels of DNA were present. With more sulphate

reducing genes being seen in 0 ppm and 10 ppm O₂ this could suggest that H₂S is more likely at these O₂ concentrations.

The absence of detectable SRB activity could be because the pH measured at the end of the experiments was much higher than expected and high pH can inhibit microbial sulphate reduction [21]. For sulphate reduction to take place the Eh also needs to be below -100 mV [22]. All of the microcosms had an Eh value above this and could be why no H₂S was detected. For CH₄ to take place the Eh needs to be below -150 mV [23] and so this indicates that the H₂/CH₄ detected by the Dräger metre is most likely H₂. As SRB were detected in the inoculated microcosms it is possible that with favourable Eh, H₂S production would still be possible.

Faint bands were seen on the DGGE for control microcosms, which indicates that there were microbes present even within the control microcosms. The inoculated microcosms that showed the least number of bands was 100 ppm O₂ with a higher numbers being seen in the O₂ concentrations that were higher and lower. This could be because 100 ppm O₂ is too low for good growth with O₂ but it also has enough O₂ reduce other processes such as H₂S production. Despite the lowest number of bands, 100 ppm O₂ still had similar levels of CO₂ to those seen in the atmospheric microcosms. This shows that the bands that are missing in the 100 ppm O₂ microcosms are not contributing greatly to CO₂ production.

The range-weighted richness was calculated for each sample. All microcosms had a range-weighted richness value of less than 10 meaning that all microcosms could allow restricted colonisation. This can be expected as the microcosms were inoculated with an enrichment culture that grew under conditions without O₂ within SRB enrichment media. The greatest range-weighted richness values were seen in the 100 ppm microcosms followed by 0 ppm microcosm. This indicates that these conditions have the biggest diversity within the microcosms. Epifluorescence microscopy will be performed on these samples to identify difference in the cell numbers under different conditions. To further help identify which microbes were present in the microcosms DNA sequencing of DGGE bands will be performed in the future. This will allow a better understanding of the potential microbial reactions occurring different conditions in this experiment.

The two main sources of CO₂ production within the microcosms would be microbiological and geochemical. The microbiological CO₂ is most likely from respiration by the O₂ utilising microbes. The formation of CO₂ through geochemical processes would be from carbonates in the sandstone. Another source for CO₂ in the atmospheric O₂ microcosms would be from the atmosphere. The inoculated microcosms for the atmospheric and 100 ppm O₂ show similar CO₂ production, both reaching a peak above 100 ppm CO₂ before dropping at day 25. These peaks at day 20 have high standard deviation values because of high variability in the microcosms. The CO₂ seen in the inoculated microcosms is likely a combination of both microbial and geochemical sources. The control microcosms for atmospheric conditions and 100 ppm O₂ have similar levels of CO₂ production until day 25 where the atmospheric control has a higher average of 145 ppm CO₂. This peak has a high standard deviation value. Although the controls should have been sterile, DNA results show that they were not and therefore the variability within the control microcosm could be because one control microcosm had a higher initial biomass than the others. The results suggest that 100 ppm O₂ could promote aerobic processes during the injection of CO₂. This could lead to some problems when using it for enhanced oil recovery as it could promote the degradation of oil. The initial degradation of oil by O₂ utilising organisms has also been linked to increased SRB activity [8] which could further lead to H₂S production and H₂S related issues.

The 10 ppm and 100 ppm O₂ inoculated microcosms show different trends in CO₂ levels. The 10 ppm O₂ inoculated microcosm shows a more gradual increase whereas the 100 ppm O₂ microcosm showed a peak in day 20 and then a drop in day 25. The peaks seen in both 10 ppm and 100 ppm O₂ microcosms have high standard deviation values because of high variability between the replicates.

Although the different O₂ concentrations produced different graph shapes, the final reading for all of the inoculated microcosms was around 100 ppm CO₂. In comparison the un-inoculated control microcosms had greater differences in their CO₂ production. This could be because further respiration and growth was limited by the availability of nutrients. Extending the experiment to observe any further increase in CO₂ levels would be one option to investigate if this is the case.

5. Conclusion

- The 100 ppm O₂ microcosms showed the fewest number of bands on the DGGE which indicates a restriction in what can grow under these conditions. If an O₂ concentration was able to restrict growth further it could be a way to prevent undesirable microbial impacts.
- The detection of SRB and bacterial genes showed that there was a greatest diversity seen in microcosms 10 ppm O₂ and below. This suggests that the SRB activity is more likely at these O₂ levels, which could lead to CCS related issues.
- Under these experimental conditions, 100 ppm O₂ inoculated microcosms show similar patterns of CO₂ production to the atmospheric inoculated microcosm. This indicates that the introduction of 100 ppm O₂ could promote the aerobic processes, such as the degradation of oil.
- Although no H₂S was detected in this experiment, there is evidence for greater microbial and SRB growth at 10 ppm O₂ and below, when compared to 100 ppm O₂ and above. Further investigation will be conducted, at more suitable pH and Eh conditions for H₂S production, to further examine the influence of O₂ concentration on H₂S production.

References

- [1] Porter R. T. J., Fairweather M., Pourkashanian M., Woolley R. M. The range and level of impurities in CO₂ streams from different carbon capture sources. *Int. J. Greenh. Gas Control*; 2015. 36:161–174.
- [2] de Visser E., Hendriks C., Barrio M., Mølnvik M. J., de Koeijer G., Liljemark S., Le Gallo Y. Dynamis CO₂ quality recommendations. *Int. J. Greenh. Gas Control*; 2008. 2(4):478–484.
- [3] Head I. M., Jones D. M., Larter S. R. Biological activity in the deep subsurface and the origin of heavy oil. *Nature*; 2003. 426(6964):344–352.
- [4] Zettlitz M., Moeller F., Morozova D., Lokay P., Würdemann H. Re-establishment of the proper injectivity of the CO₂-injection well Ktzi 201 in Ketzin, Germany. *Int. J. Greenh. Gas Control*; 2010. 4(6):952–959.
- [5] Lerm S., Westphal A., Miethling-Graff R., Alawi M., Seibt A., Wolfgramm M., Würdemann H. Thermal effects on microbial composition and microbiologically induced corrosion and mineral precipitation affecting operation of a geothermal plant in a deep saline aquifer. *Extremophiles*; 2013. 17:311–327.
- [6] Jordan L. C., Walsh J. M. Selection of an Active Souring Management Solution for a Gulf of Mexico Waterflood. *Corros*; 2004; 4759:1–11.
- [7] Sherry A., Gray N. D., Ditchfield A. K., Aitken C. M., Jones D. M., Röling W. F. M., Hallmann C., Larter S. R., Bowler B. F. J., Head I. M. Anaerobic biodegradation of crude oil under sulphate-reducing conditions leads to only modest enrichment of recognized sulphate-reducing taxa. *Int. Biodeterior. Biodegradation*; 2013. 81:105–113.
- [8] Jobson A. M., Cook F. D., Westlake D. W. S. Interaction of aerobic and anaerobic bacteria in petroleum biodegradation. *Chem. Geol*; 1979. 24(3–4):355–365, Feb. 1979.
- [9] Smedley P. L., Edmunds M. Redox Patterns and Trace-Elements Behaviour in the East Midlands Triassic Sandstone Aquifer, U.K. *Ground Water*; 2002. 40(1):44–58.
- [10] Postgate J. R.. *The Sulphate-Reducing Bacteria*. Second Edition. Cambridge University Press, Cambridge, 1984.
- [11] Sanger F., Nicklen S., Coulson R. DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. U. S. A.*; 1977. 74(12):5463–7.
- [12] Frimmersdorf E., Horatzek S., Pelnikevich A., Wiehlmann L., Schomburg D. How *Pseudomonas aeruginosa* adapts to various environments: A metabolomic approach. *Environ. Microbiol.*; 2010.12(6):1734–1747.
- [13] Dong Y., Kumar C. G., Chia N., Kim P.-J., Miller P. A., Price N. D., Cann I. K. O., Flynn T. M., Sanford R. A., Krapac I. G., Locke R. A., Hong P.-Y., Tamaki H., Liu W.-T., Mackie R. I., Hernandez A. G., Wright C. L., Mikel M. A., Walker J. L., Sivaguru M., Fried G., Yannarell A. C., Fouke B. W. *Halomonas sulfidaeris*-dominated microbial community inhabits a 1.8 km-deep subsurface Cambrian Sandstone reservoir. *Environ. Microbiol.*; 2014. 16(6):1695–708.
- [14] Morozova D., Wandrey M., Alawi M., Zimmer M., Vieth A., Zettlitz M., Würdemann H. Monitoring of the microbial community composition in saline aquifers during CO₂ storage by fluorescence in situ hybridisation. *Int. J. Greenh. Gas Control*; 2010. 4(6):981–989.
- [15] Muyzer G., Dewaal E. C., Uitterlinden A. G. Profiling of Complex Microbial Populations by Denaturing Gradient Gel Electrophoresis Analysis of Polymerase Chain Reaction-Amplified Genes Coding for 16S rRNA. *Appl. Environ. Microbiol.*; 1993. 59(3):695–700.
- [16] Geets J., Borremans B., Diels L., Springael D., Vangronsveld J., van der Lelie D., Vanbroekhoven K. DsrB gene-based DGGE for community and diversity surveys of sulfate-reducing bacteria. *J. Microbiol. Methods*; 2006. 66(2):194–205.
- [17] Wagner M., Roger A. J., Flax J. L., Brusseau G., Stahl D. Phylogeny of dissimilatory sulfite reductases supports an early origin of sulfate respiration. *J. Bacteriol.*; 1998. 180(11):2975–2982.

- [18] Muyzer G., Smalla K. Application of denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) in microbial ecology. *Antonie Van Leeuwenhoek*; 1998. 73(1):127–41.
- [19] Marzorati M., Wittebolle L., Boon N., Daffonchio D., Verstraete W. How to get more out of molecular fingerprints: Practical tools for microbial ecology. *Environ. Microbiol.*; 2008. 10(6):1571–1581.
- [20] Marschall C., Frenzl P. and Cypionka H. Influence of oxygen on sulfate reduction and growth of sulfate-reducing bacteria. *Archives of Microbiology*; 1993. 159:168-173.
- [21] O’Flaherty V., Mahony T., O’Kennedy R., Colleran E. Effect of pH on growth kinetics and sulphide toxicity thresholds of a range of methanogenic, syntrophic and sulphate-reducing bacteria. *Process Biochem.*; 1998. 33(5):555–569.
- [22] Jørgensen B. B. Bacterial sulfate reduction within reduced microniches of oxidized marine sediments. *Mar. Biol.*; 1977. 41(1):7–17.
- [23] Wang Z. P., DeLaune R. D., Patrick W. H., Masscheleyn P. H. Soil Redox and pH Effects on Methane Production in a Flooded Rice Soil. *Soil Sci. Soc. Am. J.*; 1993. 57(2):382–385.