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Soil Microbial Metabolic Quotient in Inner Mongolian Grasslands: Patterns and Influence Factors

CAO Yingqiu[1], XU Li[2], ZHANG Zhen[1], CHEN Zhi[2], HE Nianpeng[2, 3, 4]

(1. *Resources and Environment College*, *Anhui Agricultural University*, *Hefei* 230036, *China*; 2. *Key Laboratory of Ecosystem Network Observation and Modeling*, *Institute of Geographic Sciences and Natural Resources Research*, *Chinese Academy of Sciences*, *Beijing 100101*, *China*; 3.*College of Resources and Environment*, *University of Chinese Academy of Sciences*, *Beijing* 100049, *China*; 4. *Institute of Grassland Science*, *Northeast Normal University*, *and Key Laboratory of Vegetation Ecology*, *Ministry of Education*, *Changchun* 130024, *China*)

Abstract: Microbial metabolic quotient (MMQ) is the rate of soil microbial respiration per unit of microbial biomass, and represents the capacity of soil microbes to utilize soil organic matter. Understanding the regional variation and determinants of MMQ can help predict the responses of soil respiration rate to global climate change. Accordingly, we measured and analyzed MMQ-related data (e.g., soil basic respiration rate at 20℃ and soil microbial biomass) from 17 grassland sites, which located in meadow steppe, typical steppe, and desert steppe along a 1000-km transect across the Inner Mongolian grasslands, China. Results showed that MMQ varied significantly among the different grassland types ($P < 0.05$; desert > typical > meadow) and decreased from southwest to northeast ($r = – 0.81$) with increasing latitude ($r = – 0.50$), and with increasing mean annual precipitation ($r = – 0.69$). Precipitation accounted for 56% of the total variation in MMQ, whereas temperature accounted for 26%. MMQ was negatively correlated with precipitation across the Inner Mongolian grasslands. Therefore, climate change, especially in regard to precipitation, may influence soil microbial respiration and soil carbon dynamics through altering MMQ. These results highlighted the importance of spatial patterns in MMQ for accurately evaluating the responses of soil respiration to climate change at regional and global scales.

Keywords: soil respiration; soil microbial biomass carbon; precipitation; temperature; Inner Mongolian grassland

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1 Introduction

Microbial metabolic quotient (MMQ) is the rate of soil microbial respiration (R) per unit of microbial biomass, and can represent the capacity of soil microbes to utilize soil organic matter (Powlson and Jenkinson, 1976). Understanding the regional variation of MMQ and its regulating influence factors can help elucidate the adaptations of soil microbes at regional or global scales and help predict the responses of soil respiration to global climate change.

Recently, several studies have investigated the variation of MMQ at regional and global scales and have investigated roles of various factors (e.g., land-use, disturbances, heavy metal pollution) in determining MMQ (Zhou D N et al., 2013; Zheng et al., 2016; Francaviglia et al., 2017). Bogorodskaya et al. (2009) used MMQ to investigate the soil microbial complexes of forest eco-

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Corresponding author: XU Li. E-mail: xuli@igsnrr.ac.cn; ZHANG Zhen. E-mail: xjzhangzhen@163.com

systems that were subjected to fires and insect defoliation. At the global scale, Xu et al. (2017) investigated the variation of MMQ among different ecosystems. Such studies have improved the current understanding of the regulation of soil microbial respiration, including the roles of internal and external factors at different scales. Theoretically, any factors that affect the physical or chemical properties of soil could influence the quantity and activity of soil microbes, thereby affecting MMQ (Jiang et al., 2013; Steinweg et al., 2013). Some studies have reported that microbial biomass and activity were influenced by decomposition and the storage of soil organic matter (SOM; Blagodatskaya et al., 2011; Zhao et al., 2016) and that greater MMQ was accompanied by more rapid SOM decomposition (Steinweg et al., 2013).

Terrestrial ecosystems are composed of unique geographical units, each with characteristic climate, soil, vegetation, and microbial traits (Anderson, 1992). Therefore, the regional variation and main influencing factors of MMQ are likely to differ among the geographical units. The Inner Mongolian grasslands, with different temperature and precipitation gradients, are one of the largest natural grasslands in China. Understanding the regional variation and underlying influence factors of MMQ variation in this region may help us to predict the responses of soil microbial respiration to global climate change (Xu et al., 2017). Previous studies have demonstrated the variation of MMQ variation and its influencing factors in Inner Mongolian grasslands at specific sites (Zhao et al., 2016). However, it is still unclear for the regional patterns of MMQ and its underlying influence factors. In this study, we measured and analyzed MMQ-related data (e.g., soil basic respiration rate at 20℃ and soil microbial biomass) from 17 grassland sites along a 1000-km transect across the Inner Mongolian grasslands. The main objectives of the study were to: 1) explore the spatial pattern of MMQ among different grassland types across the Inner Mongolian grasslands, and 2) explore the influence and main factors that control the spatial variation of MMQ. The investigation of MMQ at regional scale may help us to better explore soil carbon cycles, and to evaluate the responses of soil respiration to climate change in future.

2 Materials and Methods

2.1 Study area

The Eurasian steppes comprise the largest area of intact grassland on Earth (1.33×10^7 km^2). The steppes extend eastward in a continuous band from Romania, through Russia and Mongolia to China. The steppes provide a natural laboratory in which to study the responses and feedback of soil respiration to climate change. The present study was conducted in the temperate grasslands of Inner Mongolia (41.14°N–43.19°N, 100.46°E–123.24°E), along a 1000-km, northeast-to-southwest transect that represented a decreasing precipitation gradient (Fig. 1).

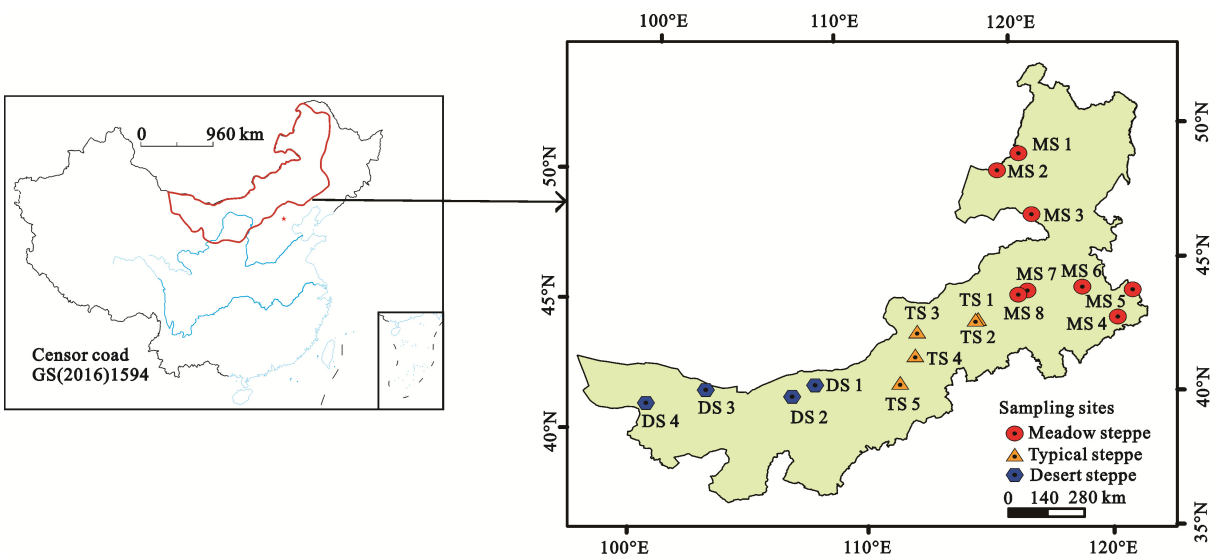

Fig. 1 Distribution of sampling sites across the Inner Mongolian grasslands in 2013

The study sites were characterized by a temperate continental climate, with large variations in mean annual precipitation (MAP) and annual mean temperature (AMT). In this region, precipitation mainly occurs sporadically from June to August. From northeast to southwest, MAP ranged from 71 to 474 mm, and AMT ranged from 6.6℃ to 1.0℃ (Table 1). The temperate grasslands were classified as meadow steppe, typical steppe, and desert steppe.

2.2 Soil sampling

Soil sampling was conducted in early August 2013. Sampling sites (n = 17) were selected along the 1000-km, northeast-to-southwest transect, taking into account the spatial distribution of meadow steppe, typical steppe, and desert steppe (Fig. 1). Four plots (10 m × 10 m) were established at each site, and in each plot, the community composition of the aboveground vegetation was measured in a 1 m × 1 m quadrat. Soil was also collected from each plot using a random sampling design and W-shaped sampling pattern. After removing litter from the soil surface, 10 soil samples (0 to 10 cm in depth) were collected from each quadrat using a 4 cm soil auger and pooled. Each pooled sample (~1 kg) was homogenized, passed through a sieve (2-mm mesh), and dried naturally in the shade, after visible litter was manually removed.

2.3 Measurements and analysis

2.3.1 Physicochemical soil characteristics

To determine the basic soil properties of each of the 17 sites, soil pH was measured using an Ultrameter-2 pH (Myron L. Co., CA, USA; determination of soil: water 1 : 1.25), soil texture was analyzed (sand, 250–2000 μm; silt, 50–250 μm; or clay, < 50 μm) using a Mastersizer-2000 laser particle instrument (Malvern Company, Worcestershire, England), and SOC content was measured using the H_2SO_4-$K_2Cr_2O_7$ oxidation method (Nelson et al., 1996).

2.3.2 Soil microbial respiration rate (R_{20})

Soil samples (30 g dry weight) were placed in 150-mL polyethylene plastic bottles (4 replicates per site) and adjusted to 55% water holding capacity (WHC, %) by adding deionized water. The WHC was measured are described in He et al. (2013). All samples were pre-incubated at 20℃ for 3 d to activate the microorganisms and to minimize the pulse effect (Fierer and Schimel, 2002; Liu and He, 2017). The plastic bottles

Table 1 Characteristics of 17 sampled sites along a 1000-km transect across the Inner Mongolian grassland in 2013

Site	Grassland types	Soil type	Longitude (°N)	Latitude (°E)	AMT (℃)	MAP (mm)	pH	Clay (%)	Silt (%)	Sand (%)
MS-1	Meadow steppe	Black calcium soil	119.28	50.05	–2.71	355.26	5.84	54.67	40.68	4.65
MS-2			118.01	49.53	–1.18	305.18	5.63	10.74	23.86	65.40
MS-3			119.30	47.66	–0.91	375.87	5.66	45.54	40.79	13.67
MS-4			122.25	43.19	6.02	473.99	5.65	49.82	35.78	14.41
MS-5			123.24	44.11	5.24	463.17	7.15	59.99	40.02	0.00
MS-6			120.96	44.58	5.37	392.73	6.88	100.00	0.00	0.00
MS-7			118.36	44.77	0.95	389.60	5.90	82.10	0.95	16.96
MS-8			117.90	44.67	–0.07	392.99	5.93	93.41	6.59	0.00
TS-1	Typical steppe	Chestnut calcium soil	115.83	43.94	2.20	283.72	8.69	73.09	20.52	6.39
TS-2			115.70	43.93	1.84	285.47	6.10	77.15	22.69	0.17
TS-3			112.92	43.71	3.49	186.59	6.74	80.75	19.25	0.00
TS-4			112.71	42.80	5.04	208.78	6.55	89.97	10.03	0.00
TS-5			111.89	41.79	2.24	334.46	6.44	87.13	12.87	0.00
DS-1	Desert steppe	Alfisols	108.05	41.87	5.40	164.75	7.00	56.68	30.9	12.43
DS-2			107.00	41.45	1.35	249.26	7.38	89.36	10.64	0.00
DS-3			103.11	41.72	7.06	70.97	6.63	100.00	0.00	0.00
DS-4			100.46	41.14	6.62	85.78	6.69	85.10	14.81	0.09

Notes: AMT: annual mean temperature. MAP: mean annual precipitation

were sealed with caps that had small holes for ventilation to reduce water loss. Water loss was measured and corrected to 55% WHC on the basis of weight at intervals of 3–4 d.

After one-week of incubation, R_{20} was measured using an automatic sampling and analysis system. Briefly, a new PRI-8800 Automatic Temperature Control Soil Flux System (PRI-8800; Pre-Eco, China) was developed to measure R_{20}, as a modification of He et al. (2013). The system measured the CO_2 concentration of each incubation bottle at a high frequency (every second) (He et al., 2013; Liu et al., 2017; Liu et al., 2018). An electric water bath was controlled using an automatic temperature regulator (Julabo, Germany) and connected to a Li-COR CO_2 analyzer (Li-7100; Li-COR, USA), which recorded the CO_2 concentration every second. R_{20} was calculated using the slope of CO_2 concentration and specific transformation factors (Eq. (1)):

$$R_{20} = \frac{k \times v \times \alpha \times \beta}{m} \quad (1)$$

where R_{20} represents the rate of soil microbial respiration (mg CO_2-C/(kg soil·d)) at 20℃; k represents the slope of CO_2 concentration in this measurement system; V represents the volume of the incubation bottle and gas tube; m represents the soil dry weight; α represents the transformation coefficient of CO_2 mass; and β represents the transformation coefficient of time.

2.3.3 Soil microbial diversity

After 1-week of incubation, soil microbial phospholipid fatty acid (PLFA) biomarker analysis was conducted following the method described by Bååth and Anderson (2003). Briefly, PLFAs were extracted from 8 g dry-weight-equivalent fresh soil using a 5 : 10 : 4 (v : v : v) mixtures of chloroform, methanol, and phosphate buffer. After extraction, the lipids were separated into neutral lipids, glycolipids, and polar lipids (phospholipids) using a silicic acid column and analyzed using a Thermo ISQ gas-chromatography mass-spectroscopy (GC-MS) system (TRACE GC Ultra ISQ).

The PLFA nomenclature used was as follows: total number of carbon atoms: number of double bonds, followed by the position (ω) of the double bond closest to the methyl end of the molecule; *Cis* and *trans* configurations are indicated using 'c' and 't', respectively (Frostegård et al., 1993; Xu et al., 2015).

The 19 PLFAs (i14 : 0, i15 : 0, a15 : 0, i15 : 1, i16 : 0, 16 : 1ω7c, 16 : 1ω9c, i17 : 0, a17 : 0, cy17 : 0, cy19 : 0, 18 : 1ω5c, 18 : 1ω7c, 18 : 1ω9c, 18 : 2ω6c, 18 : 3ω6c, 10Me16 : 0, 10Me17 : 0, and 10Me18 : 0) that were consecutive present in the samples were used for data calculation. The fatty acids i14 : 0, i15 : 0, a15 : 0, i15 : 1, i16 : 0, i17 : 0, and a17 : 0 were used as indicators of Gram-positive (G^+) bacteria, whereas the fatty acids 16:1ω7c, 16:1ω9c, cy17 : 0, 18 : 1ω5c, 18 : 1ω7c, and cy19 : 0 were used to as indicators of Gram-negative (G^-) bacteria (Dijkstra et al., 2011). The fatty-acid signatures i14 : 0, i15 : 0, a15 : 0, i15 : 1, i16 : 0, 16 : 1ω7c, 16 : 1ω9c, i17 : 0, a17 : 0, cy17 : 0, 18 : 1ω5c, 18 : 1ω7c, and cy19 : 0, which were considered to be of bacterial origin (Frostegård et al., 1993), were used as biomarkers for bacterial biomass. The fatty acid 18:1ω9c and isomers 18 : 2ω6c and 18:3ω6c were used as index of fungal biomass (Frostegård et al., 1993), whereas the fatty acids 10Me16 : 0, 10Me17 : 0, and 10Me18 : 0 were used as indicators of actinobacteria biomass. The sum of all PLFAs was calculated as a measure of viable microbial biomass.

2.4 Calculation of MMQ

Even though previous studies have calculated MMQ (g CO_2-C/(kg $C_{PLFA\ content}$·d),which represent the rate of soil microbial respiration (R) per unit of microbial biomass) using microbial biomass carbon (MBC), the present study calculated MMQ using PLFA, both because MBC measurement had a degree of difference (chloroform fumigation method) and because PLFA content is an important component of the living microorganism membrane (Yan et al., 2006):

$$\mathrm{MMQ} = \frac{R_{20}}{\mathrm{PLFA}} \quad (2)$$

where PLFA (the phospholipid fatty acid) represents the microbial biomass (mg $C_{PLFA\ content}$/g soil).

2.5 Statistical analysis

One-way analysis of variance (ANOVA) with the LSD test was used to compare the mean R_{20}, microbial biomass, and MMQ values from the different grassland types. Bivariate correlation analysis among climate (AMT and MAP), basic soil properties, microbial properties, R_{20} and MMQ was conducted using SPSS (IBM,

Inc., Chicago, IL, USA), and structural equation model(SEM) were used to explore the relative contribution of climate and soil characteristics to the spatial pattern of MMQ using R (version 2.15.2; R Development Core Team, 2012). A statistical probability of $P < 0.05$ was considered significant.

3 Results

3.1 Variation in R_{20} among steppe types

Under relatively optimal incubation conditions (20℃ and 55% WHC), the R_{20} values were approximately 24.50, 18.30, and 25.70 mg CO_2-C/(kg soil·d) in meadow steppe, typical steppe and desert steppe respectively (Fig. 2); however, R_{20} was not significantly affected by type of steppe.

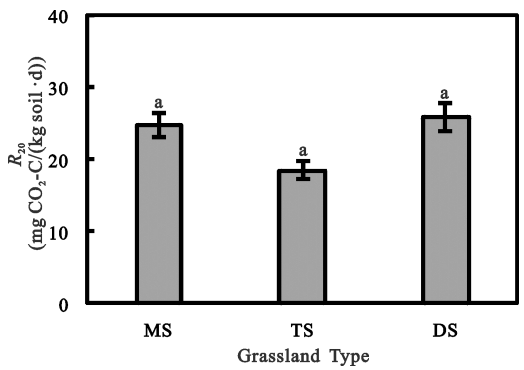

Fig. 2 Effect of steppe type on microbial respiration rate. R_{20}, microbial respiration rate at 20℃ and 55% water holding capacity; MS, meadow steppe; TS, typical steppe; DS, desert steppe. The same lowercase letters indicate no significant differences at the $P = 0.05$ level.

3.2 Variation in soil microbe community across steppe types

The PLFA of grasslands was significantly affected by steppe type ($P < 0.05$) and decreased in the following order: meadow steppe (4.00×10^{-4} mg $C_{microbial}$/g soil) > typical steppe > desert steppe (1.30×10^{-4} mg $C_{microbial}$/g soil) (Fig. 3A). Furthermore, bacteria (*Ba*), Gram- positive bacteria (G^+), Gram-negative bacteria (G^-), fungi (*Fu*), actinobacteria (*Acti*), and the total number of bacteria were significantly greater in meadow steppe than in desert steppe ($P < 0.05$, Fig. 3B).

The soil PLFA of the Inner Mongolian grasslands increased with increasing longitude ($r = 0.59$, $P < 0.05$) and latitude ($r = 0.78$, $P < 0.01$) (Fig. 4), from northeast to southwest, increased with increasing MAP($r = 0.50$, $P < 0.05$), and decreased with decreasing AMT ($r = –0.85$, $P < 0.01$) (Fig. 5).

3.3 Variation and influencing factors in MMQ across steppe types

Unexpectedly, the MMQ of the desert steppe (with mean value of 20.67×10^{-4} g CO_2-C/(kg $C_{PLFA\ content}$·d)) was significantly higher than that of either typical steppe (6.89×10^{-4} g CO_2-C/(kg$C_{PLFA\ content}$·d)) or meadow steppe (6.76×10^{-4} g CO_2-C/(kg$C_{PLFA\ content}$·d))($P < 0.05$). However, there was no significant difference in the MMQ values between typical steppe and meadow steppe (Fig. 6).

The MMQ values from the Inner Mongolian grasslands decreased with increasing longitude ($r = –0.81$)

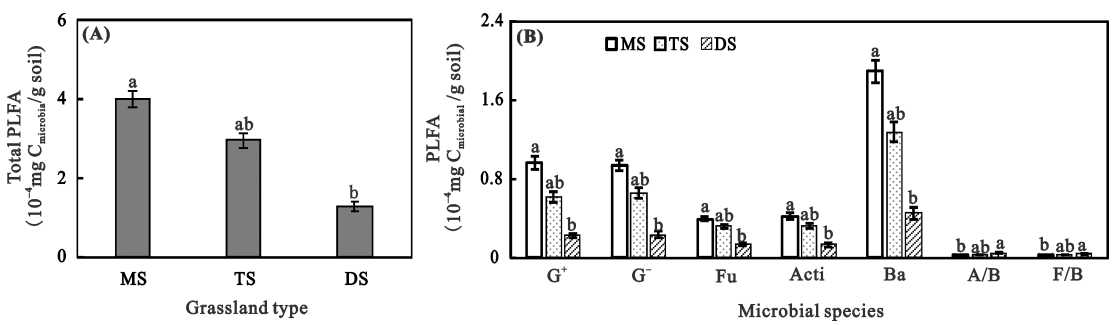

Fig. 3 Effect of steppe type on soil microbial community. MS, meadow steppe; TS, typical steppe; DS, desert steppe; G^+, Gram-positive bacteria; G^-, Gram-negative bacteria, *Fu*, fungi; *Acti*, Actinomycetes; *Ba*, bacteria; A/B, Actinomycetes/bacteria; F/B, fungus/bacteria; PLFA, phospholipid fatty acid.Different lowercase letters indicate significant differences at the $P = 0.05$ level

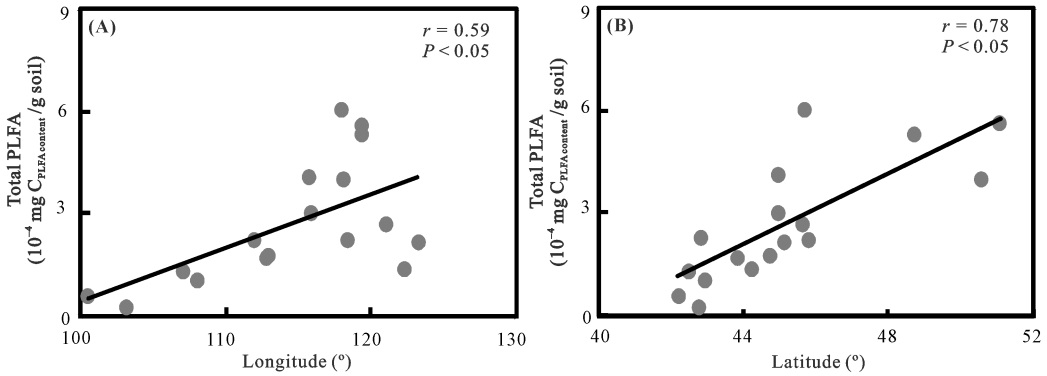

Fig. 4 Effect of location on steppe soil levels of phospholipid fatty acids (PLFAs). Panels depict the linear relationships between total PLFAs and longitude (A) and latitude (B) in the Inner Mongolian grasslands.

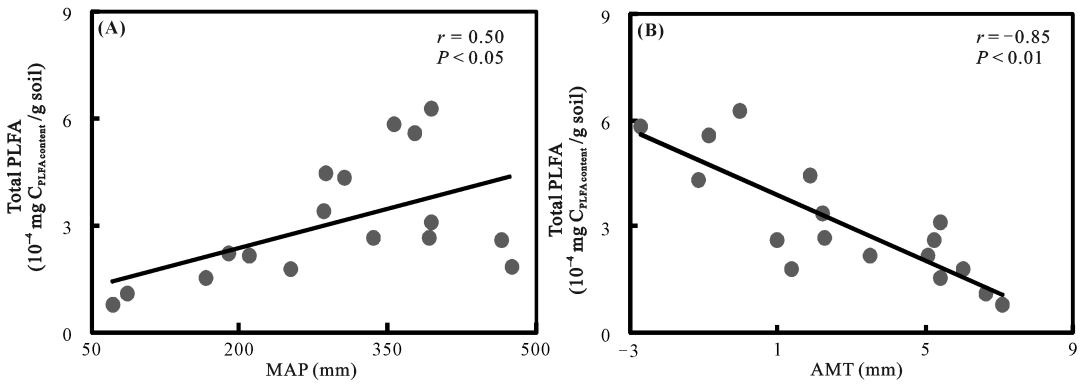

Fig. 5 Effect of climate on steppe soil levels of phospholipid fatty acids (PLFAs). Panels depict the linear relationships between total PLFAs and mean annual precipitation (MAP; A) and annual mean temperature (AMT; B) in the Inner Mongolian grasslands

and latitude (r = –0.50) (Fig. 7), as well as with increasing MAP (r = –0.69), and increased with increasing AMT (r = 0. 48) (Fig. 8). The Structural equation model (SEM) indicated that MAP accounted for 56% of the total variation in MMQ across the Inner Mongolian grasslands, whereas AMT accounted for 26% (Fig. 9).

4 Discussion

4.1 MMQ differs across steppe types

The results of this study indicate that MMQ varies significantly across the grassland types. The significant differences in MMQ could be due to differences in precipitation. For example, the abundant precipitation, higher temperature, and soil environment of the meadow steppe was highly suitable for microbial growth, so that the number of soil microbes of the meadow steppe were significantly greater than those of the desert steppe and with the lower MMQ than the desert steppe. Under

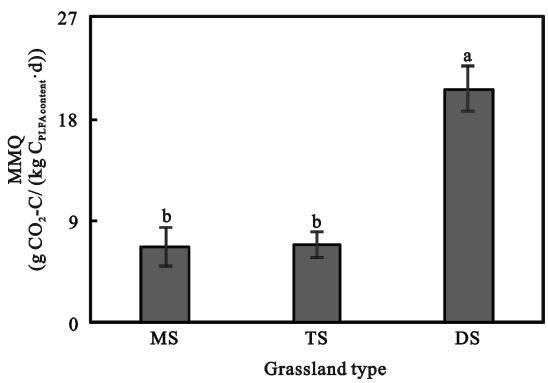

Fig. 6 Effect of steppe type on soil microbial metabolic quotient (MMQ). MS, meadow steppe; TS, typical steppe; DS, desert steppe. Different lowercase letters indicate significant differences at the P < 0.05 level

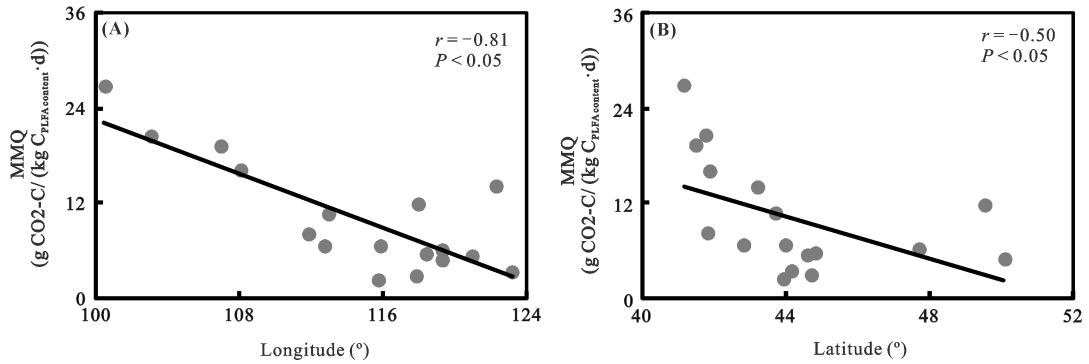

Fig. 7 Spatial patterns of soil microbial metabolic quotient (MMQ) across longitude (A) and latitude (B) in the Inner Mongolian grasslands

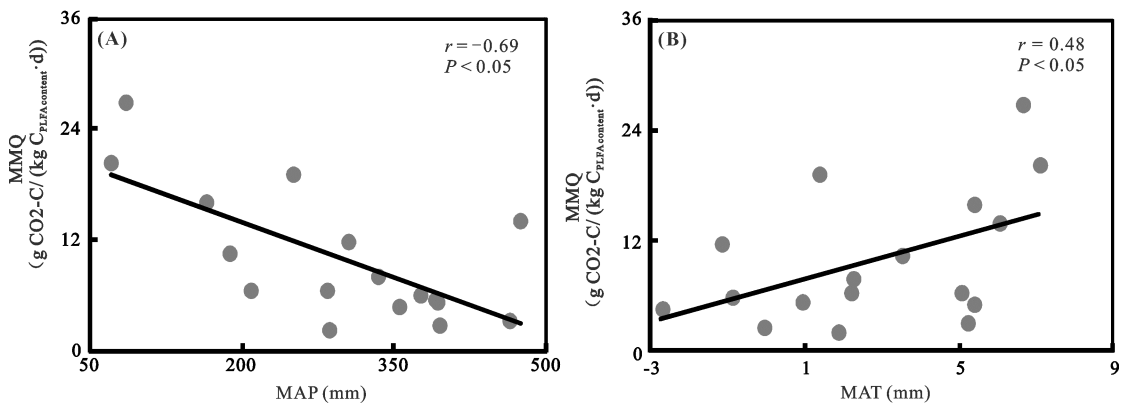

Fig. 8 Effect of climate on soil microbial metabolic quotient (MMQ). Panels depict the linear relationships between MMQ and mean annual temperate (AMT; A) and mean annual precipitation (MAP; B) in the Inner Mongolian grasslands

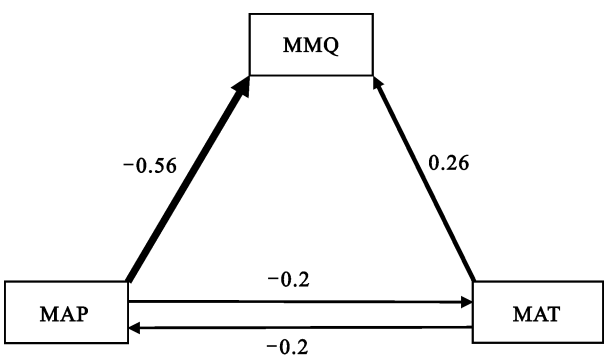

Fig. 9 Structural equation model (SEM) for the influence of climate on microbial metabolic quotient (MMQ). AMT, annual mean temperature; MAP, mean annual precipitation. Line thickness indicates the weight of the variable in the model. '+' represents positive correlation, '–' represents negative correlation.

environmental stress (mainly MAP and AMT), soil microbial activity may decrease with decreasing carbon use efficiency (CUE) (Saggar et al., 1999). The relatively low precipitation, temperature, and SOM of desert steppe could reduce available microbial carbon. However, at 20℃ and 55% WHC incubation, the MMQ of desert steppe was higher than that of meadow steppe.

Some studies have demonstrated the influence of land-use change, heavy metal pollution, and overgrazing on MMQ, which was an indicator of soil microbial metabolic activity (Zhao et al., 2007; Aldezabal et al., 2015). However, few studies have investigated the variation of MMQ among different biotypes (e.g., natural grassland and forest) or the effects of precipitation and temperature on soils microbial communities. Li and Chen (2004) reported that the mean MMQ of the upper 5 cm of Inner Mongolian steppe soil (incubated at 28℃) was ~30.2 μmol/(mmol·d), whereas Chen et al. (2004) reported that the mean MMQ of New Zealand grasslands soil was ~0.38 μg CO_2-C /(mg $C_{microbial}$·h), and Chen et al. (2001) reported that the MMQ of soil from southwest Karst region of south China was 0. 707 × 10^{-3}

μg CO_2-C/(g soil·h). Difference between these studies and this study (10.07×10^{-4} g CO_2-C/(kg $C_{PLFA\ content}$·d)) was that the fumigation-incubation method, rather than the PLFA method, was used to measure MBC (microbial biomass carbon).

4.2 Precipitation and temperature influences spatial pattern of MMQ

As expected, MMQ exhibited a southwest-to-northeast spatial pattern with a decreased variation across the Inner Mongolian grasslands and increased with increasing AMT and decreasing MAP. The SEM analyses indicated that MAP was the determinant of that variation in MMQ across the steppes. Insam (1990) reported that MMQ was significantly correlated with MAP. In the present study, MAP declined gradually across the Inner Mongolia steppes from northeast-to-southwest accompanied by decreasing AMT and a transition from a Central Asian inland climate (arid) to an East Asian monsoon climate (semi-humid). Furthermore, as MAP decreased, soil water content decreased, and soil water availability became a limiting factor for soil microbial activity compared to temperature (Wang et al., 2004; Liu et al., 2012). In drier desert steppe, more energy and nutrients from SOM decomposition would be allocated to the metabolism of soil microbes, whereas in humid meadow steppe, the energy or nutrients from SOM decomposition would be allocated to microbial growth and reproduction. Therefore, the soil microbes in arid regions yielded higher MMQ values and lower CUE values. Similar strategies have been reported for the CUE of plants (He, 2012) and represent the long-term adaptation of microorganisms to environmental stresses. Microorganisms can alter microbial growth efficiency (as an assimilation matrix for producing energy after assigning the proportions of biomass and enzyme production and consumption breathing; Conant et al., 2011) to divert more energy into respiration and metabolism, so that SOM decomposition is mostly distributed into CO_2, but very low during microbial growth or reproduction. As higher MAP or soil moisture in meadow steppe, the energy and nutrients from SOM decomposition may be used for soil microbial growth and reproduction. Zhou D N et al. (2013) reported that soil microbial metabolic activity decreased with increasing precipitation. Furthermore, sufficient precipitation can provide more suitable environments for microbial growth and development, thereby reducing MMQ.

Also, temperature is an important factor in the regulation of soil microbial activity, which soil microbial respiration generally increases with increasing temperature (Li et al., 2014). As temperature rises, the enzyme activity of soil microbes increases, thereby increasing soil respiration. The rate of SOM decomposition may increase with increasing MMQ (Schimel and Bennett, 2004; Raiesi and Beheshti, 2014). In Inner Mongolia grasslands, which have a hot and rainy season, insufficient precipitation (85–355 mm/yr) is the main factor that limits plant primary production and soil microbial activity and is more influential than temperature (Chen et al., 2015). In New Zealand grassland (temperate climate), precipitation and temperature are both sufficient. Therefore, the dissolved organic carbon, total nitrogen, and total phosphorus of the soils collectively determine the spatial variation of MMQ (Chen et al., 2004). These results demonstrate that the main controlling factors and spatial patterns (along longitude or latitude) of MMQ differ among different geographic units. However, Xu et al. (2017) reported global patterns for MMQ, along with the cost of ignoring their unique properties at a large extent.

4.3 Potential influence of climate change on soil carbon cycling

The spatial pattern and main determinants of MMQ reflect soil microbial activity and its adaptation mechanism to some extent (Powlson and Jenkinson, 1976). High MMQ values indicate faster soil organic matter decomposition rate and lower carbon turnover efficiency, which in turn indicates the increase of carbon emissions (per unit microbial biomass). Global climate change may result in more extreme weather events, such as high-frequency precipitation events and higher temperature, which may increase the complexity of soil carbon cycles.

We found that MMQ exhibits a spatial pattern that increased from northeast to southwest, across the Inner Mongolian grasslands, where precipitation is its main controlling factor and then temperature. Under a climate scenario of increasing precipitation and temperature (Zhao et al., 2015; Donat et al., 2016), it is likely that MMQ would decrease eastwards, which could directly affect soil microbial respiration and ecosystem carbon cycle (Canarini et al., 2017). However, it appears that

the overall precipitation of Inner Mongolia has decreased over the past 50 yr, whereas temperature has increased (Hu et al., 2015; Wang et al., 2017). Increasing soil temperature may promote soil microbial activity and SOM decomposition (Suseela et al., 2014; Wang et al., 2015; Zhou X Q et al., 2013), which indicates that MMQ could increase, which would reduce CUE and increase soil carbon emissions.

5 Conclusions

The present study investigated the spatial pattern and determinants of microbial metabolic quotient (MMQ) across the Inner Mongolian grassland. MMQ varied from 6.76×10^{-4} to 20.67×10^{-4} g CO_2-C/(kg $C_{PLFA\ content}$ ·d), with the average value of 10.07×10^{-4} g CO_2-C/(kg $C_{PLFA\ content}$ ·d) in this region The MMQ of desert steppe was significantly greater than other two steppe types ($P < 0.05$), but there was no difference between meadow steppe and typical steppe. Interestingly, MMQ significantly decreased from southwest to northeast, and both precipitation and temperature jointly affected the spatial variation of MMQ, although precipitation was the main controlling factor which accounted for 56% of the total variation in MMQ, temperature accounted for 26%. Totally, the apparent patterns of MMQ and its determinants in specific regions highlight new approaches for investigating the response of soil microbial respiration to climate change that may be integrated into ecological models in future.

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