Microbial community analyses of produced waters from high-temperature oil reservoirs reveal unexpected similarity between geographically distant oil reservoirs

Daehyun D. Kim, Corynne O’Farrell, Courtney R. A. Toth, Oscar Montoya, Lisa M. Gieg, Tae-Hyuk Kwon and Sukhwan Yoon

1 Department of Civil and Environmental Engineering, KAIST, Daejeon, Korea. 2 Department of Biological Sciences, University of Calgary, Calgary, AB, Canada.

Summary
As a preliminary investigation for the development of microbial-enhanced oil recovery strategies for high-temperature oil reservoirs (~70 to 90°C), we have investigated the indigenous microbial community compositions of produced waters from five different high-temperature oil reservoirs near Segno, Texas, U.S. (~80 to 85°C) and Crossfield, Alberta, Canada (~75°C). The DNA extracted from these low-biomass-produced water samples were analysed with MiSeq amplicon sequencing of partial 16S rRNA genes. These sequences were analysed along with additional sequence data sets available from existing databases. Despite the geographical distance and difference in the physicochemical properties, the microbial compositions of the Segno and Crossfield produced waters exhibited unexpectedly high similarity, as indicated by the results of beta diversity analyses. The major operational taxonomic units included acetoclastic and hydrogenotrophic methanogens (Methanosetaeaceae, Methanobacterium and Methanoculleus), as well as bacteria belonging to the families Clostridaceae and Thermotogaceae, which have been recognized to include thermophilic, thermotolerant, and/or spore-forming subtaxa. The sequence data retrieved from the databases exhibited different clustering patterns, as the communities from close geographical locations invariably had low beta diversity and the physicochemical properties and conditions of the reservoirs apparently did not have a substantial role in shaping of microbial communities.

Introduction
Petroleum remains as the primary source of energy, in spite of the recent surge in energy production from alternative, renewable sources (Sieminski, 2015). The total global reserve of petroleum is by no means scarce; however, the deposits of easily recoverable crude oil that can be put into production using conventional production technology are dwindling. Most of potential deposits of conventional oil have already been explored and remaining unexplored deposits often pose challenges for economical production due to their remoteness or environmental sensitiveness (Muggeridge et al., 2014). To enhance the recovery efficiencies of the developed oilfields, various enhanced oil recovery (EOR) techniques, for example injection of miscible gas (e.g., CO₂ and N₂), steam flooding and injection of polymers and/or surfactants, have been developed and implemented (Youssef et al., 2009). Another EOR technique that has gathered significant interest is the microbial-enhanced oil recovery (MEOR) technique, wherein microbial activities are utilized to partially degrade long-chain hydrocarbons, produce gases and organic acids, and/or alter wettability of solid surfaces, all aiming to enhance oil mobility (Jack, 1991; Youssef et al., 2009).

Although MEOR is an attractive energy-efficient and environmentally friendly alternative, it has not been widely implemented. One of the barriers to broad implementation of MEOR practices is the paucity of reliable...
data from scientific investigations that can be used to predict behaviour of the indigenous microbial community upon in situ biostimulation or bioaugmentation (Youssef et al., 2009; Lewin et al., 2014). Since the 1980s, scientific investigations, both culture-based and culture-independent, have been performed to better understand the microbial community structures and metabolic potentials in developed oil reservoirs (Mueller and Nielsen, 1996; Orphan et al., 2000, 2003). More recently, high-throughput sequencing techniques (e.g., pyrosequencing and Illumina HiSeq/MiSeq sequencing technologies) have been implemented to analyse the microbial community compositions and metagenomes of oil reservoirs (An et al., 2013; Lewin et al., 2014; Frank et al., 2016; Hu et al., 2016; Vigneron et al., 2017). These investigations have demonstrated that stable active microbial populations are established in the subsurface oil reservoirs with temperatures up to 80°C and even higher, and also that anthropogenic alterations, for example injection of nitrate to treat souring, may lead to perturbation of the indigenous microbial populations and their metabolic properties. Nevertheless, the data acquired in previous research projects are yet too quantitatively limited to cover the diverse environmental conditions that can characterize subsurface oil reservoirs. Due primarily to the difficulty in sample collection and limited public disclosure of information from the oil industry sector, the availability of sequencing data in public databases remains limited.

In this study, the microbial community compositions in produced waters collected from four separate high-temperature oil wells in the Segno oilfield near Houston, TX, USA (80–85°C) and an oil well in the Crossfield oilfield, AB, Canada (75°C) were analysed to enhance the understanding of the microbial community structure in the deep subsurface high-temperature (>80°C) oil reservoirs, as a preliminary investigation for developing MEOR strategies for these types of reservoirs. Microbial community compositions of such high-temperature reservoirs have rarely been investigated. Furthermore, we analysed these microbial community profiles alongside those from oil reservoirs (produced water samples) across the globe having diverse physicochemical properties. These investigations revealed an unexpected level of similarity among the microbial communities of the high-temperature oil reservoirs in two geographically distant locations that have not yet been observed in oil reservoir microbiomes.

Results and discussion

The physicochemical properties of the produced water samples

The physicochemical properties of the produced water samples (CFW: Crossfield well sample; CFS: Crossfield separator sample; SG30, SG54, SG80, and SG85: Segno well samples from wells 30, 54, 80, and 85, respectively) were analysed before sequencing (Table S1). The pH of the four produced water samples from Segno oil fields varied from 5.53 to 8.03. The produced water samples from oil well at the Crossfield site was weakly acidic (pH 4.70), while the produced water collected from the separator was measured to be pH 7.33. All of the produced water samples contained relatively high concentrations of organic acids including acetate, propionate, and formate, which may serve as labile electron donors for indigenous microbial population. The produced water from the oil well at the Crossfield site (CFW) had higher concentrations of SO_4^{2−} (23.7 mg l−1) compared to the four production water samples from Segno site (3.3–12.7 mg l−1). The NO_3 concentrations in all produced water samples fell below the detection limit (<1 mg l−1), suggesting NO_3 respiration is unlikely. Ferric iron was detected only from SG30 at 4.8 mg l−1; however, ferrous iron was detected in three of the four Segno samples (46.5–80.5 mg l−1) and the Crossfield (13.9 mg l−1 sample) at substantially larger concentrations. The low concentrations of these potential electron acceptors suggested that the microbiomes of these subsurface oil reservoirs may be electron acceptor-limited. Phosphate (PO_4^{3−}) concentrations were below the detection limit (1 μg l−1) in the produced water samples from both Segno and Crossfield sites, suggesting that lack of bioavailable phosphorous may also limit microbial growth in situ. The qPCR assays targeting universal 16S rRNA genes demonstrated that the microbial populations in the produced water samples, 172 ± 52 to 489 ± 178 copies (mL produced water)^−1, were orders of magnitudes lower than the cell numbers observed in produced waters from previously investigated oil reservoirs with comparable temperature ranges (Gittel et al., 2009; Li et al., 2017). Such low microbial cell counts were previously reported only in hyperarid Atacama soils and high Arctic permafrost samples, both of which are hostile to microbial habitation (Yergeau et al., 2010; Fletcher et al., 2011).

Microbial community profiles in the produced water samples

The microbial community compositions of the produced water samples from Crossfield and Segno were analysed with 16S rRNA amplicon sequencing using an Illumina MiSeq sequencing platform. After quality screening and merging of the paired-end sequences, amplicon sequencing of the produced water samples yielded an average of 65 230 reads (45 944–103 164 reads) per sample (Table S2). The Good’s coverage indices of >99% and saturated rarefaction curves (Fig. S1) indicated that most microbial diversities in the samples were
covered with the 16S amplicon sequencing analyses. The Shannon-Wiener indices of the samples ranged from 5.202 to 6.689, while the index value for the Crossfield separator sample was 2.370. The microbial community profiles of the produced water collected from the oil wells were strikingly similar considering the geographical distance between Segno and Crossfield oil fields and the differing chemical compositions; however, the microbial community composition of the Crossfield separator sample deviated greatly from the produced water collected from the oil well at the same site with relatively similar chemical composition (Fig. 1).

Archaea constituted 18.6–33.4% of the total microbial population in the produced water samples. In all produced water samples, >90% of the archaeal OTUs were affiliated to organismal groups identified as methanogens. The archaeal population profiles were virtually indistinguishable among the produced water samples from the oil wells, with Methanosaeta, an acetoclastic methanogen, as the most abundant archaeal genus (45.9–49.8% of archaeal population) in each of the produced water samples. Hydrogenotrophic (Methanobacterium, Methanothermococcus, Methanoculleus, Methanolallis, Candidatus Methanoregula, and Methanolovia: 42.5–47.2% of the archaeal populations) and methylotrophic methanogens (Methanolobus and Methanomethyloversans: 1.0–3.7% of the archaeal populations) were also found in the produced water samples, suggesting that multiple methanogenic pathways may coexist in the examined oil reservoirs despite the presence of dissolved SO$^2_-$ and presumed sulphate reduction activities that may inhibit methanogenesis (Fig. 1A). Uncharacterized WSA2 class (phylum Euryarchaeota) was also recovered, although at much lower relative abundances (0.7–1.4%).

The OTUs affiliated to members of the classes Clostridia and Alphaproteobacteria dominated the bacterial populations in the production water samples from the oil wells. Clostridia constituted the most abundant taxa (of all bacteria and archaea) in the samples CFW, SG30, SG54, and SG85, while members of the Alphaproteobacteria were dominant in the sample SG80 (Fig. 1B). Members of Clostridia are known to thrive in moderately thermophilic regimes and are known to be spore-forming, and thus, may be suited to survive amid shifting temperature and pressure conditions (de Rezende et al., 2012; Aülo et al., 2013). Within the Clostridia class, only 14.6–20.9% of OTUs could be identified at the genus level and 38.7% of these OTUs were identified as Desulfotomaculum, a genus generally known as thermophilic sulphate-reducing bacteria (Table S3) (Aülo et al., 2013). Several isolates and enrichments of Desulfotomaculum spp. have also been found to form syntrophic associations with hydrogenotrophic methanogens, which may be one of the pathways contributing to CH$_4$ production in the examined oil reservoirs (Imachi et al., 2006). Alphaproteobacteria class was also abundant in the produced water samples. Especially in the CFW sample, a member of Alphaproteobacteria (assigned to the order Rhizobiales) was the most abundant group of microorganisms, accounting for 37.7% of the total microbial population (Table S3). The order Rhizobiales, members of which are known as anaerobic hydrocarbon degraders, was previously identified as one of the major groups of organisms inhabiting several thermophilic (55–70°C) Chinese oil reservoirs (Zhang et al., 2012).

Apart from Clostridia and Alphaproteobacteria, Deltaproteobacteria also constituted a substantial proportion of the produced water samples (8.9–16.6% of the

Fig. 1. The compositions of (A) archaeal and (B) bacterial population in produced waters from oil reservoirs near Segno, Texas (SG30, SG54, SG80, SG85) and Crossfield, Alberta (CFW, CFS). The notations in the legend f, c, o, and g stand for the OTUs assigned to family, class, order and genus levels respectively. The processed reads were clustered into OTUs by assigning to the Greengenes v13.8 reference database or de novo clustering (for reads with no matches in the database) with a cut-off value of 97%.

© 2018 The Authors. Microbial Biotechnology published by John Wiley & Sons Ltd and Society for Applied Microbiology, Microbial Biotechnology, 11, 788–796
Coomparative analyses of oil reservoir microbial communities

The microbial community profiles of the Crossfield and Segno produced waters were analysed in depth alongside the microbial community profiles of produced waters from other oil reservoirs of varying geographical locations and physicochemical characteristics (Table S4). Comparisons were constructed with the raw 16S rRNA amplicon sequence data sets acquired from the NCBI Sequence Read Archive (SRA) and through personal communication (Lewin et al., 2014; Gao et al., 2015; Hu et al., 2016; Shelton et al., 2016; Li et al., 2017; Vigneron et al., 2017). As expected from the nearly identical microbial compositions of the Crossfield and Segno samples, tight clustering was observed for the microbial communities in these samples, regardless of the metrics used for beta diversity calculation (Fig. 2). Except for the Segno and Crossfield produced water communities, no obvious clustering of the communities from produced waters collected from distant geographical regions was observed. The two produced water samples from the separate oil reservoir formations (~3 km apart) in the Norwegian Sea, previously reported to exhibit unusual similarity (Lewin et al., 2014), clustered closely when analysed with Bray-Curtis or unweighted Unifrac distance metrics, but were distantly plotted with weighted Unifrac distance metrics. The only instance of tight clustering between communities constructed with data sets from two independent studies was observed between the communities from the oil wells in the Norwegian Sea and Halfdan oil field in the Danish North Sea, albeit only when analysed with unweighted Unifrac distance metric. This close phylogenetic association between the OTUs in these samples may still be attributed to their geographical proximity (Fig. S2) (Lewin et al., 2014; Vigneron et al., 2017). The physicochemical characteristics of the tightly-clustered oil reservoirs exhibited little consistency (Table S4) and the clustering patterns appeared to depend primarily on the geographical proximity, rather than any specific physicochemical parameter. The close association of the produced water microbial communities in Segno and Crossfield sites, two geographical locations separated by 2850 km (1771 miles) of discontinuous terrain, was thus a unique observation.

An OTU network analysis was performed to observe the clustering patterns of the produced water communities based on sharing of OTUs among the communities. The clustering of OTUs in the centre of the field indicated that a large number of microbial taxa were shared by the produced water communities; however, formations of distinct clusters among the communities were also evident in the network. Sharing of unique OTUs resulted in tight clustering of the communities from close geographical locations, corroborating the result from the nonmetric multidimensional scaling (NMDS) plots. Such dependence on the geographical distances is clearly distinct from what is observed in soils and aquatic environments with more populated microbiomes, and this difference may be attributed to the extremely slow generation time of the microorganisms residing in the adverse subsurface environments (Lozupone and Knight, 2005; Chu et al., 2010; Lewin et al., 2014). Once again, all of the SG and CF communities were clustered within a single tight group, while this group was clearly separated from any other cluster. Also, notable in this analysis was that the CFS community clustered tightly with the CFW and SG communities, sharing a large number of the OTUs unique to these communities, supporting that the microorganisms in the CFS community originated from the CFW community (Fig. 3).

Cross contamination of the produced water samples or extracted DNA may be raised as a possibility; however, several lines of evidence arguing against this possibility can be found in the experimental results. (i) The produced water samples from the Segno and Crossfield sites were sampled and processed separately on different dates and sequenced in separate MiSeq
sequencing runs. (ii) A close association was observed between the CFW and CFS communities on the OTU network, indicating that the CFS microbial community originated from the CFW community. The separator DNA sample was less susceptible to contamination with Segno DNA samples due to its high DNA concentration and thus, the resemblance of OTU composition between CFS and the CFW provides an indirect evidence that the similarity between SG and CFW communities was not due to cross contamination. (iii) Contamination of the SG DNA samples with the CFW DNA sample was unlikely, as the four Segno microbial communities exhibited very similar microbial compositions, which are distinguishable from that of the CFW microbial community (Fig. 1). The similarity of the CFS community constructed with the 16S rRNA sequences in the shotgun metagenome to that constructed with amplicon sequences precludes another possibility that PCR bias in amplicon sequencing may have been the cause (Fig. S3).

The microbial communities in the produced waters from the Halldan oil field in the North Sea, with reservoir temperatures similar to the Segno and Crossfield sites (73–76°C), were plotted distantly from the SG and CFW communities on any of the NMDS plots and in the OTU network analysis. With limited information, it is not yet possible to identify the rationale for the divergence among these high-temperature reservoirs. Despite these differences, one common observation that can be made of these microbial communities from the high-temperature oil reservoirs is that members of the class Clostridia were among the most abundant taxa in these communities. The abundance of the organisms affiliated to the Clostridia class in these high-temperature oil reservoirs was also consistent with previous reports that this group of Gram-positive bacteria often constitute major portions of the microbial populations in deep subsurface environments stressed with high temperature and high pressure (Gittel et al., 2009; Aüullo et al., 2013; Frank et al., 2016). This relative abundance was attributed to the spore-forming capability that may have helped these organisms withstand the shifting environmental conditions during the long sedimentation and burial processes of the geologic formations, as well as their capability to survive under high temperature and pressure (Aüullo et al., 2013).
Co-occurrences of key oil reservoir microbial taxa

To check for potential relationships among key microbial taxa in the oil reservoir microbiomes, co-occurrence patterns of major microbial taxa (microbial orders found at >1% abundance in at least one sample) were analysed and presented on a co-occurrence network (Fig. 4). The microbial taxa that appeared as major populations in the largest number of data sets, i.e., Clostridiales (in 35 data sets), Pseudomonadales (in 38 data sets), Burkholderiales (in 34 data sets), Rhizobiales (in 33 data sets), Methanococcales (in 33 data sets), and Synergistales (in 32 data sets), were positioned in the periphery of the co-occurrence network, suggesting that these taxa have little reliance on other specific taxa of organisms for colonization. Most notable was Clostridiales, one of the most abundant groups of microorganisms in the high-temperature oil reservoirs including the Segno and Crossfield sites, in that virtually no significant co-occurrence relationship was found with any group of microorganisms other than the weak correlation with uncultured Cyanobacteria sp. ML635J-21. A strong co-occurrence relationship was observed among the orders Sphaerochaetales, Desulforomadales, Oceanospirillales, and Bacteroidales, which are all known to harbour taxa that are obligately anaerobic hydrocarbon-utilizing organisms, suggesting that the anoxic, hydrocarbon-rich oil reservoirs favour colonization of these obligate anaerobes. The co-occurrence analysis also suggests that these organisms are not likely to compete for a common limiting substrate (more likely to be electron acceptor or nutrients, as supple hydrocarbon availability is guaranteed in the oil reservoirs) and possibly share a symbiotic or syntrophic relationship (Head et al., 2014). All of these taxa were relatively abundant in the Segno and Crossfield samples and are likely to contain thermophilic and barotolerant subgroups able to survive in such adverse subsurface environments.

Implications for MEOR

As suggested by low cell counts, the examined high-temperature oil reservoirs appear to be hostile to microbial habitation despite the abundance of organic materials as the potential source of carbon and energy. Developing suitable MEOR techniques targeting such reservoirs would be no easy undertaking, due to the difficulty in establishing a viable population of metabolically active microorganisms able to withstand these...
adversities. Paradoxically, the scantiness of established microbial population may also work in favour of MEOR as the success of MEOR often depends primarily on the competition of these externally introduced organisms with indigenous microorganisms (Gray et al., 2008; Youssef et al., 2009). Successful enrichment of useful microorganisms is not guaranteed from such sparse inoculum; however, the similarity observed between microbiomes of the high-temperature produced water samples and the relative abundance of the previously enriched microbial taxa, e.g., Chlostridia and methanogens, are certainly positive signs. The high temperature, per se, should not be the adverse environmental parameter limiting the microbiome to such low population. The availability of readily utilizable organic electron donors in situ suggests against the possibility of electron donor starvation. Enrichment efforts should thus focus on finding electron acceptors or nutrients that would stimulate microbial growth, as potential electron acceptors (e.g., Fe³⁺ and NO₂⁻) and nutrients (e.g., PO₄³⁻) were deficient in the examined samples. The decision as to which mechanism should be the major target for development of MEOR technology for such high-temperature reservoirs awaits the success of these initial enrichment efforts.

Acknowledgements

The authors would like to express special thanks to Alexander Wentzel (SINTEF, Norway), Jenna L. Shelton (U.S. Geological Survey), Adrien Vigneron (Newcastle University, United Kingdom) and Nicolas Tsesmetzis (Shell International Exploration and Production Inc.) for kindly providing the access to their sequence data sets. We are also grateful to Jake Jungteck Lim (Energy Holdings Group, Korea) for arranging for the sampling trips. This research was financially supported by the Korea Institute of Energy Technology Evaluation and Planning (KETEP) and the Ministry of Trade, Industry and Energy (MOTIE) of the Republic of Korea (20152520100760) and the “R&D Center for reduction in Non-CO₂ Greenhouse gases” (2017002420002) funded by Korea Ministry of Environment (MOE) as ‘Global Top Environment R&D Program’. The authors were also financially supported by Korea Ministry of Land, Infrastructure and Transport (MOLIT) as U-City Master and Doctor Course Grant Program and the Brain Korea 21 Plus Project (Grant 21A20132000003).

Conflict of interest

The authors declare no conflict of interest.
References

An, D., Caffrey, S.M., Soh, J., Agrawal, A., Brown, D., Budwell, K., et al. (2013) Metagenomics of hydrocarbon resource environments indicates aerobic taxa and genes to be unexpectedly common. *Environ Sci Technol* 47: 10708–10717.

Aulio, T., Ranchou-Peyruse, A., Ollivier, B. and Magot, M. (2013) *Desulfotomaculum* spp. and related gram-positive sulfate-reducing bacteria in deep subsurface environments. *Front Microbiol* 4, 362.

Chu, H., Fierer, N., Lauber, C.L., Caporaso, J.G., Knight, R., and Grogan, P. (2010) Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. *Environ Microbiol* 12: 2998–3006.

Coates, J.D., Woodward, J., Allen, J., Philip, P., and Lovley, D.R. (1997) Anaerobic degradation of polycyclic aromatic hydrocarbons and alkanes in petroleum-contaminated marine harbor sediments. *Appl Environ Microbiol* 63: 3589–3593.

Fletcher, L.E., Conley, C.A., Valdivia-Silva, J.E., Perez-Montano, S., Condori-Apaza, R., Kovacs, G.T.A., et al. (2011) Determination of low bacterial concentrations in hyperarid Atacama soils: comparison of biochemical and microscopic methods with real-time quantitative PCR. *Can J Microbiol* 57: 953–963.

Frank, Y.A., Kadnikov, V.V., Gavrilov, S.N., Banks, D., Gerasimchuk, A.L., Podosokorskaya, O.A., et al. (2016) Stable and variable parts of microbial community in Siberian deep subsurface thermal aquifer system revealed in a long-term monitoring study. *Front Microbiol* 7: 2101.

Gao, P., Tian, H., Li, G., Sun, H., and Ma, T. (2015) Microbial diversity and abundance in the Xinjiang Luliang long-term water-flooding petroleum reservoir. *MicrobiologyOpen* 4: 332–342.

Gittel, A., Sørensen, K.B., Skovhus, T.L., Ingvorsen, K., and Schramm, A. (2009) Prokaryotic community structure and sulphate reducer activity in water from high-temperature oil reservoirs with and without nitrate treatment. *Appl Environ Microbiol* 75: 7098–7096.

Gray, M., Yeung, A., Foght, J., and Yarrington, H.W. (2008) Potential microbial enhanced oil recovery processes: a critical analysis, in SPE Annual Technical Conference and Exhibition, ATCE2008, Denver, USA, Society of Petroleum Engineers, Colorado, 114676, pp.1-25.

Gray, N., Sherry, A., Grant, R., Rowan, A., Hubert, C., Callbeck, C., et al. (2011) The quantitative significance of *Syntrophaceae* and syntrophic partnerships in methanogenic degradation of crude oil alkanes. *Environ Microbiol* 13: 2957–2975.

Head, I.M., Gray, N.D., and Larer, S.R. (2014) Life in the slow lane; biogeochemistry of biodegraded petroleum containing reservoirs and implications for energy recovery and carbon management. *Front Microbiol* 5: 566.

Hu, P., Tom, L., Singh, A., Thomas, B.C., Baker, B.J., Piceno, Y.M., et al. (2016) Genome-resolved metagenomic analysis reveals roles for candidate phyla and other microbial community members in biogeochemical transformations in oil reservoirs. *mBio* 7, e01669–15.

Imachi, H., Sekiguchi, Y., Kamagata, Y., Loy, A., Qiu, Y.-L., Hugenholtz, P., et al. (2006) Non-sulfate-reducing, syntrophic bacteria affiliated with *Desulfotomaculum* cluster I are widely distributed in methanogenic environments. *Appl Environ Microbiol* 72: 2080–2091.

Jack, T.R. (1991) Microbial enhancement of oil recovery. *Curr Opin Biotechnol* 2: 444–449.

Lewin, A., Johansen, J., Wentzel, A., Kotlar, H.K., Drablos, F., and Vallø, S. (2014) The microbial communities in two apparently physically separated deep subsurface oil reservoirs show extensive DNA sequence similarities. *Environ Microbiol* 16: 545–558.

Li, X.-X., Liu, J.-F., Zhou, L., Mbadinga, S.M., Yang, S.-Z., Gu, J.-D., and Mu, B.-Z. (2017) Diversity and composition of sulfate-reducing microbial communities based on genomic DNA and RNA transcription in production water of high temperature and corrosive oil reservoir. *Front Microbiol* 8: 1011.

Lozupone, C., and Knight, R. (2005) UniFrac: a new phylogenetic method for comparing microbial communities. *Appl Environ Microbiol* 71: 8228–8235.

Mueller, R.F., and Nielsen, P.H. (1996) Characterization of thermophilic consortia from two souring oil reservoirs. *Appl Environ Microbiol* 62: 3083–3087.

Muggeridge, A., Cockin, A., Webb, K., Frampton, H., Collins, I., Moulds, T., and Salino, P. (2014) Recovery rates, enhanced oil recovery and technological limits. *Phil Trans R Soc A* 372: 20120320.

Nazina, T.N., Sheshakova, N.M., Semenova, E.M., Korshunova, A.V., Kostrukova, N.K., Tourou, T.P., et al. (2017) Diversity of metabolically active bacteria in water-flooded high-temperature heavy oil reservoir. *Front Microbiol* 8: 707.

Orphan, V.J., Taylor, L.T., Hafenbradl, D., and Delong, E.F. (2000) Culture-dependent and culture-independent characterization of microbial assemblages associated with high-temperature petroleum reservoirs. *Appl Environ Microbiol* 66: 700–711.

Orphan, V.J., Goffredi, S.K., Delong, E.F., and Boles, J.R. (2003) Geochemical influence on diversity and microbial processes in high temperature oil reservoirs. *Geomicrobiol J* 20: 295–311.

de Rezende, J.R., Kjeldsen, K.U., Hubert, C.R.J., Finster, K., Loy, A., and Jørgensen, B.B. (2012) Dispersal of thermophilic *Desulfotomaculum* endospiros into Baltic Sea sediments over thousands of years. *ISME J* 7: 72–84.

Shelton, J.L., Akob, D.M., McIntosh, J.C., Fierer, N., Spear, J.R., Warwick, P.D., and McGray, J.E. (2016) Environmental drivers of differences in microbial community structure in crude oil reservoirs across a methanogenic gradient. *Front Microbiol* 7: 1535.

Sieminski, A. (2015) Annual energy outlook 2015. US Energy Information Administration.

Sung, Y., Fletcher, K.E., Ritalahti, K.M., Apkarian, R.P., Ramos-Hernández, N., Sanford, R.A., et al. (2006) *Geobacter lovleyi* sp. nov. strain SZ, a novel metal-reducing and tetrachloroethene-dechlorinating bacterium. *Appl Environ Microbiol* 72: 2775–2782.

Vigneron, A., Alsop, E.B., Lomans, B.P., Kyrpides, N.C., Head, I.M., and Tsitselis, N. (2017) Succession in the petroleum reservoir microbiome through an oil field production lifecycle. *ISME J* 11: 2141–2154.

Yergeau, E., Hugues, H., Whyte, L.G., and Greer, C.W. (2010) The functional potential of high Arctic permafrost
revealed by metagenomic sequencing, qPCR and microarray analyses. ISME J 4: 1206.
Youssef, N., Elshahed, M.S., and McInerney, M.J. (2009) Microbial processes in oil fields: culprits, problems, and opportunities. Adv Appl Microbiol 66: 141–251.
Zhang, T., Gannon, S.M., Nevin, K.P., Franks, A.E., and Lovley, D.R. (2010) Stimulating the anaerobic degradation of aromatic hydrocarbons in contaminated sediments by providing an electrode as the electron acceptor. Environ Microbiol 12: 1011–1020.
Zhang, F., She, Y.-H., Chai, L.-J., Banat, I.M., Zhang, X.-T., Shu, F.-C., et al. (2012) Microbial diversity in long-term water-flooded oil reservoirs with different in situ temperatures in China. Sci Rep 2: 760.

Supporting information
Additional Supporting Information may be found online in the Supporting Information section at the end of the article:

Fig. S1. Rarefaction curves of the OTUs recovered from the produced water samples.
Fig. S2. Geographical locations of the oil well sites where the produced water samples were collected for microbial community analyses.
Fig. S3. Comparison of microbial community profiles of the CFS sample constructed with 16S amplicon sequencing and shotgun metagenome sequencing.
Table S1. Physiochemical characterization of the produced water samples from Segno and Crossfield oil wells.
Table S2. Summary of 16S rRNA amplicon sequencing of the produced water samples.
Table S3. Relative abundance of taxa found in the produced water samples from Segno and Crossfield.
Table S4. Imported physicochemical characterization data for the produced water samples whose microbial communities were analysed in this study.
Table S5. The OTU table of produced water samples from Segno and Crossfield sites including the sample collected from the oil-water separator.
Appendix S1. Materials and methods.
Appendix S2. Supplementary results.