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High-Throughput Microbial Isolation from Tibetan Plateau Wetlands Using Single-Cell Microdroplet Platform

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Abstract

Wetland soils of the Tibetan Plateau are the habitat for various microbial resources, these microbes are of great importance in ecosystem functions and biogeochemical cycles. However, traditional agar plate isolation suffers from low efficiency and susceptibility to contamination, limiting the acquisition of low-abundance and rare microbial strains. In order to maximize the recovery and cultivation rate of microorganisms from this unique environment. Here, we utilized the single-cell microliter-droplet screening system (MISS cell, Tmaxtree Biotechnology, Jiangsu, China) to perform high-throughput single-cell isolation and cultivation of microorganisms from soil samples of the Yellow River source wetland on the Tibetan Plateau. We also compared microbial diversity of MISS cell isolates with those obtained from traditional agar plates. The results demonstrated that the number of isolates using the microdroplet single-cell method (Droplet, 4,208) yielded > 9-fold more culture-positive units than the plate isolation method (Plate). Diversity analysis based on 16S rRNA sequencing revealed a 6.7% diversity increase at the genus level with the droplet method. Further species-level analysis confirmed that this method effectively captured low-abundance soil strains—e.g., *Brevundimonas diminuta* and *Acinetobacter radioresistens*—that are uncultured by plating, markedly expanding the detected microbial diversity. This research not only obtains microbial resources from the Tibetan Plateau wetland, but also confirms the robustness of the single-cell based microdroplet technique in isolating. Our work provides new insights in exploring the “microbial dark matter” in extreme environment.

Keywords: high-throughput microdroplets; MISS cell; strain isolation; Tibetan Plateau;

Introduction

Wetlands are the dynamic interface between terrestrial and aquatic systems and have long been known as the “kidneys of the earth”. Wetlands sustain biodiversity and provide critical ecosystem services such as food-web support, climate regulation, and water purification [1]. On the Tibetan Plateau (mean altitude > 4000 m), alpine wetlands cover 1.32×10^5 km², forming the largest high-altitude wetland system worldwide. Long-term low temperature, intense UV radiation, and strong hypoxia impose severe environmental filters that select for specialized soil microbiota. Despite these constraints, plateau wetland soils retain high microbial diversity and drive key terrestrial biogeochemical processes [2]. Empirical studies consistently link soil microbial richness to ecosystem multi-functionality, including net primary productivity, nutrient cycling, and the greenhouse effect [3]. Harnessing the microbial resources in this unique environment is the first step in developing microbial species based products for environment protection and bio-engineering strains.

Currently, the main methods for analyzing microbial diversity include high-throughput sequencing and microbial isolation and cultivation [4, 5]. High-throughput sequencing technology enables the direct extraction of DNA from samples for sequencing, providing an initial understanding of microbial community composition in the wetlands of the Qinghai-Tibet Plateau [6, 7]. However, this method cannot accurately reflects the physiological state of cultivable microorganisms in the environment and their interactions. Moreover, it is difficult to analyze microbial characteristics and functions at the strain level within ecosystems. Therefore, microbial isolation and cultivation remain essential approaches for exploring and analyzing microbial resources. The solid agar plate method is currently the most widely used technique for bacterial isolation in laboratory conditions. Although simple to operate, this method is time-consuming, inefficient, and prone to contamination. Furthermore, it has limitations in recovering rare or slow-growing

species, due to interspecific competition and differences in growth rates. Research indicates that pure cultures obtained using traditional agar plate methods represent only approximately 0.1%–1.0% of the total microbial diversity [8]. Consequently, the vast majority of microorganisms remain “uncultured” or “difficult to culture”, and are often referred to as “Microbial Dark Matter (MDM)” [9].

Over the past decade, single-cell isolation and cultivation techniques have emerged as a practical tool for accessing the “microbial dark matter”. By isolating individual microbial cells before cultivation, these methods minimize inter-species competition and weaken environmental factors, thereby enhancing the cultivability of previously unculturable microorganisms. At present, the most frequently adopted techniques are flow cytometry-based cell sorting (FCCS) and raman-activated cell sorting (RACS), both of which rely on expensive equipment and demand multi-step operational procedures [10]. To overcome these drawbacks, droplet-based microfluidics emerged as a cost-effective alternative. Individual cells can be encapsulated in separate microdroplets, thereby avoiding cross-contamination and enabling large-scale parallel culture [11]. The single-cell microliter-droplet screening system (MISS cell, Tmaxtree Biotechnology, Jiangsu, China) based on this principle enables single-cell-level isolation and culture, long-term incubation (up to 60 days), and target sorting guided by optical signals (e.g., optical density and fluorescence) [12]. These capabilities have established droplet-based microfluidics as a widely used high-throughput screening platform for enzyme kinetics [13], single-cell cultivation [14], nucleic-acid analysis [15], and protein crystallisation [16]. Notably, this technology has also been widely applied to the isolation and cultivation of microorganisms. For example, Hengoju et al. [17] invented a high-throughput droplet-microfluidic platform. Compared with traditional agar plate isolation approaches, it remarkably expands the recoverable gut microbial diversity. Li et al. [18] added resuscitation factors prior to single-cell encapsulation and recovered 18 biphenyl-degrading strains from Tibetan Plateau soils that had resisted

standard cultivation. Liu et al. [19] applied high-throughput droplet encapsulation to Southern Ocean sediments and achieved a marked rise in both the detection rate and the phylogenetic breadth of recoverable taxa, reinforcing droplet microfluidics as a key tool for exploring the “microbial dark matter”.

Nevertheless, the application of droplet microfluidics to the isolation and cultivation of wetland soil microorganisms on the Qinghai-Tibet Plateau remains unexplored, and systematic comparisons with traditional plate culture methods are lacking. The low temperatures, high radiation, and oligotrophic conditions characteristic of this extreme habitat may unpredictably affect cultivation outcomes. Consequently, this study applied the single-cell microliter-droplet screening system (MISS cell) to wetland soils in the Three-River-Source Nature Reserve on the Qinghai-Tibet Plateau, aiming to isolate and cultivate microorganisms. It also compared this method with traditional agar plate isolation techniques in terms of cultivation efficiency, species diversity, and the ability to capture functional groups, with the aim of providing methodological guidance for the high-throughput isolation of microorganisms from extreme environments. The specific experimental workflow is shown in **Figure 1.**

Materials and Methods

Study Site and Sample Collection

Soil was sampled on 30 July 2023 from the Yellow River Source wetland on the Tibetan Plateau (98°26′ E, 34°22′ N; 4576 m Altitude). Soil sample from 0-10 cm was collected using a soil core sampler from the wetland, the standing water table is about 10 cm depth. Immediately after collection, samples were sealed in sterile plastic bags, transported on ice, and stored at 4°C for cultivation, -80°C for DNA extraction, separately in the laboratory until use. Before use, soil core was mixed thoroughly.

Composition of the Culture Medium

Both solid plate and microdroplet cultures used traditional LB medium, the composition of which was as follows (g/L): tryptone 10; yeast extract 5; sodium chloride (NaCl) 10.

Traditional Agar Plate Isolation

Two grams of fresh soil were suspended in 10 mL of sterile saline solution containing 1 mm glass beads and shaken at 30 rpm, 25°C for 16 h. After 10 minutes of sedimentation, the supernatant was used as bacterial suspension. Serial dilutions were prepared and motile cells were enumerated in a haemocytometer; non-motile particles were excluded to avoid counting soil debris. The final density of the bacterial suspension was adjusted to 2×10^9 CFU/mL. The detailed dilution target and target concentrations for gradient dilution are shown in **Table 1**. All the plate derived isolates were divided into three groups (A, B, and C), each comprising approximately 20 agar plates. Each plate was spread with 100 μL supernatant and incubated at 25°C. Plates were inspected daily until the colony number showed no further increase over two days. Then, plates of the same group were washed with 1× PBS and colonies from the plates were gathered into a 5 mL centrifuge tube, centrifuged and total DNA was extracted using the HiPure Soil DNA Mini Kit (Magen), following the manufacturer's protocol. DNA concentration was determined using Nanodrop One (Thermo, USA) and adjusted to 20 ng/μL, and submitted for sequencing.

High-Throughput Microdroplet Bacteria Encapsulization, Incubation and Sorting

Microdroplet generation and high-throughput single-cell cultivation were performed with the Single-Cell Microliter-Droplet Screening System (MISS cell, Tmaxtree Biotechnology, Jiangsu, China). MISS cell is a compact, high-throughput platform that integrates droplet-based microfluidics with single-cell cultivation and optical sorting [20]. A single run routinely produces 5000-20000 monodisperse droplets, corresponding to 500-4000 single-cell encapsulations. The droplet array is incubated in gas-permeable fluoropolymer tubing for up to 60 days, allowing steady oxygen and metabolite exchange. After incubation, the droplets

are passed through an in-line optical detector that records absorbance and fluorescence. **Table 1** shows the dilution rates for each group and the expected single-cell encapsulation frequencies. Suspensions from groups D-F were loaded into the MISS cell chip and incubated at 25°C for 7 days. Optical density (OD) measurements were performed every 24 hours to monitor droplet growth until the single-cell encapsulation rate remained stable for two consecutive days. An OD-based threshold of 1.5 was applied to sort positive droplets into a 96-well plate, and the corresponding data (including OD_{600}, well positions, and plate ID) were recorded. The collected droplets were split into two aliquots (1 μL each), one for subsequent cultivation and the other for 16S rRNA sequencing.

DNA Extraction and 16S rRNA Sequencing Analysis

Genomic DNA was extracted from (i) wetland soil sample, (ii) pooled isolates recovered by droplet-based microfluidics, and (iii) pooled isolates from traditional agar plates, using the SPINeasy DNA Pro Kit for Soil (MP Biomedicals) according to the manufacturer's instructions. Library preparation and sequencing were performed by Shanghai Majorbio Bio-Pharm Technology (Shanghai, China). For diversity profiling, the V3-V4 region was amplified using 341F/806R primers and sequenced on an Illumina MiSeq platform. For strain-level resolution, full-length 16S rRNA genes were amplified using 27F/1492R primer set and sequenced on a PacBio Sequel IIe platform.

All the sequencing data were trimmed and denoised, and ASVs were generated using the DADA2 algorithm in qiime2 version 2023.9 [21]; taxonomic classification was performed against the SILVA 138 database [22]. Downstream analyses (alpha-diversity, NMDS, PERMANOVA) and visualizations were conducted in R 4.3.1 with vegan v2.6-4 and ggplot2 v3.4.

Results

Bacterial Single Cell Isolation Using MISS Cell Platform Droplets and OD Scatter Plot of MISS-Cell Droplet Array

According to Table 1, the microdroplet experiment consisted of three groups: D, E and F. Group D contained 20 96-well plates sorted following 15 days' incubation at 25°C, groups E (20 plates) and F (13 plates) were sorted after 40-45 days of culture. The single-cell bacterial isolation rate for each droplet-plate group is shown in Fig. 2a. Some well-plates exhibited abnormally high isolation rates (greater than 24%), possibly due to the multi-cell encapsulation, rather than successful single-cell isolation. After excluding these well-plates, the average single cell rates for well plates in Groups D, E, and F were 5.20%, 13.03%, and 8.15%, respectively. The total number of sorted droplets from the three groups was 66,882, with the OD_{600} threshold set to 1.5 on the MISS cell-sorting deck. Totally, 4,208 single cell isolates were recovered in this study (Fig. 2b), whereas traditional agar plating yielded only 466 colonies (the total number of colonies in 20 agar plates), fewer than one-ninth of the droplet approach.

α Diversity Analysis

Alpha diversity analysis revealed that Chao and Sobs index values for bulk soil significantly exceeded those for both microdroplet cultures and traditional agar plates (Fig. 3). This is attributed to the presence of a vast array of complex, unculturable microorganisms within wetland soil. Microdroplet cultures exhibited marginally higher diversity indices than plate cultures, indicating that compartmentalised single-cell cultivation enhances the recovery of rare taxa and increases species diversity, as reported in other studies [23, 24].

Microbial Community Composition Comparations Among Different Methods

16S rRNA amplicon sequencing was used to characterize bacterial community composition in bulk soil, agar plate culture isolates, and high-throughput microdroplet cultures (Fig. 4a). At the phylum level,

Pseudomonadota dominated all samples, accounting for 37.6–55.5% of the total relative abundance, with the highest proportion found in microdroplet cultures (55.5%). Bacteroidota and Actinobacterota were the second and third most predominant phyla, comprising 9.0-33.5% and 7.9-14.3% of the community, respectively. The microdroplet method significantly increased the relative abundance of Bacillota to 21.8%. Sequencing results indicated that most soil microorganisms, with the exception of the Acidobacteria phylum, grew well on both microdroplets and solid agar medium. However, the relative abundance of microorganisms varied between the two methods; most microorganisms exhibited higher relative abundances in microdroplets than on agar plates. Further analysis of the genus-level microbial community structure (Fig. 4b) revealed that in the plate culture method, *Flavobacterium* (27.91%), *Aeromonas* (18.56%), *Pseudarthrobacter* (14.30%), and *Pseudomonas* (8.31%) were the predominant genera. In contrast, the microdroplet method significantly increased the relative abundance of *Bacillus* (21.5%), *Brevundimonas* (14.6%), and *Brucella* (10.7%), while nearly depleting *Flavobacterium* and *Aeromonas*. More importantly, several genera—including *Brevundimonas* (14.64%), *Acinetobacter* (5.91%), and *Stenotrophomonas* (9.54%)—were entirely undetectable on agar plates but were successfully enriched and isolated exclusively in microdroplets. These results highlight the suitability of the microdroplet method for isolating and culturing soil microorganisms from the Tibetan Plateau wetlands, and demonstrate its ability to recover microorganisms missed by traditional plate culture. To resolve species-level diversity within the dominant genera recovered by microdroplet isolation, we also performed full-length 16S rRNA gene sequencing on the PacBio Sequel II platform. The microdroplet method significantly increased the relative abundance of strains such as *Bacillus cereus* (33.5%), *Stenotrophomonas maltophilia* (16.62%) *and Acinetobacter radioresistens* (6.3%), which were present in extremely low abundances in the original soil samples, indicating that the microdroplet method is capable of enriching rare microorganisms in soil.

These results further demonstrate the robustness of the microdroplet method in enriching low-abundance microorganisms within complex environments (Fig. 4c).

Analysis of OTU Abundance in Soil Microbial Communities

Venn analysis of soil microbial OTUs (Fig. 4d) showed that the droplet and plate methods shared a core set of OTUs while each features method-specific OTUs. The microdroplet isolation yielded a higher total number of OTUs than the agar plate method. At the genus level, the microdroplet method identified 64 OTUs (11 unique), while the agar plate method identified 60 OTUs (17 unique). Consequently, the microbial communities obtained by the microdroplet method exhibited approximately 6.7% higher diversity than those from the agar plate method. To resolve the phylogeny of OTUs unique to each cultivation method, we constructed a maximum-likelihood tree of 16S rRNA sequences retrieved exclusively by droplet cultivation or by traditional agar plating (Fig. 5). The results revealed distinct clustering patterns among the unique OTUs in both groups: the agar plate-based method yielded multiple clusters on the phylogenetic tree (e.g., branches including *Lachnospiraceae NK4A136 group OTU27* and *Prevotella OTU22*), indicating a more concentrated phylogenetic relationship within this microbial community and suggesting the potential presence of specific dominant taxa. In contrast, microdroplet-unique OTUs were scattered across the tree, reflecting a broader phylogenetic diversity. Recovery of these microdroplet-specific OTUs shows that the method captures rare microbes with trace abundance in the original soil, which would escape detection with routine sequencing strategy. This significantly improves the discovery rate of soil microbial resources on the Tibetan Plateau [25].

Disscussion

This study demonstrated that droplet microfluidics outperformed traditional agar plating in recovering soil bacterial diversity from the Qinghai–Tibetan Plateau. The microdroplet method significantly recovered

both low-abundance and functionally important microbial communities from wetland soils. Among the dominant bacterial phyla identified, Pseudomonadota, Bacteroidota (9.0%-33.5%), and Actinobacteriota (7.9%-14.3%) have been reported to play pivotal roles in the carbon, nitrogen, and phosphorus cycles of permafrost wetland soils. The competitive advantage of Pseudomonadota in consuming readily available organic carbon likely explains this dominance under cold, nutrient-pulsed conditions [26, 27]. Bacteroidota and Actinobacteriota are resistant to drought and high-intensity ultraviolet radiation. These groups synergistically degrade complex organic matter and participate in carbon, nitrogen, and phosphorus cycling, thereby supporting soil fertility and plant growth [28, 29]. Their synergistic action enhances organic–inorganic nutrient transformation in alpine ecosystems, making them core microbial groups maintaining soil ecological functions in permafrost regions. Furthermore, Firmicutes were markedly enriched in the microdroplet method; their efficient DNA repair mechanisms likely underpinned survival under high-radiation environments [30]. At the species level, *Bacillus cereus* (33.5%) was the dominant species in the microdroplet system. However, as a major food-borne pathogen, it produced toxins that can be lethal to livestock such as cattle, sheep, and horses, posing a serious threat to pastoral economies [31, 32]. *Stenotrophomonas maltophilia* (16.62%) exhibited root-promoting potential under certain conditions, and studies reported its ability to stimulate the secondary metabolism of Hypericum perforatum, indicating potential medicinal value [33, 34]. *Brevundimonas diminuta* accounted for 9.78% in the microdroplet system. This bacterium is widely distributed in soil, freshwater, seawater, and extreme environments, and shows high potential for phytoremediation, including plant-growth promotion and heavy-metal removal [35, 36]. Additionally, the microdroplet method successfully isolated *Acinetobacter radioresistens* (6.3%). This radioresistant bacterium survives the high-radiation environment of the Tibetan Plateau and contributes to the degradation of soil organic pollutants such as polycyclic aromatic hydrocarbons (PAHs)

239 [37]. The genus *Pseudomonas* was represented by *Pseudomonas aeruginosa* (2.9%) and *Pseudomonas*
240 *mandelii* (1.3%). *P. aeruginosa* maintains metabolic activity under anoxic and hypersaline conditions,
241 facilitating organic matter decomposition and soil C/N cycling. Its exopolysaccharides also promote
242 aggregate formation and improve soil structure [38]. *P. mandelii*, a Gram-negative bacterium widespread in
243 permafrost soils of polar and alpine regions, plays a key role in soil nitrogen cycling [39].

244 Droplet microfluidics achieved higher cultivability by encapsulating single cells or small cell numbers
245 in monodisperse picoliter droplets, which acted as independent microreactors. This compartmentalization
246 minimized cross-feeding, intercellular competition, and growth-rate bias, thereby preventing the
247 competitive exclusion of slow-growing or rare taxa—a phenomenon commonly observed on traditional
248 agar plates [40]. Meanwhile, the limited contact area between microorganisms and culture medium in
249 traditional plate methods restricted nutrient diffusion and availability in solid media [41]. In contrast, MISS
250 microcarriers enhanced cultivability by providing rapid mass transfer and a high surface-to-volume ratio
251 within each droplet [42]. However, both droplet and plate cultivation imposed a negative selective pressure
252 on Acidobacteriota—a prominent soil phylum in the native community—resulting in their near-complete
253 exclusion from the enriched fractions. This outcome was ascribed to the acidophilic nature of
254 Acidobacteriota, which rendered their enrichment incompatible with the circum-neutral pH maintained in
255 the cultivation assay, thereby creating a pronounced habitat filter against their recovery [43]. Dominant
256 bacterial genera such as *Flavobacterium* and *Aeromonas*, which were only isolated and cultured on agar
257 plates, were not detected in the microdroplet method. This observation was explained by the fact that
258 complex microbial interactions—mutualism, commensalism and competition—depended on continuous
259 physical contact and cross-feeding. Droplet compartmentalization severed these contacts and disrupted
260 metabolic cooperation, thereby suppressing the growth of obligate symbionts that require such interactions

[44]. Guo [45] manipulated the number of gut bacterial strains per microdroplet to quantify interaction effects on diversity. They found that species richness in low-interaction groups was lower than in complex interaction groups, and species diversity decreased when mutually antagonistic species were co-encapsulated in the same droplet. Jung et al. [46] revealed that co-culture within confined spaces, enabled by microfluidic co-encapsulation at the single-cell level, significantly altered the growth kinetics and interactions between *Staphylococcus epidermidis* and *Staphylococcus aureus*.

Conclusion

Here we recruited the high-throughput MISS single-cell isolation system to recover microbes from wetland soil of Tibetan Plateau, and evaluated the robustness of the system by comparing the isolation capacity and diversity with traditional agar plating. Results showed that droplet isolation yielded high-throughput bacteria isolates, with lower cost and automatically. In the same period, it yielded 4,208 strains, whereas plate culture produced only 466 colonies. The robustness of droplet based isolation also improved cultivable microbes at genus-level diversity by 6.7%, and furthermore, enabling the isolation of low-abundance bacterial species from soil, such as *Bacillus cereus* and *Brevundimonas diminuta*. Our results provide a new insight into recovering microbial resources in alpine wetlands. future studies focusing on the strain level utilization and functional microbial strains should be taken to further explore the "microbial dark matter" in this extreme environment.

Data availability

The 16S rRNA gene sequencing raw data generated from this study are deposited in NCBI Sequence Read Archive (SRA) under accession number from SRX30174083 to SRX30174087, the BioProject number is PRJNA1308673.

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Author contributions

Yujie Wu contributed to writing – original draft, visualization, formal analysis and data curation. Lerui Zhou contributed to writing – review & editing. Yongcui Deng contributed to writing – review & editing and resources. Juanli Yun contributed to writing – review & editing, supervision, project administration, investigation, funding acquisition and conceptualization. Xiaojie Guo contributed to writing – review & editing and methodology. All authors read and approved the final manuscript.

Declarations

Ethics approval Not applicable.

Competing interest The authors declare no competing interests.

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Table 1. Target cell suspension concentration, dilution target and bacterial single cell rate for plate (A-C) and microdroplet (D-F) groups.

Sample	Target concentration	Dilution target	Bacterial single cell rate
A	2500~5000 CFU/mL	4×10^5~8×10^5	Not available
B	25000~50000 CFU/mL	4×10^4~8×10^4	Not available
C	250000~500000 CFU/mL	4×10^3~8×10^3	Not available
D	500~1000 CFU/mL	2×10^6~4×10^6	10%~20%

Sample	Target concentration	Dilution target	Bacterial single cell rate
E	5000~10000 CFU/mL	2×10^5~4×10^5	10%~20%
F	50000~100000 CFU/mL	2×10^4~4×10^4	10%~20%

Figure Captions

Fig. 1 Schematic workflow of this study. Soil collected from the Tibetan Plateau was prepared as a suspension, divided into three parts: one is used for DNA extraction and original microbial diversity analysis, while the other two are for high-throughput microdroplet sorting and traditional agar plate cultivation, respectively. The three parts were compared subsequently via 16S rRNA sequencing analysis to determine microbial diversity

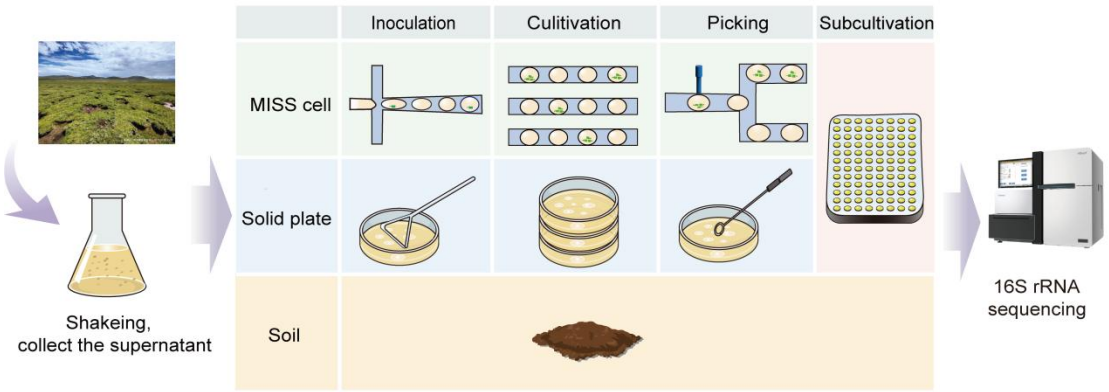
Fig. 2 MISS cell microdroplet sorting results: (a) Bacterial single cell rate in sorted droplets; (b) OD

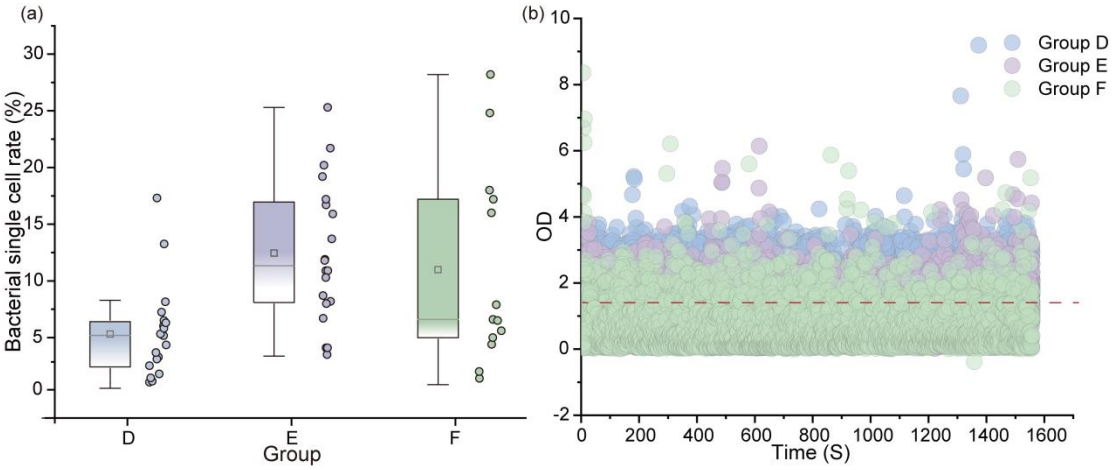
distribution in Droplet Plate

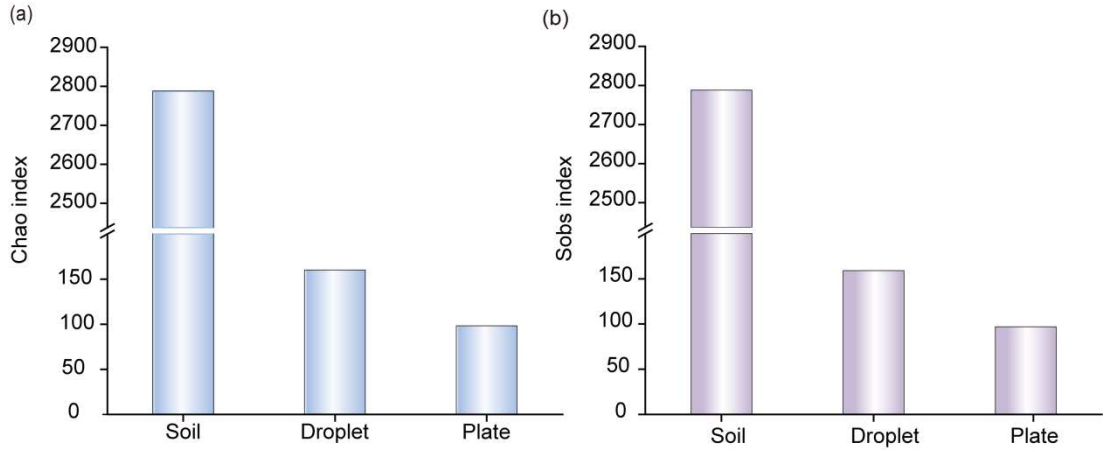
Fig. 3 Alpha diversity indices of bacterial communities from the original soil, agar plate cultivation, and microdroplet cultivation: (a) Chao, (b) Sobs

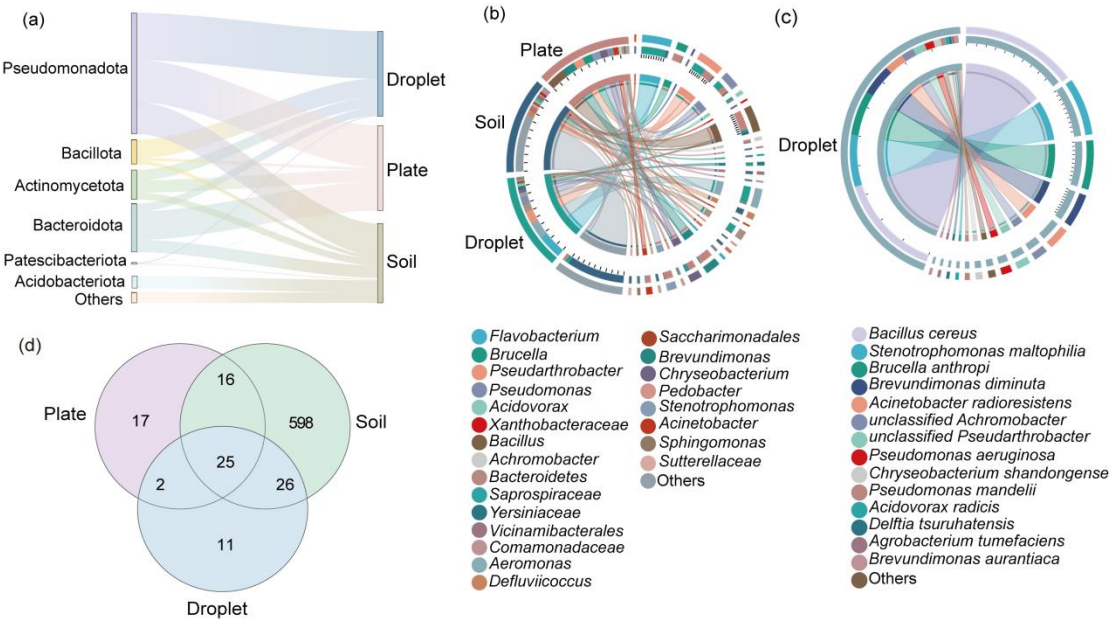
Fig. 4 Community characteristics of soil bacteria recovered by traditional agar plate and microdroplet cultivation. Bacterial community composition of the original soil, traditional agar plates, and microdroplet cultures at (a) phylum level; (b) genus level and (c) species level within the dominant genera (microdroplet method); (d) Venn diagram of bacterial OTUs among the three treatments

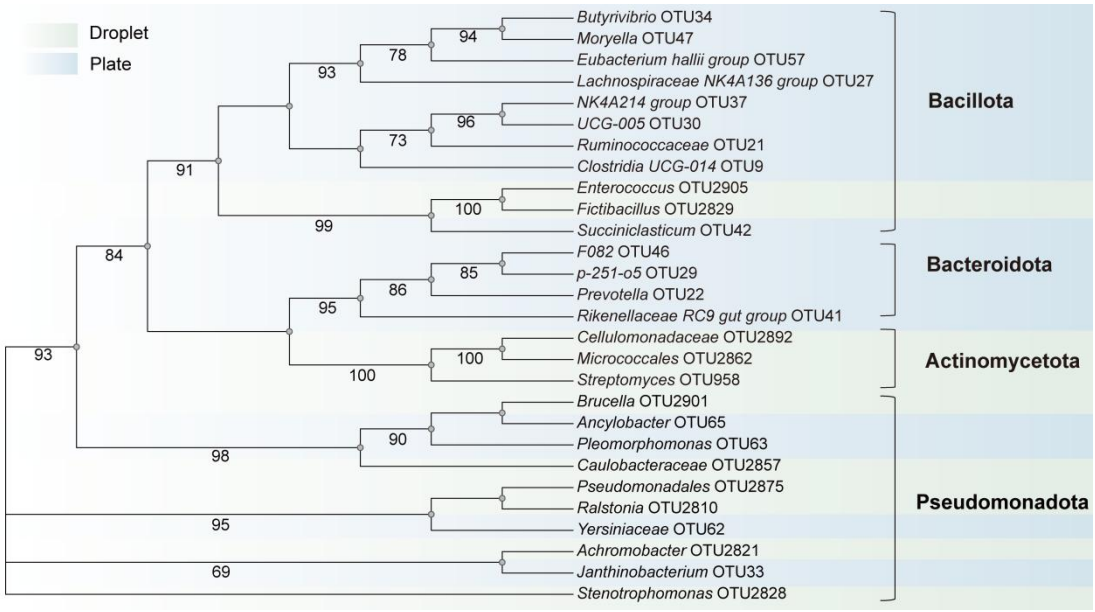
Fig. 5 Phylogenetic analysis of soil bacteria recovered by traditional agar plates and microdroplet cultivation




(a)
Bacterial single cell rate (%)
Group
D
E
F
(b)
OD
Time (S)
Group D
Group E
Group F


(a)
Chao index
Soil
Droplet
Plate
(b)
Sobs index
Soil
Droplet
Plate


(a)
Pseudomonadota
Bacillota
Actinomycetota
Bacteroidota
Patescibacteriota
Acidobacteriota
Others
Droplet
Plate
Soil
(b)
Plate
Soil
Droplet
(c)
Droplet
(d)
Plate
Soil
Droplet
16
17
598
25
2
26
11
Flavobacterium
Brucella
Pseudarthrobacter
Pseudomonas
Acidovorax
Xanthobacteraceae
Bacillus
Achromobacter
Bacteroidetes
Saprospiraceae
Yersiniaceae
Vicinamibacterales
Comamonadaceae
Aeromonas
Defluviicoccus
Saccharimonadales
Brevundimonas
Chryseobacterium
Pedobacter
Stenotrophomonas
Acinetobacter
Sphingomonas
Sutterellaceae
Others
Bacillus cereus
Stenotrophomonas maltophilia
Brucella anthropi
Brevundimonas diminuta
Acinetobacter radioresistens
unclassified Achromobacter
unclassified Pseudarthrobacter
Pseudomonas aeruginosa
Chryseobacterium shandongense
Pseudomonas mandelii
Acidovorax radicis
Delftia tsuruhatensis
Agrobacterium tumefaciens
Brevundimonas aurantiaca
Others


Droplet
Plate
Butyrivibrio OTU34
Moryella OTU47
Eubacterium hallii group OTU57
Lachnospiraceae NK4A136 group OTU27
NK4A214 group OTU37
UCG-005 OTU30
Ruminococcaceae OTU21
Clostridia UCG-014 OTU9
Enterococcus OTU2905
Fictibacillus OTU2829
Succiniclasticum OTU42
F082 OTU46
p-251-o5 OTU29
Prevotella OTU22
Rikenellaceae RC9 gut group OTU41
Cellulomonadaceae OTU2892
Micrococcales OTU2862
Streptomyces OTU958
Brucella OTU2901
Ancylobacter OTU65
Pleomorphomonas OTU63
Caulobacteraceae OTU2857
Pseudomonadales OTU2875
Ralstonia OTU2810
Yersiniaceae OTU62
Achromobacter OTU2821
Janthinobacterium OTU33
Stenotrophomonas OTU2828
Bacillota
Bacteroidota
Actinomycetota
Pseudomonadota