Abundance and Diversity of RuBisCO Genes Responsible for CO₂ Fixation in Arid Soils of Northwest China

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ABSTRACT

Arid soils where water and nutrients are scarce occupy over 30% of the Earth’s total surface. However, the microbial autotrophy in the harsh environments remains largely unexplored. In this study, the abundance and diversity of autotrophic bacteria were investigated, by quantifying and profiling the large subunit genes of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) form I (cbbL) responsible for CO₂ fixation, in the arid soils under three typical plant types (Haloxylon ammodendron, Cleistogenes chinensis, and Reaumuria soongorica) in Northwest China. The bacterial communities in the soils were also characterized using the 16S rRNA gene. Abundance of red-like autotrophic bacteria ranged from 3.94 × 10⁵ to 1.51 × 10⁶ copies g⁻¹ dry soil and those of green-like autotrophic bacteria ranged from 1.15 × 10⁶ to 2.08 × 10⁶ copies g⁻¹ dry soil. Abundance of both red- and green-like autotrophic bacteria did not significantly differ among the soils under different plant types. The autotrophic bacteria identified with the cbbL gene primer were mainly affiliated with Alphaproteobacteria, Betaproteobacteria and an uncultured bacterial group, which were not detected in the 16S rRNA library. In addition, 25.9% and 8.1% of the 16S rRNA genes were affiliated with Cyanobacteria in the soils under H. ammodendron and R. soongorica, respectively. However, no Cyanobacteria-affiliated cbbL genes were detected in the same soils. The results suggested that microbial autotrophic CO₂ fixation might be significant in the carbon cycling of arid soils, which warrants further exploration.

Key Words: autotrophic bacteria, carbon cycling, cbbL, harsh environments, real-time polymerase chain reaction


Soils store at least three times as much organic carbon as that found in the atmosphere on a global scale (Lal, 2004). Future atmospheric CO₂ concentrations will largely depend on the balance of soil organic carbon storage. Biological processes in soil leading to CO₂ production and consumption comprise of root respiration, heterotrophic decomposition and microbial CO₂ assimilation (Hanson et al., 2000; Kuzyakov, 2006). Root respiration and heterotrophic decomposition are deemed as major processes and are well studied previously (Hanson et al., 2000; Kuzyakov, 2006). Autotrophic microbes assimilate CO₂ from atmosphere or originating from root and microbial respiration, forming an “internal carbon cycling” in soil, which is elusive and usually neglected (Kuzyakov, 2006; Yuan et al., 2011).

Most microbes fix CO₂ through the Calvin-Benson-Basham (CBB) reductive pentose phosphate pathway (Badger and Bek, 2008; Tabita et al., 2008). The first and rate-limiting step in the CBB cycle is catalyzed by ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO), which exists in four forms in nature, i.e., forms I, II, III and IV (Badger and Bek, 2008; Tabita et al., 2008). Form I enzymes have eight large and eight small subunits, forming a hexadecamer structure, and have been evolved into four distinct clades: IA, IB, IC, and ID (Badger and Bek, 2008; Tabita et al., 2008). Forms IA and IB belong to a green-like group and are found in Proteobacteria, Cyanobacteria, green algae and higher plants (Badger and Bek, 2008). Forms IC and ID are members of red-like group, occurring in Proteobacteria, Cyanobacteria, green algae and higher plants (Badger and Bek, 2008). Selesi et al., 2005; Tolli and King, 2005; Vide-
mšek et al., 2009). Later on, the diversities of CO₂-fixing microbes in a range of soils have been explored (Selesi et al., 2005; Tolli and King, 2005; Nigro and King, 2007; Videmšek et al., 2009). It was found that the abundance of autotrophic bacteria is closely related with CO₂ fixation activity (Yuan et al., 2012a, b).

Recently, it was found that a barren high-elevation soil harbors a highly diverse photoautotrophic microbial community and continues to take up CO₂ assimilating bacteria in these soils remain largely unexplored. In the present study, we investigated the abundance (by real-time polymerase chain reaction, PCR) and diversity (by cloning and sequencing) of cbbL genes responsible for CO₂ fixation in three typical arid soils under plant types of Haloxylon ammodendron, Cleistogenes chinensis, and Reaumuria soongorica in Northwest China. The abundance and diversity of total bacteria was also investigated using the 16S rRNA gene.

MATERIALS AND METHODS

Site description

The study was conducted at a site (88.02° E, 44.33° N; elevation: 472 m) 8 km northeast of Fukang Station of Desert Ecology, Chinese Academy of Sciences, which is located at the southern periphery of the Gurbantünggút Desert and in the hinterland of the Eurasian continent (Xie et al., 2009). Mean annual precipitation of this region is 160 mm and mean annual temperature is 6.6 °C. The tested soil was desert calcic soil (Wang et al., 2007). The pH of surface soil (0–5 cm) ranged from 7.96 to 8.57, soil moisture from 24.0 to 29.3 g kg⁻¹, and soil organic matter content from 1.9 to 4.8 g kg⁻¹. H. ammodendron, C. chinensis and R. soongorica are dominant plant species in this region.

Soil sampling and soil properties

Soil samples were taken from 3 plots located at least 20 m apart under each vegetation type. Five soil cores of surface soil (1–5 cm) from each plot were composed and homogenized. The soil samples were kept at 4 °C and brought to the laboratory immediately for further analysis. Soil samples for DNA extraction were stored at −20 °C. Soil water content was measured by oven-drying soil at 105 °C for 8 h. Soil pH was measured at a soil:water ratio of 1:5 (w/w). Soil organic carbon content was determined by a TOC analyzer (TOC 5000A with SSM 5000A module, Shimadzu, Japan). Microbial biomass carbon in fresh soil was determined by ethanol-free chloroform fumigation extraction method. Fumigated and unfumigated soils were extracted with a 0.5 mol L⁻¹ K₂SO₄ at a soil:water ratio of 1:4 (w/w). Carbon concentrations in supernatants were determined on a TOC analyzer (Multi N/C 3100, Jena, Germany).

DNA extraction

DNA was extracted from 500 mg soil samples with the Fast DNA SPIN kit for soil and the FastPrep-24 machine (MP Biomedicals, USA), according to the manufacturer’s instructions. DNA extracts were examined on a 1% agar gel and stored at −80 °C for further use.

Real-time quantitative PCR (qPCR)

All qPCR assays were carried out in duplicate on a real-time iCycler system (Bio-Rad, USA) using SYBR green I chemistry and the data were analyzed by Bio-Rad IQ5 version 2.0, as reported previously (Fan et al., 2011, 2012). The primers for 16S rRNA gene, green-like cbbL gene and red-like cbbL gene quantification were Eub338/Eub518, cbbLRF1/cbbLRR1 and cbbLG1F/cbbLG1R, respectively (Fierer et al., 2005; Selesi et al., 2005). A standard curve spanning 10⁻¹⁰⁸ gene copies was constructed by 10-fold serial dilution of known copy number vectors pMD19-T (TaKaRa, Japan) with partial 16S rRNA or cbbL gene inserts. Each 20 µL reaction cocktail contained 10 µL 2 × SuperMix (Bio-Rad, USA), 2 µL 20-fold diluted extracted DNA, 0.4 µL each primer (10 mmol L⁻¹) and 7.2 µL sterilized Millipore water. The thermo-cycling conditions for amplifications of the 16S rRNA gene, green-like cbbL gene and red-like cbbL gene were as follows: denaturing at 95 °C for 3 min; 40 cycles of denaturing at 94 °C for 30 s, annealing at 57 °C for 30 s, extension at 72 °C for 45 s and data collection at 83 °C for 10 s; 1 cycle of 95 °C for 60 s, 55 °C for 10 s and a melt data acquisition procedure. The amplification specificity was confirmed by generating a melting curve from the PCR products.

PCR amplification, cloning and sequencing

PCRs for cloning were performed on a DNA engine peltier thermal cycler (Bio-Rad). The primers for 16S rRNA gene amplifications were 27f and 1492r. The primers for green-and red-like cbbL gene amplifications were the same as those used for qPCR. Each 25 µL reaction mixture contained: 1 µL 10-fold diluted ex-
extracted DNA, 2.5 µL of 10 × Ex Taq buffer, 0.625 U of Ex Taq polymerase, 200 µmol L⁻¹ of dNTP mixture, 200 nmol L⁻¹ of each primer and 2.5 µg mL⁻¹ bovine serum albumin. Thermo-cycling conditions for the 27f/1492r primer were: denaturing at 95 °C for 3 min; 25 cycles of denaturing at 94 °C for 30 s, annealing at 57 °C for 30 s, and extension at 72 °C for 60 s with a final cycle of 72 °C for 10 min. The thermo-cycling conditions for cbbL1F/cbbL1R and cbbLG1F/cbbLG1R were the same as for 27f/1492r except that products were amplified for 35 cycles.

Triplicate PCR products of each treatment were pooled, gel purified and cloned into the vector pMD19-T, which was then transferred into Escherichia coli JM109 competent cells (TaKaRa). Overnight grown white transformant colonies were PCR screened directly for the presence of inserts. Positive clones were further analyzed. Identity of green- and red-like cbbL genes was analyzed by Blast in the National Center for Biotechnology Information (NCBI) database (http://www.ncbi.nlm.nih.gov). Phylogenetic tree was constructed with neighbor-joining procedure (bootstrap replication = 1 000) in MEGA 4.0. Clone frequencies were calculated as the proportion of clone number to total clone number of each lineage to total clone number of each sample. Triplicate PCR products of each treatment were cloned and edited with MEGA 4.0 (Tamura et al., 2004) and removed in further analysis. In this study, 0, 2 and 8 sequences were detected as chimera in green- and red-like cbbL and 16S rRNA gene clone library. Finally, 136, 125 and 90 sequences in green- and red-like cbbL and 16S rRNA gene clone library were further analyzed. Identity of green- and red-like cbbL genes was analyzed by Blast in the National Center for Biotechnology Information (NCBI) database (http://www.ncbi.nlm.nih.gov). Phylogenetic tree was constructed with neighbor-joining procedure (bootstrap replication = 1 000) in MEGA 4.0. Clone frequencies were calculated as the proportion of clone number to total clone number of each lineage. Identity and clone frequency of 16S rRNA gene were analyzed with classifier in the Ribosomal Database Project (RDP) with a confidence threshold of 80% (Cole et al., 2007). Soil bacterial communities were compared by LibCompare in RDP. Partial sequences of green- and red-like cbbL genes and 16S rRNA gene were deposited in the European Molecular Biology Laboratory database under the accession numbers FR849249-FR849384, FR849122-FR849248 and FR849385-FR849682, respectively.

**Statistical analysis**

One-way analysis of variance (ANOVA) was conducted to test the significance of vegetation effects on soil properties and gene abundances with SAS 8.0 (SAS Institute Inc., USA).

**RESULTS**

**Soil properties**

Water content of the surface soils under *H. ammodendron*, *C. chinensis* and *R. soongorica* communities ranged from 24.0 to 29.3 g kg⁻¹ (Table I), with no significant difference (*P* = 0.67) between plant vegetation types. Soil pH in the *H. ammodendron* and *R. soongorica* soils (pH = 8.57 and 8.45, respectively) were significantly higher (*P* < 0.01) than that in the *C. chinensis* soil (pH = 7.96). Soil organic carbon content in the *C. chinensis* soil was significantly lower (*P* = 0.05) than those in the *H. ammodendron* and *R. soongorica* soils. Average soil microbial biomass varied greatly, but did not significantly differ (*P* = 0.24) among vegetation types.

**Abundance of autotrophic and total soil bacteria**

The amplification efficiency of real-time PCR for the 16S rRNA gene, green-like cbbL gene and red-like cbbL gene were 87.7%, 96.5% and 94.6%, respectively. Corresponding slopes were −3.659, −3.408 and −3.460 and corresponding correlation coefficients (*R²*) were 0.991, 0.993 and 0.991, respectively. Copy numbers of associated 16S rRNA genes in the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica* ranged from 2.51 × 10⁶ to 9.07 × 10⁹ copies g⁻¹ dry soil (Fig. 1), but did not differ significantly (*P* = 0.14) from each other. Mean copy numbers of green-like cbbL genes were 2.08 × 10⁶, 1.15 × 10⁶ and 1.84 × 10⁶ copies g⁻¹ dry soil for the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively (Fig. 2). Me-

**TABLE I**

<table>
<thead>
<tr>
<th>Plant</th>
<th>Moisture g kg⁻¹</th>
<th>pH</th>
<th>Soil organic carbon g kg⁻¹</th>
<th>Microbial biomass µg g⁻¹ dry soil</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>H. ammodendron</em></td>
<td>24.0±2.3a¹ b</td>
<td>8.57±0.06a</td>
<td>4.76±0.95a</td>
<td>284.98±18.24a</td>
</tr>
<tr>
<td><em>C. chinensis</em></td>
<td>27.6±3.9a</td>
<td>7.96±0.06b</td>
<td>1.90±0.56b</td>
<td>176.29±40.74a</td>
</tr>
<tr>
<td><em>R. soongorica</em></td>
<td>29.3±3.3a</td>
<td>8.45±0.07a</td>
<td>3.90±0.29ab</td>
<td>198.10±66.19a</td>
</tr>
</tbody>
</table>

¹Means±standard errors (*n* = 3).

²Means followed by the same letter(s) within each column are not significantly different at *P* < 0.05.
Fig. 1 Abundance of bacterial 16S rRNA genes in the arid soils under three plant types of *Haloxylon ammodendron* (HA), *Cleistogenes chinensis* (CC) and *Reaumuria soongorica* (RS). Vertical bars indicate standard errors of the means (n = 3). Bars with the same letter are not significantly different at P < 0.05.

Fig. 2 Abundance of green-like and red-like *cbbL* genes in the arid soils under three plant types of *Haloxylon ammodendron* (HA), *Cleistogenes chinensis* (CC) and *Reaumuria soongorica* (RS). The *cbbL* genes encode the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) form I. Vertical bars indicate standard errors of the means (n = 3). Bars with the same letter are not significantly different at P < 0.05.

an copy numbers of red-like *cbbL* genes were 1.41 × 10^6, 0.39 × 10^6 and 1.51 × 10^6 copies g^-1 dry soil for the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively. Copy numbers of both green- and red-like *cbbL* genes did not differ significantly (P > 0.05) among plant types.

**Compositions of autotrophic and total soil bacteria**

A total of 41, 48 and 45 green-like *cbbL* sequences were retrieved from the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively. No chimeric green-like *cbbL* sequence was detected. Diversities of green-like autotrophic bacterial communities in the soils under the three plant types were low (Fig. 3). All the green-like *cbbL* sequences were grouped as Alphaproteobacteria and were affiliated with *Nitrobacter vulgaris* (accession number L22885) with an average similarity of 93%, except for one clone that was affiliated with *Bradyrhizobium* sp. BTAI1 (accession number CP000494) with a similarity of 95%.

After removal of two chimeric sequences, 39, 44 and 44 red-like *cbbL* sequences were retrieved from the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively (Fig. 4). These sequences were tentatively grouped into seven clusters. Cluster 1 and 2 did not match closely with any sequences in the NCBI database. Cluster 3 was grouped with the Betaproteobacterium *Burkholderia xenovorans* LB400 (accession number CP000271). Cluster 4 was grouped with the Betaproteobacteria *Variovorax paradoxus* S-110 (CP001635), *Caprivadus taiwanensis* LMG19424 (CU633750) and *Ralstonia eutropha* H16 (AY305378). Cluster 5 was affiliated with the Alphaproteobacterium *Sinorhizobium meliloti* M119 (DQ898620). Cluster 6 was grouped with the Alphaproteobacteria *Rhodospirillum centenum* ATCC (CP000613), *Nitrospira winogradskii* Nb-255 (CP000115) and *Bradyrhizobium japonicum* USDA110 (CU633750). Cluster 7 was grouped with the uncultured bacterium clone HKOR7 (AY572135).

Clusters 1, 2 and 7, which were not affiliated with known cultured bacteria, accounted for 74.4%, 70.5% and 84.1% of the red-like *cbbL* clone library in the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively (Fig. 5). *Burkholderia*-like *cbbL* sequences (Cluster 3) accounted for 5.1%, 2.3% and 4.5%; while cluster 4 accounted for 5.1%, 6.8% and 4.5% of the red-like *cbbL* clone library in the soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, respectively. Clusters 5 represented 12.8%, 15.9% and 2.3% and Cluster 6 2.6%, 4.5% and 4.5%, respectively.

Thirteen bacterial phyla were detected by 16S rRNA gene sequence analysis in the soils tested, namely Acidobacteria, Actinobacteria, Armatimonadetes, Bacteroidetes, Cyanobacteria, Chloroflexi, Deinococcus-Thermus, Gemmatimonadetes, Nitrospira, Planctomycetes, Proteobacteria, TM7 and Verrucomicrobia (Fig. 6). Cyanobacteria dominated in the soil under *H. ammodendron*, followed by the unclassified bacteria, Acidobacteria, Actinobacteria, Deinococcus-Thermus, Bacteroidetes and Proteobacteria. No Armatimonadetes, Chloroflexi, Gemmatimonadetes, Nitrospira, Planctomycetes, TM7 and Verrucomicrobia were detected in

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**Fig. 1** Abundance of bacterial 16S rRNA genes in the arid soils under three plant types of *Haloxylon ammodendron* (HA), *Cleistogenes chinensis* (CC) and *Reaumuria soongorica* (RS). Vertical bars indicate standard errors of the means (n = 3). Bars with the same letter are not significantly different at P < 0.05.

**Fig. 2** Abundance of green-like and red-like *cbbL* genes in the arid soils under three plant types of *Haloxylon ammodendron* (HA), *Cleistogenes chinensis* (CC) and *Reaumuria soongorica* (RS). The *cbbL* genes encode the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) form I. Vertical bars indicate standard errors of the means (n = 3). Bars with the same letter are not significantly different at P < 0.05.
the soil under *H. ammodendron*. Actinobacteria and unclassified bacteria accounted for 42.3% and 15.4%, respectively, of the soil under *C. chinensis* (Fig. 7) and no Chloroflexi, Cyanobacteria, Deinococcus-Thermus, Nitrospira and Verrucomicrobia were detected. Clone frequencies of Acidobacteria, Actinobacteria and unclassified bacteria were 18.9%, 29.7% and 13.5%, respectively. No Armatimonadetes, Gemmatimonadetes and Planctomycetes were detected in the soil under *R. soongorica*. Comparison of soil bacterial communities using LibCompare in RDP showed that the clone frequency of Cyanobacteria differed (*P* = 0.01) between the soils under *H. ammodendron* and *C. chinensis* (25.9% versus 8.1%). Total bacterial communities in the soils under *C. chinensis* and *R. soongorica* were not significantly different (*P* > 0.05) from each other.

**DISCUSSION**

The abundance of autotrophic bacteria was quantified in all three arid soils under different vegetation types (Fig. 2). For example, red-like *cbbL* genes were 0.39 × 10^6 to 1.51 × 10^6 copies g^-1 dry soil in these soils (Fig. 2). A higher abundance of red-like *cbbL* genes (6.8 × 10^6 to 3.4 × 10^7 copies g^-1 soil) was found in a German agricultural soil using the same primer pair (Selesi *et al.*, 2007). Videmšek *et al.* (2009) showed a
Fig. 4 Neighbor-joining phylogenetic tree of red-like \textit{cbbL} genes in the arid soils under three plant types of \textit{Haloxylon ammodendron}, \textit{Cleistogenes chinensis} and \textit{Reaumuria soongorica}. The \textit{cbbL} genes encode the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) form I. Bootstrap values ($n = 1000$) are indicated at the nodes and the scale bar represents 10\% sequence divergence. Sequences from this study are represented as closed circles.
similar trend (6.2 × 10^6 to 1.4 × 10^7 copies g^{-1} soil) in the soils with low atmospheric CO_2 concentration near a natural CO_2 spring. Green-like autotrophic bacteria were rarely quantified in previous studies. Videmšek et al. (2009) did not detect green-like cbbL genes in the soils near a CO_2 spring where red-like cbbL genes were abundant. In the soils analyzed in this study, copy numbers of green-like cbbL genes were found to be 1.15 × 10^6 to 2.08 × 10^6 copies g^{-1} dry soil (Fig. 2). However, high proportions of Cyanobacteria in the soils under *H. ammodendron* and *R. soongorica* (25.9% versus 8.1%) suggest that the diversity of green-like autotrophic bacteria in some soils of this region was probably underestimated (Fig. 7). Assuming that the copy numbers of cbbL genes are equal to those of 16S rRNA genes in Cyanobacteria, green-like cbbL genes in the soils under *H. ammodendron* and *R. soongorica* would be up to 1.5 × 10^9 and 0.5 × 10^9 copies g^{-1} dry soil, which are similar to, or even higher than those observed in the paddy soils (0.02 × 10^8 to 8.14 × 10^8 copies g^{-1} soil) (Yuan et al., 2012a, b). The presence of abundant autotrophic bacteria in the arid soils suggests microbial autotrophy may be an important component in C cycling within the arid ecosystems as is the case in other soils.

The green-like cbbL sequences of all three arid soils were mainly affiliated with the Alphaproteobacterium *Nitrobacter* (Fig.4), which was not dominant in the 16S rRNA clone library. Predominance of *Nitrobacter* in green-like autotrophic bacteria agrees with the findings in a German agricultural soil (Selesi et al., 2005). Cyanobacteria detected in this study were closely related to *Crinalium epipsammum* and *Planktothricoides raciborskii* (Fig.6). In silico analysis showed that the primer pairs used in the present study could not amplify the cbbL genes in *C. epipsammum*, while no cbbL sequence in *Planktothricoides raciborskii* was available in the NCBI database. In addition, green-like cbbL sequences obtained in this study were not grouped closely with any Cyanobacterial cluster (Fig. 3). Therefore, the primer pair targeting green-like cbbL genes used in this study may bias against Alphaproteobacteria. Less than 30% red-like cbbL sequences of each clone library were distributed amongst the Betaproteobacteria and Alphaproteobacteria (Figs. 4 and 5), while over 70% of red-like cbbL sequences obtained in this study were novel or uncultured in all the three tested soils. There is uncertainty as to whether or not these newly dominant red-like cbbL sequences are affiliated with dominant lineages in Proteobacteria or other phyla identified using the 16S rRNA gene (Fig. 6). Therefore, further research should be conducted using culture or specific culture independent methods, such as stable isotope probing, to further investigate the microbial ecology of autotrophic CO_2 fixation in alkaline arid regions.

Previous studies showed that the microbial autotrophic community is significantly affected by edaphic factors (Selesi et al., 2005; Toll and King, 2005; Nigro and King, 2007; Videmšek et al., 2009; Yuan et al., 2012b). In our study we found that the abundance of cbbL and 16S rRNA genes were lowest (although not statistically significant) in the soils under *C. chinensis* where organic carbon and pH were lowest (Figs. 1 and 2, Table I). The absence of Cyanobacteria in the soils under *C. chinensis* indicated that the structure of the autotrophic bacterial community associated with this soil was different from those in the other two soils (Fig. 7). This suggested that soil properties were also important regulators in shaping autotrophic bacterial communities in arid soils.

CONCLUSIONS

An abundance of green- and red-like autotrophic bacteria were detected in three arid soils under *H. ammodendron*, *C. chinensis* and *R. soongorica*, in Northwest China. The abundance and diversity of autotrophic bacteria in the soils under *H. ammodendron* and *R. soongorica* were probably underestimated as a high proportion of Cyanobacteria detected with the 16S rRNA gene were not detected with the cbbL gene in
Fig. 6 Neighbor-joining phylogenetic tree of 16S rRNA genes in the arid soils under three plant types of Haloxylon ammodendron, Cleistogenes chinensis and Reaumuria soongorica. Bootstrap values (n = 1000) are indicated at the nodes and the scale bar represents 10% sequence divergence. Sequences from this study are represented as closed circles.
these soils. The abundance and diversity of autotrophic bacteria in the three typical arid soils studied suggested that microbial autotrophic CO$_2$ fixation might play an important role in carbon cycling in the arid soils of Northwest China, which warrants further investigation.

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