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Identify the core bacterial microbiome of hydrocarbon degradation and a shift of dominant methanogenesis pathways in oil and aqueous phases of petroleum reservoirs with different temperatures from China

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Abstract

Microorganisms in petroleum reservoirs mediate hydrocarbon degradation coupling with methanogenesis process as the terminal step, they also contribute to microbial enhanced oil recovery (MEOR) worldwide with great economic and environmental benefits. Here, a molecular investigation, using the 16S rRNA and *mcrA* gene profiles based on MiSeq sequencing and clone library construction method, was conducted on oil and water (aqueous) phases of samples with high, moderate and low temperatures from seven petroleum reservoirs in China. A core bacterial microbiome with a small proportion of shared OUT, but a high proportion of sequences among all reservoirs was discovered, including aerobic degraders, sulfate/nitrate reducing bacteria, fermentative bacteria and sulfur cycling bacteria distributed mainly in *Proteobacteria*, *Bacteroidetes*, *Deferribacteres*, *Deinococcus-Thermus*, *Firmicutes*, *Spirochaetae* and *Thermotogae*. Their prevalence in the reported petroleum reservoirs and successive enrichment cultures suggest their common roles and functions involved in aliphatic and aromatic hydrocarbon degradation. Dominant methanogenesis process generally shifts from hydrogenotrophic pathway in water phase to acetoclastic pathway in oil phase in high temperature reservoirs, but the opposite is true for low temperature reservoirs. No differences were detected between two phases in moderate temperature reservoirs. Physiochemical factors, including pH, temperature, phase conditions, and nitrate, Mn^{2+}, and Mg^{2+} concentrations are the main ones correlating to the microbial compositional and functional profiles significantly. LEfSe analysis shows distribution differences of microbial groups towards pH, temperature, and oil/water. Tax4Fun functional profiling indicates major functional metabolism differences between the two phases, including amino acids, hydrocarbons in the oil phase, and carbohydrates in the water phase.

Keywords: Reservoir; Core microbiome; oil and water phases; temperature; methanogenesis; hydrocrbon

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1 Introduction

Microbial enhanced oil recovery (MEOR) is one of the most feasible and profitable technologies for extracting residual oil from low-productivity reservoirs by utilizing microorganisms for hydrocarbon transformation via fermentation and methanogenesis as the major functional players in MEOR applications (Magot et al., 2000; Mbadinga et al., 2011; Mesle et al., 2013). Implementation of MEOR could also attenuate side-effects by injection of nitrate into oil wells to stimulate the propagation of nitrate-reducing bacteria (NRB) and inhibit the growth of sulfate-reducing bacteria (SRB), subsequently reducing sulfidogenic negative effects on corrosion and oil quality deterioration (Gao et al., 2013). Currently, investigations on compositional and functional profiles of petroleum reservoir microbiome have attracted attention from both scientists and engineers because the information will improve the current understanding on microbial diversity and function in oil reservoir systems and implement MEOR through manipulating microbial community composition and activities (Magot et al., 2000; Mesle et al., 2013; Youssef et al., 2009).

Petroleum reservoir is often characterized as a high temperature, high salt content, and high pressure subterranean ecosystem, but low temperature reservoirs also exist around the world (Grabowski et al., 2005; Li et al., 2013; Voordouw et al., 1996; Li et al., 2014). The physiochemical and geographic differences among petroleum reservoirs together with exogenous injection of microorganisms and nutrients during MEOR operation could affect the composition and functional groups of the indigenous microbial community. Many previously discovered bacterial and archaeal groups have important functional roles, e.g., sulfate reducing, nitrate/nitrite reducing and fermentative bacteria, thermophilic archaeal hydrocarbon degraders and methanogens as well as exogenous aerobic hydrocarbon degraders in the microbial community (Gao et al., 2015a; Gao et al., 2015b; Lenchi et al.,

2013; Li et al., 2012a; Orphan et al., 2003; Wang et al., 2012; Grabowski et al., 2005; Pham et al., 2009). The common and specific roles and functions of these microorganisms in petroleum reservoirs are of great value to be understood fully.

Methanogens cooperate with hydrocarbon degraders and fermentative bacteria synergistically to make the overall degradation processes thermodynamically favorable under largely anaerobic conditions (Mbadinga et al., 2011). Fermentative products from hydrocarbon degradation provide the essential growth substrates for methanogens with two major pathways, namely hydrogenotrophic and acetoclastic methanogenesis, and in many cases the syntrophic acetate oxidization pathway coupling with hydrogenotrophic methanogenesis is prevalent in both *in situ* and enrichment incubation *ex situ* (Mesle et al., 2013; Liang et al., 2015; Wang et al., 2012; Lee et al., 2015; Mayumi et al., 2011). However, very little is known on the influencing factors that shape the methanogenesis pathways and methanogen community structure and composition.

Petroleum reservoirs are a complex system consisting of porous sandstone with oil and water and air. The microorganisms attached to the oil phase of petroleum fluids are largely neglected in majority of the pervious investigations due to technical difficulties in DNA extraction and then sequencing (Kryachko et al. 2012). Oil-attached microorganisms influence the oil-water interface properties by production of biosurfactants and metabolites or forming adsorbed colloidal particles to enhance oil recovery performance (Kobayashi et al., 2012; Kryachko et al., 2012; Wang et al., 2014). The distribution, function and contribution of these microorganisms to MEOR success could be very different from those of the aqueous phase (Kobayashi et al. 2012). Oil-degrading microorganisms, including thermophilic hydrocarbon-degrading archaea and methanogens, play different roles in MEOR process (Mbadinga et al., 2011), their compositional patterns and functional profiles towards

temperature and oil/aqueous phase, are of great value to understand the mechanism of MEOR operation. In this study, the objectives were to study the compositional and functional differences of petroleum reservoir inhabiting microorganisms under different temperatures; the methanogenesis pathways in oil and aquesous phases of these samples; and the influence of physiochemical factors on microbial community composition.

2 Materials and Methods

2.1 Characterization of geographic properties of sampling reservoirs

Petroleum production fluid samples were collected from seven areas across China, covering oilfields of different geographical locations and temperatures. The reservoirs and crude oil properties together with the aqueous phase chemical characteristics of this study are listed in Table 1. Detail reservoir properties are described in the Supplementary Materials.

2.2 Sample collection, ion concentration measuring and DNA extraction

Each sample containing a mixture of crude oil and water was collected on site into a sterilized container after flushing each wellhead for at least 3-5 min. The containers were screw capped to avoid air invasion and transported to the nearby laboratory immediately for further processing. The mixture was gently heated to 50°C and then separated into oil and aqueous phases in a separatory funnel. Ion concentrations of the aqueous phase were measured using Dionex 600 ion chromatography (Triad Scientific, Inc., Manasquan, NJ, USA) following the manufacturer's instructions.

To obtain aqueous phase DNA, the aqueous phase of sample after oil and water separation was first filtered through a 0.22 polycarbonate membrane filter and a slice of the membrane was used to extract DNA by AxyPrep™ Bacterial Genomic DNA Miniprep Kit according to

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manufacturer's instruction (Axygen Biosciences, USA). For the oil phase, three volumes of isooctane (2, 2, 4-trimethylpentane) were used to dissolve the crude oil, and then centrifuged at 5000 rpm for 30 min to concentrate non-dissolved particulate and microbial cells for at least three times to obtain enough materials. Repetitive DNA extractions were then conducted on these materials and combined to meet the quantity requirement for quality control. Finally, all DNA samples from water and oil phases were measured by Nanodrop for concentration and checked for DNA integrity by electrophoresis before further steps in analysis.

2.3 Clone library construction and analysis

The methyl-CoA enzyme encoding gene (*mcrA*) primer pair, ME3MF&ME3MF-e/ME2r'(Narihiro and Sekiguchi, 2011) and the 16S rRNA gene primer pair targeting methanogens, MetA86f/ARC915r (Wright and Pimm, 2003; Narihiro and Sekiguchi, 2011; Yu et al., 2008), were used to generate gene clone libraries for each sample (aqueous and oil phases separately) according to the method established previously (Zhou et al., 2015)(Table 2).

FunGene pipeline chimera check was applied to check *mcrA* gene sequences using the UCHIME *de novo* mode (Edgar et al., 2011). USEARCH software was used to check chimeras of methanogenic 16S rRNA gene sequences using QIIME compatible SILVA 119 release SSURef database ("rdp_gold fasta") file as a reference. Then, for *mcrA* gene sequences, *de novo* OTU picking method was applied by QIIME at a cutoff value of 0.05 (Caporaso et al., 2010). Representative OTU sequences were aligned and inserted into the *mcrA* gene ARB database by maximum parsimony method without changing the initial tree topology (Angel et al., 2012; Ludwig et al., 2004). The phylogenetic affiliation was assigned, and taxonomic composition results were processed by QIIME accordingly (Figure S1). For

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141 methanogenic 16S rRNA gene sequence clustering and diversity analysis, the same method
142 was applied via QIIME as described in the followings.

143 **2.4 MiSeq sequencing and QIIME based analysis**

144 The prokaryotic universal primer pair 515F/909R (Caporaso et al., 2012; Wang and Qian,
145 2009) and archaeal universal primer pair Arch347F/Arch806R (Takai and Horikoshi, 2000)
146 were used to amplify samples of this study (both with barcodes attached to the forward
147 primers, Table 2). Two PCR reactions were conducted and then combined to yield enough
148 PCR products to compromise variations between different batches. Then, pooled PCR
149 products of each sample with approximately 100 ng or 200 ng DNA were subjected to one
150 MiSeq run. Sequencing samples were prepared using TruSeq DNA Kit according to the
151 manufacturer's instruction. The library was uploaded to an Illumina MiSeq platform for
152 sequencing with reagent kit v2 (2× 250 bp) or v3 (2× 300 bp) as described in the
153 manufacturer's manual.
154
155 After merging paire-end reads from raw sequencing data by FLASH-1.2.8, fastx-toolkit was
156 applied to split merged reads from one run into individual samples according to the primer
157 barcodes (Magoc and Salzberg, 2011). Then, all sequences were split into each library with
158 the name of each sample attached according to the barcode map using QIIME command
159 "split_libraries" (Caporaso et al., 2010). The criterion for filtering out underqualified
160 sequences was "-s 15 -k -a 6 -r -l 150 -b 12 -M 5 -e 0". Chimera checking was conducted by
161 USEARCH software using QIIME compatible SILVA 119 release SSURef database
162 ("rdp_gold" fasta) file as the reference (Edgar, 2010). Clustering, picking OTU, taxonomy
163 assignment, aligning, filtering alignments and phylogenetic tree construction, taxonomic
164 composition summarizing, alpha and beta diversity analyses were conducted step-by-step by
165 the QIIME pipeline with QIIME compatible SILVA 119 SSURef database as the reference

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(Caporaso et al., 2010). In clustering, “pick_open_reference_otus.py” command was used to conduct OTU dividing and BLAST method was used to assign taxonomy to input sequences. This subsampled open reference OTU picking method was the performed-optimized and optimal strategy suggested by the developers (Rideout et al., 2014). After OTU table “biom” files were generated, in order to get the bacterial community composition information from prokaryotic 16S rRNA gene primer amplified libraries, “filter_taxa_from_otu_table.py” command was introduced to only retain bacterial OTUs in the “biom” file. Similarly, exclusive archaeal and methanogenic OTU table files could also be processed from archaeal 16S rRNA gene primer amplified libraries. Summary information of each sample OTU abundance could be calculated by “biom summarize-table” command, and then the lowest number over all samples was chosen as the subsampling size to make each library acquire an even size using “multiple_rarefaction_even_depth.py” command. The taxonomic compositional table was drawn according to the subsampled biom file. Since there was no lanemask file available in this SILVA compatible 119 release SSURef database, alignment filtering method was performed independently with entropy threshold as 0.1 and gap filter threshold as 0.9 after obtaining aligned sequences by PyNAST method. Diversity parameters of each library could be generated by alpha diversity calling, with rarefaction curve, Good’s coverage value, Shannon, Chao1, Simpson and PD whole tree indices calculated. Beta diversity, which delineates dissimilarity relationship among samples, was generated and visualized through unweighted & weighted UniFrac matrix and non-phylogenetic Bray-Curtis matrix method. The pairwise-shared OTU numbers were calculated from “biom” by the command “shared_phylotypes.py”. Core microbiome (shared OTU table in a specific sample category) was identified by “compute_core_microbiome.py” command.

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2.5 Diversity and statistical analysis

The statistical significance of community composition of samples among different categories was valued by anosim and adonis method, implemented in "compare_categories" command in QIIME. Mantel Test was used to compare the distance matrix of physicochemical parameters and UniFrac/Bray-Cutis distance matrix from beta diversity analysis by QIIME. For aqueous phase samples, both of the *in situ* physicochemical parameters and ion concentrations were used in the analysis; while only *in situ* physicochemical parameters were included for oil phase samples. The compositional bar chart and bubble chart were modified and illustrated from taxonomic summary results. Tax4Fun was used to predict the functional capabilities based on abundance profiles of microbial 16S rRNA gene datasets (Asshauer et al., 2015). LDA Effect Size (LEfSe) analysis was applied to illustrate the biomarker species with high statistical significance in different sample categories and the functional profiles statistically distributed in different sample categories (Segata et al., 2011).

2.6 Quantitative PCR on *mcrA* gene abundance

The quantitative PCR measurement was conducted using iTaq™ Universal SYBR® Green Supermix Kit (BIO-RAD). The qPCR mixture contained in 15 μl: 7.5 μl of supermix, 16 μg of BSA (Roche), and 1 μM final concentration of primer pair [ME3MF&ME3MF-e (250:1) and ME2r']. Annealing temperature was set to be the same as the clone library PCR setting, and the rest thermocycling settings were according to the manufacturer's instructions. Randomly picked one pMD18-T plasmid with *mcrA* gene inserted was used to make the standard curve. The DNA template concentration was adjusted to 0-40 ng/μl. Results, which deviated significantly from values in the replicate groups, were omitted and undetermined results were also deleted. The property of final adjusted standard curve is $r^2 = 0.995$ and Eff% = 83.32.

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2.7 Sequencing result deposition

For clone library sequences, KT314862-KT315353, were assigned to methanogenic 16S rRNA gene sequences; KT314340-KT314835 were assigned to *mcrA* gene sequences. For high throughput sequencing data based on Illumina MiSeq platform, PRJEB9855 was assigned to prokaryotic 16S rRNA gene sequencing data; PRJEB10996 was assigned to archaeal 16S rRNA gene sequencing data.

3 Results and Discussions

3.1 Common OTU among different categories and core bacterial microbiome

Community composition results shows 21 bacterial phyla were obtained with an average abundance of more than 0.1% (Figure 1a), and three major archaeal phyla are *Thaumarchaeota*, *Euryarchaeota* and *Crenarchaeota* (Figure 1b). Pairwise shared OTU numbers of all samples indicated that, irrespective of combinations between aqueous and oil phase samples, the average numbers of shared bacterial OTUs ranged from 199.9 to 292.4, accounting for 26.6-36.2% of the total OTU numbers within individual samples; average numbers of shared archaeal OTUs ranged from 1.8 to 11.9, accounting for 8.5-23.4% of total OTU numbers within individual samples (Table S4). Core bacterial OTU numbers among aqueous, oil and all samples were 73, 57 and 46, which accounted for 7.1-10.1%, 5.9-10.3% and 4.5-8.3% of OTU numbers in individual samples. Core archaeal OTU number among aqueous samples was only 3, accounting for 3.9-8.1% of OTU numbers in individual samples, and no archaeal OTU was shared among oil phase samples.

However, by investigating taxonomic profiles of core bacterial OTUs, the shared OTUs were 49, 41 and 34 genera in aqueous, oil and all samples, corresponding to 65.5%, 59.9% and 58.8% of average sequences in the total bacterial community, respectively (Tables S5 and S6).

Most of them belonged to the most abundant 36 genera, of which numbers of shared genera among aqueous, oil and all samples were 28, 23 and 23, respectively (Figure 2, and Tables S5 and S6).

There was no significant difference of shared bacterial OTU numbers in and between aqueous and oil phase samples, suggesting a core microbiome shared among all components. The core OTUs covered around 2/3 of the total bacterial sequences, even though the percentages of core/total OTU number for individual samples were 4.5% to 10.3%. The core microbiome shared among all petroleum reservoirs could be the key participants mediating critical microbial processes, such as activation, degradation, fermentation, oil-emulsification and methane generation (Yamane et al., 2008; Wang et al., 2014; Pham et al., 2009; Orphan et al., 2000; Magot et al., 2000). This spectrum of core microbiome shares common functional roles in facilitating MEOR and is modified by the *in situ* physicochemical conditions of different reservoirs (Figure 2 and Table S5). Moreover, substantial portions of aerobic bacteria discovered in the core bacterial microbiome across reservoirs implies that exogenous bacteria introduced into reservoirs by water flushing can also represented in the core composition and play important roles in enhancing oil recovery (Gao et al., 2015b; Youssef et al., 2009).

Bacterial community in aqueous phase showed association with temperature by Mantel Test using unweighted UniFrac matrix method, and temperature also affected the dissimilar distance of PCoA coordinates of bacterial community by Adnois statistical analysis (Tables S3, S7 and S8). However, temperature changed the proportions of the taxa of the core microbiome significantly, but not the presence/absence (Tables S3, S7 and S8). Consequently, the common genera discovered from this study show that despite of geographic and physiochemical differences, there is core microbiome with small OTU numbers but large

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sequence proportions in these petroleum reservoirs across China for possibly mediating hydrocarbon degradation processes. Prevalent core genera discovered in this study also appear to be the most abundant components in petroleum reservoirs besides China (Gao et al., 2015a; Gao et al., 2015b; Li et al., 2012a; Orphan et al., 2003; Orphan et al., 2000; Tang et al., 2012; Yamane et al., 2008; Dahle et al., 2008; Li et al., 2015; Liang et al., 2015; Li et al., 2014) and enrichment cultures from petroleum reservoirs worldwide (Gray et al., 2011; Li et al., 2012b; Liang et al., 2015; Wang et al., 2011).

3.2 Shift of major methanogenesis pathways between oil and water phases

The dominant methanogenesis process generally shifts from hydrogenotrophic pathway in aqueous phase to acetoclastic pathway in oil phase in high-temperature reservoirs. The opposite is ture for low temperature samples, but no difference was detected between the two phases in moderate temperature reservoirs (Figure 3). It is also observed that a shift of the major methanogenesis mechanisms in aqueous and oil phases with different patterns was evident in different temperature petroleum reservoirs of this study. Quantitative measurements of *mcrA* gene in all samples are summarized in Supplementary Material.

The underlying methanogenesis mechanism could change substantially in reservoirs with distinctive geochemical properties (Magot et al., 2000). The dominance of methanogenesis process mediated by methylotrophic methanogens is rarely observed in petroleum reservoirs. It is claimed that there is a very low possibility that methyl-compounds could be generated during the degradation of kerogen (Mesle et al., 2013). However, dominance of obligate methylotrophic *Methanolobus* was found in all water, rock and coal samples in a coalbed methane reservoir within Eastern Ordos Basin of China (Guo et al., 2012). It could be extrapolated that prevalence of methylotrophic methanogenesis under certain conditions is directly fueled by the existence and availability of methyl-containing substances.

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289 Numerous studies on aqueous phase of reservoir fluids claimed that syntrophic acetate
290 oxidation associated with hydrogenotrophic methanogenesis is the major hydrocarbon
291 degradation pathway *in situ* or in enrichment incubation microcosms (Wang et al., 2012;
292 Mayumi et al., 2011; Lee et al., 2015; Mbadinga et al., 2012; Gray et al., 2011). The
293 dominance of hydrogenotrophic methanogenesis in subsurface ecosystem could be due to the
294 external hydrogen originated from maturation of organic matters and/or mineral hydrolysis
295 (Head et al., 2003), and the synergistic effect in association with acetate oxidizers, whereby
296 acetate was firstly oxidized to H_2 and CO_2, then utilized by methanogenesis (Liu and
297 Whitman, 2008). Additionally, a stable isotope labeling experiment on oil-degrading
298 microcosm showed that despite of coexistence of acetoclastic methanogenesis and acetate
299 syntrophic oxidization in the initial state, the latter process prevailed over the former one
300 after introducing low initial acetate concentration (Gray et al., 2011). This suggests that
301 acetate syntrophic oxidization could exceed acetoclastic methanogenesis and contribute
302 essential substrates H_2 and CO_2 to hydrogenotrophic methanogenesis process.

303

304 It is still hard to claim whether temperature has directly participated in the alteration of the
305 methanogenesis pathways. Reservoir fluid constituents may affects methanogenic
306 degradation because crude oil and creosote inhibit acetoclastic methanogenesis (Warren et al.,
307 2004) and volatile hydrocarbons (nC$_5$-nC$_{10}$) inhibit methanogenic degradation rate without
308 changing the abundances of both hydrogenotrophic and acetoclastic methanogens (Sherry et
309 al., 2014). Since results available are on the microbial assemblages within injection or
310 production water, new understanding on the local microbiome distribution and changes shall
311 focus on oil or hydrophobic fraction of the reservoir fluids (Kobayashi et al., 2012; Tang et
312 al., 2012; Lenchi et al., 2013). Consequently, the alteration pattern of major methanogenesis
313 in aqueous and oil phases under different temperature conditions could be further delineated.

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A combination of methods, including synthesis and quantification of degradation intermediate (Bian et al., 2015), stable isotope labeling on tracing substrate transformation (Gray et al., 2011) and molecular analysis of the metabolically active microorganisms can advance the anaerobic degradation and methanogenesis processed in reservoir systems.

3.3 Physicochemical influence and Taxa & Function profiles

Temperature is an important physical factor shaping the community structure of bacterial (anosim & adonis $P < 0.01$) and methanogenic communities of the samples in this study (anosim $P < 0.05$ & adonis $P < 0.01$)(Figure 4 and Table S7). Furthermore, a significant difference of taxa abundance among the three temperature categories for both bacterial and archaeal communities was evident by LEfSe analysis (Figure 5). For bacterial community, aqueous and oil phases of any of the samples and temperature (anosim & adonis $P < 0.01$), and pH (adonis $P < 0.05$) showed significant differences. For archaeal community significant difference was detected with sample type and temperature (both adonis $P < 0.05$) and pH and phase (anosim & adonis $P < 0.05$). For methanogenic community, sample type and temperature were identified significant (Group: anosim & adonis $P < 0.05$; Temperature: anosim $P < 0.05$ & adonis $P < 0.01$) (Table S7).

Nitrate concentration dissimilarity matrix was significantly associated with all unweighted/weighted UniFrac and Bray-Cutis matrices (all $P < 0.05$) for aqueous bacterial community (Table S8). Meanwhile, methanogenic community in oil phase was significantly affected by reservoir depth, temperature, pH and water flooding operation yearsby association analysis of weighted UniFrac matrix but not unweighted UniFrac matrix (all $P < 0.05$) (Table S8), indicating that it was the abundance difference of certain taxa affecting the compositional pattern. More detailed relationships between physicochemical factors and bacterial/archaeal/methanogenic communities are summarized in Tables S7 and S8.

339

340 Nitrate dissimilarity matrix was significantly correlated with dissimilarity matrices of all
341 aqueous phase bacterial communities using both unweight/weight UniFrac and Bray-Curtis
342 matrices (all $P < 0.05$) (Table S8). Nitrate is an important chemical used in the injection
343 water to inhibit corrosion and maintain crude quality (Gao et al., 2013). Nitrate stimulates the
344 growth of nitrate-reducing bacteria and inhibits the growth of SRB (Nemati et al., 2001; Gao
345 et al., 2013). Consequently, nitrate injection shapes the microbial communities in petroleum
346 reservoirs. Mn^{2+} and Mg^{2+} were shown to be strongly associated with bacterial community of
347 aqueous phase based on Bray-Curtis matrix (both $P < 0.05$) (Table S8). Iron can be electron
348 acceptor for direct or indirect hydrocarbon degradation under anaerobic conditions
349 (Mbadinga et al., 2011). Iron reducers could also utilize electrons from syntrophic partners to
350 further facilitate direct aromatic hydrocarbon degradation (Kunapuli et al., 2007).

351

352 Differences on taxa and function profiles in oil and aqueous phases were analyzed based on
353 LEfSe and Tax4Fun (Figures S2 and S3, and Table S9). For bacterial communities, amino
354 acid metabolism, xenobiotics biodegradation and metabolism were distributed more in oil
355 phase, while carbohydrate metabolism was more in aqueous phase. For archaeal communities,
356 ubiquinone and other terpenoid quinone biosynthesis, butanoate and tryptophan metabolism
357 together with other glycan degradation pathways were more in oil phase, while folding,
358 sorting and degradation as well as several infectious diseases related pathways, such as
359 *Salmonella* infection, tuberculosis, were more in the aqueous phase. Since FTU values of
360 archaeal communities (fraction of taxa could be mapped to existing KEGG pathway) were
361 unevenly distributed from sample to sample, the reliability of these functional prediction is in
362 question (Table S9). To date, there are still very limited studies on investigating inhabiting
363 preference of microbiome in petroleum reservoirs and their functional contributions to

aqueous and oil phases, further efforts are needed on this topic (Kryachko et al., 2012; Wang et al., 2014; Kobayashi et al., 2012).

4 Conclusions

A core bacterial microbiome of a small proportion OTU but a relatively large sequence proportion mediating hydrocarbon degradation and fermentation were revealed by analysis of oil reservoirs with different temperatures. The core and common bacterial microbiome were shared among geographically and physicochemically different reservoirs for major biodegradation. A shift of the dominant methanogenesis pathway between aqueous and oil phase within samples by temperature was detected. Factors of pH, temperature, phase conditions, and nitrate, Mn^{2+}, and Mg^{2+} concentrations shaped the microbial compositional and functional profiles significantly. Moreover, biomarker groups of bacteria and archaea associated with different pH, temperature and phase indicate major differences in function of amino acid metabolism, xenobiotics metabolism enriched in the oil phase, and carbohydrate metabolism enriched in the aqueous phase.

Author contributions. ZZ, BL, L-YW, B-ZM, HS and J-DG conceived the project and designed experiments. ZZ, BL and L-YW conducted the sampling, chemical and molecular experiments. J-FL, B-ZM and J-DG managed sample collection, supervised on data interpretation. ZZ performed the original data analysis and drafted the original manuscript. All members contributed to refine the manuscript and approved the final version.

Competing interests. The authors declare no conflict of interest.

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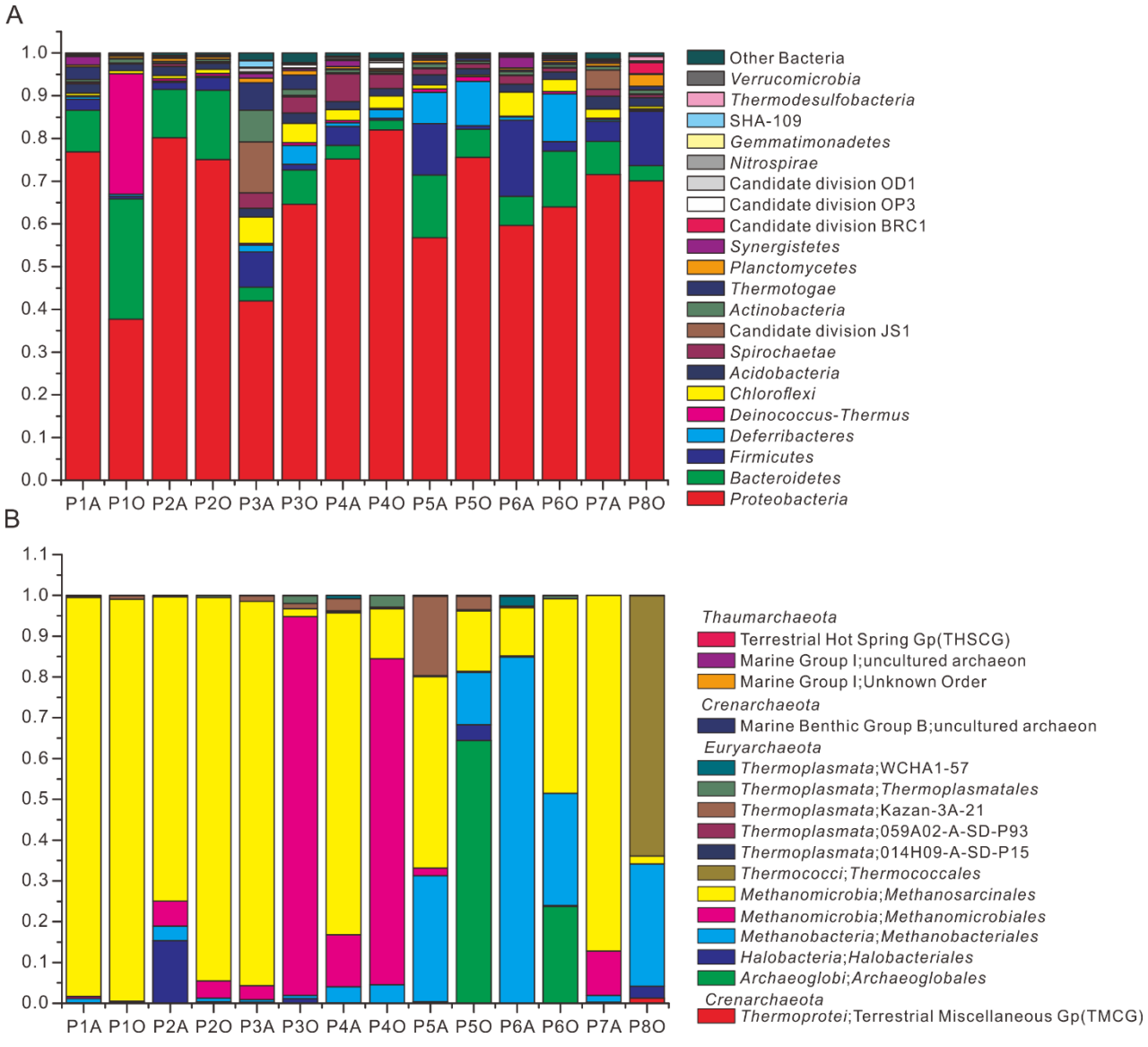

Figure 1. Relative abundance of bacteria (A) and archaea (B) from 14 aqueous and oil phase samples. Bacterial community was taxonomically assigned at the level of phylum. Those phyla with average abundance of all samples below 0.1% were combined into "Other Bacteria" category. Archaeal community was taxonomically assigned at the level of class.

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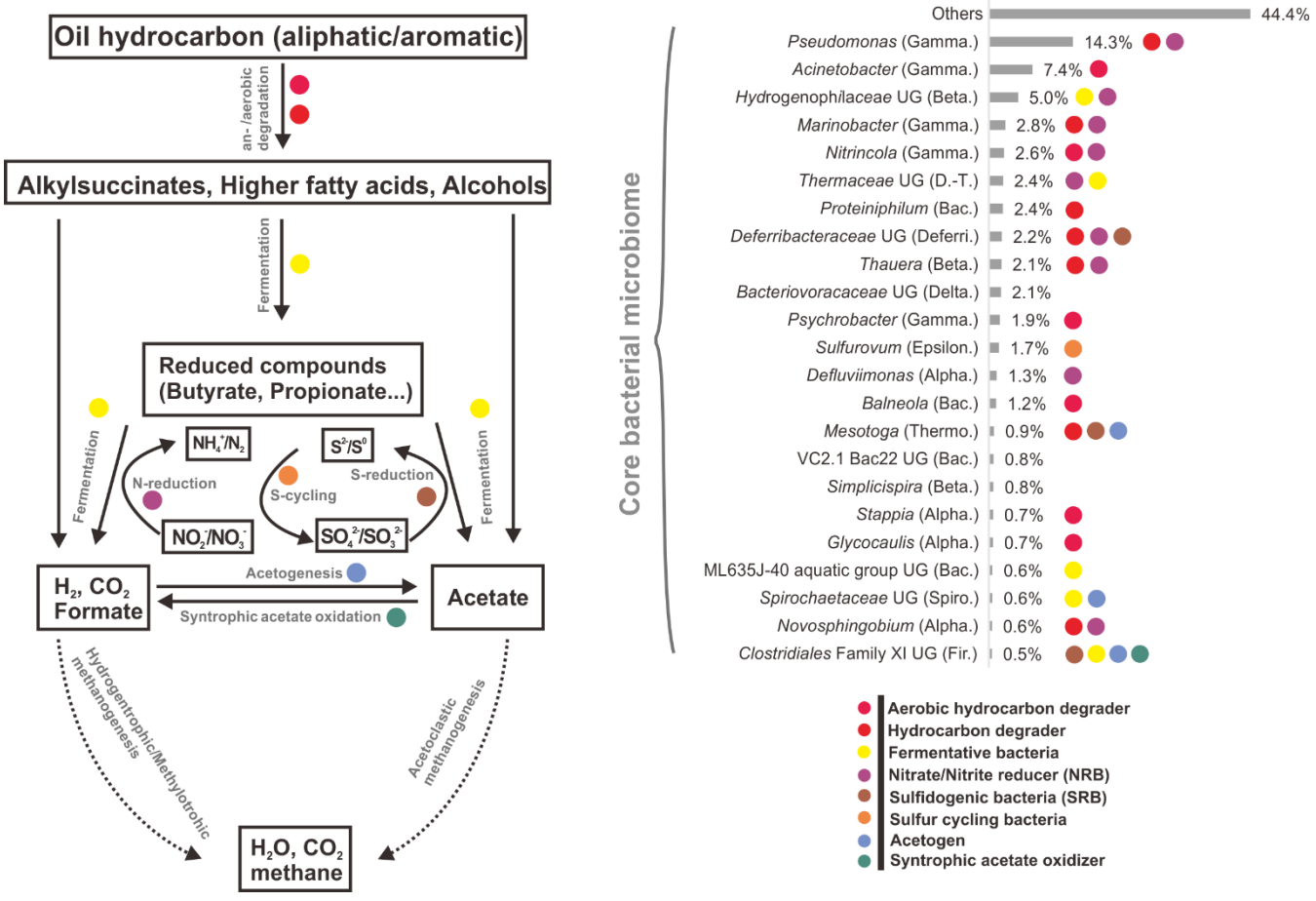

Figure 2. Average abundances and functional roles of core bacterial microbiome in all petroleum samples (including aqueous and oil phase samples). Core microbial OTUs (23 OTUs) were affiliated to the most abundant genera. The functional roles were assigned according to reference publications (Supplementary Material). Degradation pathway was modified from Mbadinga et al., 2011. Abbreviations: Alpha., Beta., Gamma., Delta., Epsilon (*Alpha-*, *Beta-*, *Gamma-*, *Delta-*, *Epsilonproteobacteria*), D.-T. (*Deinococcus-Thermus*), Bac. (*Bacteroidetes*), Deferri. (*Deferribacteres*), Delta. (*Deltaproteobacteria*), Thermo. (*Thermotogae*), Spiro. (*Spirochaetae*) and Fir. (*Firmicutes*). UG stands for uncultured genus.

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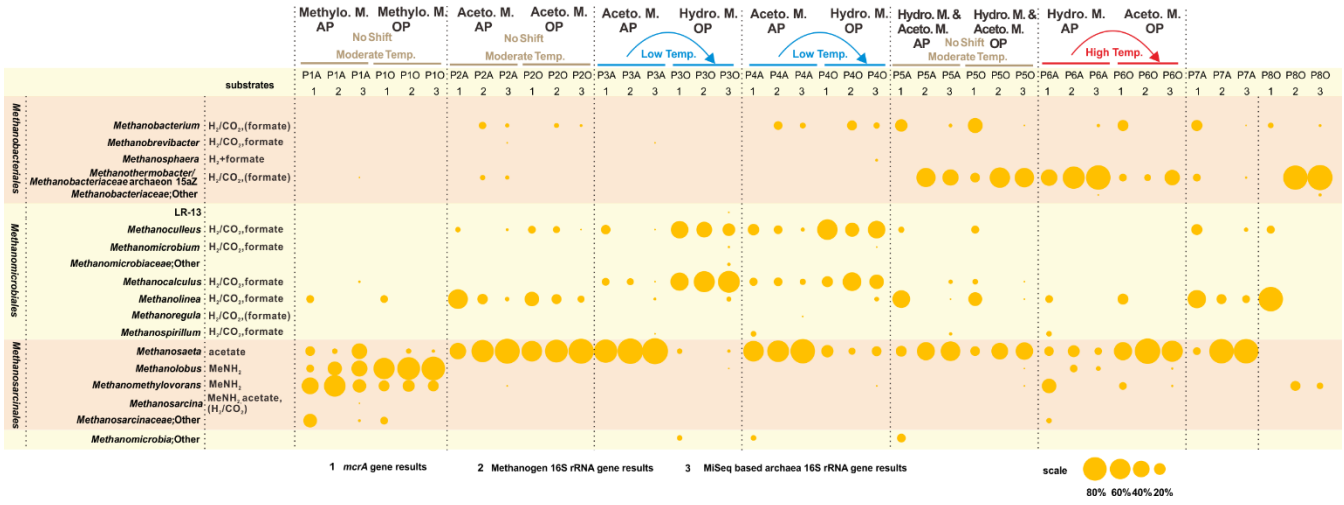

Figure 3. Bubble chart of proportional composition of methanogens based on MiSeq sequencing results of archaeal 16S rRNA genes and clone sequencing results of *mcrA* gene and methanogenic 16S rRNA gene. The major substrate utilization properties were originated from Liu et al., 2008. $MeNH_2$ is methylamine and substrates in parentheses refer to being utilized by some but not all species. *Methanothermobacter thermautotrophicus* strain Delta H is the phylogenetically closest cultured clone to *Methanobacteriaceae* archaeon 15aZ. Thus, the combination of *Methanothermobacter* and *Methanobacteriaceae* archaeon 15aZ was used. Methanogenesis shift was based on the transition of major methanogenesis pathway. Abbreviations: Aceto. M., Hydro. M. and Methylo. M. (Acetoclastic methanogenesis, Hydrogenotrophic methanogenesis and Methylotrophic methanogenesis).

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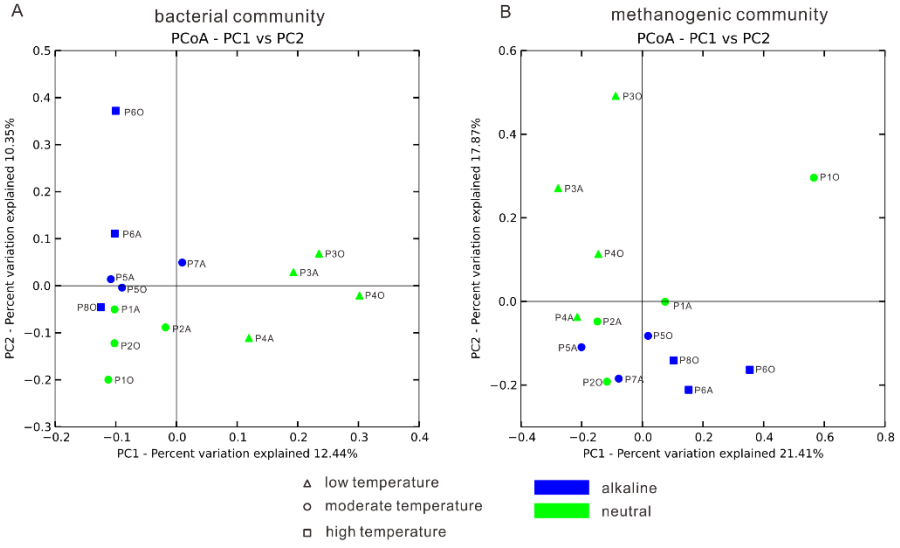

Figure 4. Principal Coordinate Analysis plot figures based on unweighted UniFrac matrices. Bacterial (A) and methanogenic (B) communities of 14 samples were separately analyzed to delineate the dissimilarity distances between each sample based on phylogenetic classification. The sample dots were categorized in terms of temperature (dot shape) and pH condition (color).

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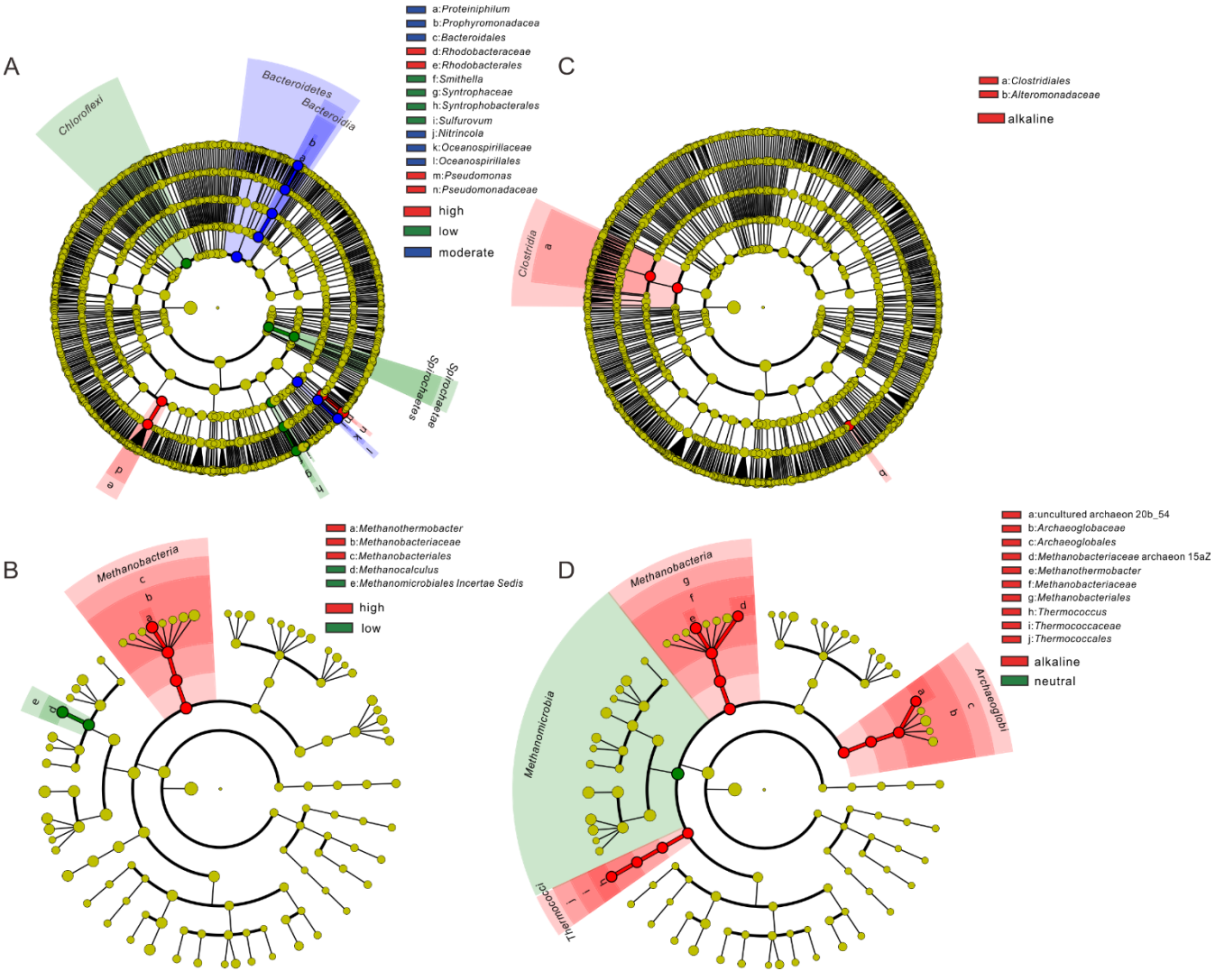

Figure 5. Cladogram based on LEfSe analysis results on bacteria (A, C) and archaea (B, D) in terms of temperature (A, B) and pH (C, D) categories. The taxonomic trees were generated from phylum to genus (inside to outside) in hierarchical structure. Biomarker taxonomic levels were labeled in color which had at least logarithmic LDA score of 3.5. Pre-sample normalization was used to format the relative abundance data. All-against-all strategy was used in multi-class analysis step.

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Table 1. Reservoir geophysical properties and physicochemical properties of aqueous phase samples

Location name	Shengli-Zhan3-26	Huabei-B51	Xinjiang (Karamay)-Liuzhong	Xinjiang (Karamay)-Qixi	Jiangsu-Wei5	Jiangsu-Gao6	Daqing (Xingbei)-Xing4	Jiangsu-Qinying
Sample name	P1	P2	P3	P4	P5	P6	P7	P8
Depth (m)	~1300	~1101	~480	~1088	1018	1970	800-1200	2280-2524
Temp (°C)	63	45	21	32	53.5	82	49	88
pH	7.1	7.2	7.0	7.1	8.62	8.88	8.5	8.2
Effective porosity (%)	30	22.2	20.5	17.4	21.7	17.4	28.3	16.5
Average permeability (× $10^{-3}\mu m^2$)	800	12.6	466	274	91.8	94.5	481	22
Oil viscosity (mPa.s)	1720	402	417	44.8	292	8.4-83.9	13.86	98-188
Water flooding operation (years)	22	4	38	46	13	18	30	0
Cl^- (mg l^{-1})	3850	819	3864	2000	7563.01	1155.95	659.31	-
SO_4^{2-} (mg l^{-1})	2244	32.4	124.8	7.7	1921.06	156.81	333.29	-
PO_4^{3-} (mg l^{-1})	0.1	Nd	Nd	Nd	139.77	6.29	Nd	-
NO^{3-} (mg l^{-1})	Nd	Nd	34.1	1.4	Nd	0.44	0.45	-
Na^+ (mg l^{-1})	3313	1064	4196	5399	7363.52	1593.55	1363.43	-
K^+ (mg l^{-1})	94.2	22.3	35.1	45.6	9.36	3.26	3.55	-
Ca^{2+} (mg l^{-1})	195.6	53.0	103.3	128.2	17.42	7.24	41.94	-
Mg^{2+} (mg l^{-1})	46.1	17.6	44.7	64.0	10.27	2.25	11.02	-
Mn^{2+} (mg l^{-1})	0.3	0.1	0.3	0.4	Nd	Nd	Nd	-
Acetate (mg l^{-1})	32	57.9	344	6.97	44.07	285.66	Nd	-

"Nd" means not detected. No aqueous phase was obtained from Jiangsu-Qinying reservoir sample.

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Table 2. PCR primers and PCR settings

	Primers	Sequences	Primer final concentration	Template DNA quantity	References
mcrA gene primer	ME3MF&ME3MF-e	ME3MF: ATGTCNGGTGGHGTMGGSTTYAC, ME3MF-e: ATGAGCGGTGGTGTCGGTTTCAC; concentration ratio = 250:1	1 μM	10-20 ng	(Narihiro and Sekiguchi, 2011)
	ME2r'	TCATBGCRTAGTTDGGRTAGT	1 μM	10-20 ng	
PCR setting	95°C2 min; 35 × (95°C 30 s, 59.5°C 30 s and 72°C 40 s); 72°C 5 min and 4°C 2 min.				
methanogenic 16S rRNA gene primer	MetA86f	GCTCAGTAACACGTGG	300 nM	10-20 ng	(Wright and Pimm, 2003; Narihiro and Sekiguchi, 2011; Yu et al., 2008)
	ARC915r	GTGCTCCCCCGCCAATTCCT	300 nM	10-20 ng	
PCR setting	95°C 5 min; 35 × (95°C for 30 s, 57°C for 30 s, and 72°C for 1 min); 72°C 10 min, 4°C 2 min.				
Prokaryotic universal primer	515F	GTGCCAGCMGCCGCGGTAA (12 nt barcode added)	1 μM	10 ng	(Caporaso et al., 2012; Wang and Qian, 2009)
	909R	GGACTACHVGGGTWTCTAAT	1 μM	10 ng	
PCR setting	94°C 3 min; 30 × (94°C 40 s, 56°C 60 s and 72°C 60 s); 72°C for 10 min, and 4°C for 2 min				
Archaeal universal primer	Arch347F	GYGCASCAGKCGMGAAW (12 nt barcode added)	1 μM	10 ng	(Takai and Horikoshi, 2000)
	Arch806R	GGACTACVSGGGTATCTAAT	1 μM	10 ng	
PCR setting	95°C for 5 min; 32 × (95°C 30 s, 50°C 30 s and 72°C 40 s); 72°C 10 min, and 4°C 2 min				