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Effect of grassland degradation on soil quality and soil biotic community in a semi-arid temperate steppe

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Abstract

Grasslands provide a number of ecosystem services for human society. Degradation of grasslands results in the loss of biodiversity and leads to the deterioration of ecosystem functions. In order to accurately assess the influence of grassland degradation on belowground ecosystems, we conducted experiments on a temperate steppe with different levels of degradation and investigated the influence of degradation on soil quality and soil biotic communities. Our results showed that grassland degradation significantly decreased soil quality, with lower values of soil quality index (SQI) observed in the degraded grassland than the meadow steppe and the grassland from the forest-steppe ecotone. Changes in the SQI along the grassland degradation gradient were positively correlated with soil carbon stock and the aboveground biomass, and negatively correlated with the root shoot ratio. Nematode trophic diversity and the ratio of fungal to bacterial PLFA were lower in the degraded grassland than the grassland from the forest-steppe ecotone. The dissimilarities in soil microbial and nematode community composition increased with the changes in soil quality index. Our results indicate that soil quality index based on the minimum data sets could effectively assess the influence of grassland degradation on soil biodiversity and ecosystem function. In order to effectively restore degraded grasslands, the key contributors to the soil quality, such as soil carbon, should be taken on priority basis for revitalizing the soil biodiversity and ecosystem function.

Keywords: Soil quality, Soil biodiversity, Grassland degradation, Soil nematode community

Introduction

Grasslands are the largest terrestrial ecosystems on earth and it covers about 40% of the earth's surface, providing a large number of ecosystem services to human society (Hu et al. 2016; Lyu et al. 2020). Grasslands in China account for 11.8% of the global grassland area and play important roles in livestock production and environmental conservation (Dong et al. 2012; Ren et al. 2008). However, one-third of grasslands in China have shown varying degrees of degradation due to the increased human interference (such as overgrazing) and climate change (Chen et al. 2014; Qi et al. 2012). Although numerous measures have been taken to restore the degraded grasslands (Guo et al. 2018; Zhang et al. 2019), one of the major issues is how to accurately assess the influence of grassland degradation (Zhang et al. 2019). Grassland degradation causes the loss of biodiversity and leads to ecosystem function degradation (Gang et al. 2014; Lyu et al. 2020; Raiesi and Salek-Gilani 2020). Therefore, elucidating the mechanisms that influence grassland degradation on the changes in soil quality and biotic communities is important so as to develop effective solutions to restore the degraded grassland ecosystems (Lal 2015; Raiesi and Salek-Gilani 2020).

Soil quality is considered as the capacity of the soil to perform ecosystem functions (Karlen et al. 2003), which can be assessed by measuring the changes of soil physical, and chemical properties induced by different land managements (Andrews et al. 2002a; Bongiorno 2020). Recently, soil quality assessments have received more and more attention to accurately evaluate the impact of land-use changes on

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degradation and sustainable land management (Guo et al. 2018; Raiesi and Salek-Gilani 2020). Using soil quality index (SQI), Li et al. (2013) have detected the extent of rangeland degradation after land-use changes and Zhang et al. (2019) found that vegetation restoration has improved the soil quality in the karst regions of southwest China. Guo et al. (2018) also found that the SQI values increased with the increasing of restoration ages on the loess hill region of China. Researches in grassland have shown that management intensification has an adverse impact on soil and plant characteristics (Askari and Holden 2014). For example, overgrazing not only reduces the biomass of palatable species (Gaitán et al. 2018) but also changes root shoot ratio and soil bulk density (Hendricks et al. 2005; Yan et al. 2020), which in turn leads to a reduction in soil carbon and nitrogen pools (Hu et al. 2016; Yan et al. 2020). Thus, soil quality index is the summarizing of these interdependent properties by choosing the best representative indicators which can comprehensively evaluate the effects of grassland degradation on soil quality and ecosystem function (Zhang et al. 2019).

Changes in soil quality can directly or indirectly influence the belowground biota and the associated ecological functions. In order to assess soil quality induced by grassland degradation more precisely, soil biotic communities should also be considered (Zhang et al. 2019). Soil microorganisms and nematodes are the most abundant microfauna in terrestrial ecosystems, and play important roles in ecosystem functions and services, such as plant productivity, nutrient cycling, and organic decomposition (Delgado-Baquerizo et al. 2020). Grassland degradation can affect soil biotic communities via changes in vegetation composition and soil characteristics (Chen et al. 2013; Wang et al. 2018). Chen et al. (2013) found that the influence of overgrazing on soil microbes led to a negative effect on soil nematode communities in a field experiment in Inner Mongolia. Thus, grassland degradation will affect the composition of soil biotic communities and ultimately influence the ecological processes they involved in. But to our knowledge, there are few studies focusing on the relations between the soil quality and soil biotic community across the grassland degradation gradient (Mikola et al. 2009).

Therefore, in order to study the influence of grassland degradation on soil quality and its relations with soil biotic communities, we conducted field experiments on the grasslands with different levels of degradations in Hulunbuir of Inner Mongolia. The degraded grassland in this study belonged to the meadow steppe which was subjected to human disturbance and overgrazing, leading to the reduction of productivity and ecosystem services (Xu et al. 2019). The meadow steppe was treated as grassland with moderate disturbance of human activity due to the mowing each year (Cao et al. 2019; Yan et al. 2016). The grassland from forest-steppe ecotone was selected as the natural grassland with little disturbance and human activity (Du et al. 2020). We hypothesized that grassland degradation will have negative influences on soil quality and soil biotic communities, with lower SQI index and diversity of soil biotic community observed in the degraded grassland compared with the meadow steppe and grassland from the forest-steppe ecotone. Since the soil microbial and nematode communities play an important role in carbon sequestration and nutrient cycling, changes in soil quality due to grassland degradation should be closely related to the changes in biotic communities along the grassland degradation gradient.

Materials and methods

Study site and design

The study site was located near Erguna Forest-Steppe Ecotone Research Station of the Chinese Academy of Sciences (50° 10′ 46.1″ N, 119° 22′ 56.4″ E) in the Hulunbuir grassland. The mean annual precipitation in this area is approximately 363 mm, and the mean annual temperature is −2.45 °C. The soil type is chernozem in World Reference Base for Soil Resources (WRB) (IUSS Working Group WRB 2006; Yang et al. 2019).

During the summer of 2017, degraded grassland (DG), meadow steppe (MG), and the grassland from forest-steppe ecotone (TG) were selected across the grassland degradation gradient. Degraded grassland was previously used as a horse ranch with the plant community dominated by *Carex duriuscula*, *Cleistogenes squarrosa*, *Potentilla acaulis*, *Artemisia frigida*, and *Serratula centauroides* (Lü et al. 2017). Meadow steppe has the plant community dominated by *Carex duriuscula*, *Leymus chinensis*, *Cleistogenes squarrosa*, *Filifolium sibiricum*, and *Stipa capillata* (Lin et al. 2017). Grassland from the forest-steppe ecotone had the richest plant community dominated by *Carex duriuscula*, *Galium verum*, *Pulsatilla chinensis*, *Thalictrum aquilegifolium*, *Sedum aizoon*, *Paeonia lactiflora*, *Artemisia scoparia*, *Leymus chinensis*, *Schizonepeta multifidi*, and *Sanguisorba officinalis* (Zhu et al. 2010).

Plant sampling and analysis

For each grassland type, four replicates (100 × 100 m^2 for each) were selected with a distance of about 1 km for each replicate. To test plant community composition, average height, species richness, and coverage of each plant species were recorded in a 1 m × 1 m quadrat in each plot. Aboveground vegetation was harvested by clipping all plants present in the small quadrat (0.4 m × 0.4 m) within each 1 m × 1 m quadrat. For measuring belowground biomass, one soil core with a diameter of 8 cm was collected from each small quadrat at 15 cm depth, then we used a 2 mm sieve to collect root

carefully. All aboveground and belowground plant tissues were oven dried at 60 °C to constant weight to obtain the aboveground and belowground biomass.

Soil sampling and analysis

Soil samples were collected using soil cores (2.5 cm) at 0–15 cm depth, and then mixed together as a composite sample for each replicate. After gentle homogenization and removal of roots, half of the fresh soil samples were stored in individual plastic bags and kept at 4 °C for soil biotic analysis. The other soil samples were sieved through a 2 mm mesh and air dried to analyze soil properties. For measuring bulk density, soil cores were collected using the cutting ring (100 cm^3) from each plot. Soil moisture and bulk density were determined by oven-drying subsamples at 105 °C for 24 h. A 1:2.5 soil: water was used for measuring soil pH by a glass electrode (Kim 1998). Total carbon (TC) and total nitrogen (TN) contents in each sample were determined using a TruSpec CN Elemental Analyzer (Leco Corporation, USA). Total phosphorus (TP) was determined by the method of molybdenum-antimony colorimetric using a spectrophotometer (Shimadzu Inc., Kyoto).

PLFA analysis

Soil microbial community was tested by phospholipid fatty acid (PLFA) analysis (Certini et al. 2004). Lipids were extracted from 4 g of freeze-dried soil using a chloroform-methanol-citrate buffer mixture (1:2:0.8), and the phospholipids were separated from neutral lipids and glycolipids on a SPE tube (Supelco Inc., Bellefonte). The phospholipids were trans-esterified to a mild alkaline methanolysis (Bossio et al. 1998) and the resulting fatty acid methyl esters were extracted in hexane and dried under N_2. Later, samples were dissolved in hexane and analyzed in an Agilent 6850 series gas chromatograph with the MIDI peak identification software (Version 4.5; MIDI Inc., Newark).

Nematode community analysis

Soil nematodes were extracted from 100 g of fresh soil according to a modified cotton-wool filter method (Oostenbrink 1960; Townshend 1963). Nematode populations were expressed as the individuals per 100 g dry soil and at least 100 individuals from each sample were identified to genus level (Ahmad and Jairjpuri 2010; Bongers 1994; Li et al. 2017). Nematodes were assigned to the following trophic groups according to their feeding habits and life-history characteristics: (i) bacterivores; (ii) fungivores; (iii) omnivore-predators, and (iv) plant parasites (Yeates et al. 1993). Trophic diversity, Shannon index, structure index, and enrichment index of the nematode community were calculated according to Ferris et al. (2001).

Soil quality index calculation

Soil quality index (SQI) was calculated by selection of minimum data set (MDS) that best representative indicators for soil functions. Using principal component analysis (PCA), principal components (PCs) with eigenvalues > 1 and explained > 5% of total variation were assumed to represent the soil quality for MDS (Andrews et al. 2002a; Brejda et al. 2000). Within each PC, the highly loaded variables within 10% of the highest loading were selected as key indicators (Andrews et al. 2002a). When more than one variable was retained within a PC, linear correlations were calculated. If the correlation coefficient between variables was more than 0.60, the variable was considered redundant and eliminated from the MDS (Andrews et al. 2002a, 2002b).

We then used the following sigmoidal type curve to normalize and score the MDS indicators (Andrews et al. 2002a; Brejda et al. 2000).

$$\mathrm{NL-SF}\,(Y) = \frac{a}{\left(1 + \left(\frac{x}{x_0}\right)^b\right)}$$

Where NL–SF (Y) is the nonlinear score of each indicator ranging from 0 to 1, a is the maximum value (a = 1), x is the value of the selected indicator, and x_0 is the mean value of each indicator. b is the slope of the equation and is set as −2.5 for "more is better" functions and 2.5 for "less is better" functions.

The final step for the soil quality assessment combined the selected indicators into an overall SQI using the following weighted additive equation (Andrews et al. 2002a, 2002b).

$$\mathrm{SQI} = \sum_{i=1}^{n} W_i S_i$$

Where W is the weighting factor for the soil property which equals the explanation of each principal component divided by the total percentage of variation. S is a nonlinear (NL–SQI) score. Then SQI is considered to be the overall assessment of soil quality, with higher values meaning better soil quality.

Statistical analysis

Before analysis, nematode abundances were ln (x + 1) transformed, other data that do not meet the assumptions of normality and homogeneity were also log-transformed. A mixed linear model (nlme) was used to test the differences across the degradation gradient with grassland type as a fixed factor and replicates as random factors. A Tukey HSD test was used for multiple comparisons. Microbial and nematode community compositions were visualized by PCA analysis. We calculated the beta diversity of microbial and nematode community

composition using the Bray-Curtis dissimilarity (Bray and Curtis 1957). Mantel tests (Spearman's rank correlation) were conducted to test the relationships between soil quality index (Euclidean distance) and soil biotic community (Bray-Curtis distance). Further, we calculated the Pearson correlation coefficient between soil quality index and soil abiotic characteristics.

Results

Effect of grassland degradation on soil quality index

Grassland degradation significantly influenced plant biomass (Table 1), with lower aboveground biomass observed in the degraded grassland (DG) than that in meadow steppe (MG) and the grassland from forest-steppe ecotone (TG), but the root biomass did not differ among three grassland types (Table 1). The root shoot ratio was higher in DG than that in MG and TG. Grassland degradation also significantly affected soil nutrient contents, with higher contents of total carbon, nitrogen, and phosphorus observed in TG than in MG and DG (Table 1).

The principal component analysis based on the soil physicochemical parameters showed that the eigenvalues of the first two PCs were > 1 and explained 78.3% of the total variance (Table 2). Total carbon and root shoot ratio were highly weighted indicators retained in PC1 and PC2 (Table 2). Soil total carbon had the highest contribution (74%) to the SQI values followed by root shoot ratio (26%). The values of SQI were significantly lower in DG (0.16–0.39) than those in MG (0.33–0.48) and TG (0.63–0.85). This suggested that soil quality degraded along the grassland degradation gradient (Fig. 1).

Effect of grassland degradation on soil biotic community

Grassland degradation also affected soil microbial community, with higher contents of total and fungal PLFAs observed in MG and TG in comparison with DG (Fig. 2). The ratio of fungal to bacterial PLFA (F/B) was significantly lower in DG than that in MG and TG (Fig. 2). Grasslands with different levels of degradation were obviously discriminated in the PCA ordination plot. Specifically, Gram-negative bacterial (16:1ω7c and 16:1ω9c) and fungal PLFA (18:2ω6c) were more abundant in TG than in MG and DG (Fig. S2). Similar patterns were also found in the soil nematode community. The abundances of total nematodes and omnivores-predators were higher in TG than in MG and DG (Fig. 3). Ecological indices of the nematode community showed the same trends with higher values of trophic diversity, Shannon index and enrichment index observed in the TG than in MG and DG (Fig. 3).

Relations between soil quality and soil biotic and abiotic characteristics

Soil quality index was positively correlated with the aboveground biomass and soil carbon stock, and negatively correlated with the root shoot ratio (Fig. 4). Positive correlations were found between SQI and the fungal and AMF PLFAs, and the F/B ratio. Similar patterns were also found between SQI and the number of omnivores-predators and nematode ecological indices (Fig. 5). Further, the distance of the soil quality index was positively correlated with the beta diversity of microbial and nematode communities (Fig. 6). Changes in soil quality could explain 19% and 15% of the variations in microbial and nematode community, and the tested environmental parameters explained 48% of the total

Table 1 Basic soil and plant characteristics along the grassland degradation gradient

	DG	MG	TG
Soil environment			
Soil moisture (%)	19.92 ± 0.52c	35.23 ± 5.29b	55.45 ± 7.77a
Bulk density (g/cm^3)	1.16 ± 0.01a	1.03 ± 0.05b	0.75 ± 0.06c
pH	6.67 ± 0.05b	6.93 ± 0.05a	6.21 ± 0.1c
Soil nutrient			
Total C (g/kg)	29.30 ± 0.83b	31.33 ± 0.59b	75.45 ± 2.77a
Total N (g/kg)	2.92 ± 0.07b	2.79 ± 0.04b	5.94 ± 0.22a
Total P (g/kg)	0.46 ± 0.01b	0.46 ± 0.02b	0.97 ± 0.04a
Plant			
Aboveground biomass (g/m^2)	143.71 ± 23.29c	292.16 ± 26.46b	411.72 ± 20.11a
Belowground biomass (g/m^2)	2866.81 ± 297.47	2570.06 ± 151.84	4447.15 ± 994.38
Root shoot ratio	24.83 ± 3.65a	9.26 ± 0.7b	11.24 ± 2.71b

DG degraded grassland, *MG* meadow steppe, *TG* the grassland from the forest-steppe ecotone
Means with different letters in the same row indicate significant differences at $P < 0.05$
Data are shown as mean ± SE

Table 2 Principal component analysis of soil quality indicators

Principal component	PC1	PC2
Eigenvalues	5.22	1.83
Variance (%)	57.96	20.34
Cumulative (%)	57.96	78.3
Aboveground biomass	0.33	0.27
Belowground biomass	0.18	−0.53
Root shoot ratio	−0.14	**−0.63**
Water content	0.32	0.15
Bulk density	−0.35	−0.27
pH	−0.31	0.37
Total C	**0.43**	−0.08
Total N	0.42	−0.12
Total P	0.4	−0.06

Notes: Bold factors are retained in the minimum data set (MDS)
PC1 and PC2 indicated the first and second principal component

variations in soil biotic community composition (Table S1).

Discussion

Effects of grassland degradation on soil quality

Grassland degradation induced by overgrazing destroys the ecological environment, which had negative influences on the plant and soil communities (Wu et al. 2014). In our study, soil total carbon was selected as an effective indicator of soil quality. Soil total carbon is a key factor affected by grazing (Hu et al. 2016; Mcsherry and Ritchie 2013) which is the most frequently used trait in soil quality calculation (Askari and Holden 2014). The reduced carbon inputs from above- and belowground biomass in the degraded grassland may be the main drivers for the lower content of total carbon (Shen et al. 2020; Wilson et al. 2018; Yan et al. 2020). In the meadow steppe, we also found that soil carbon stock was lower than the TG (Fig. S3), which may be due to that mowing reduced the accumulation of litter and then decreased the carbon input into soil (Chen et al. 2019; Li et al. 2020). The negative impacts of grassland degradation on aboveground biomass and non-significant effects on belowground biomass in this study resulted in an increase in root shoot ratio, which can change the plant biomass allocation (Gao et al. 2008). The root shoot ratio was also used as an indicator of MDS, which was higher in degraded grassland in comparison with that in the meadow steppe and grassland from transition ecotone. The increase in root shoot ratio is also related to the decrease of vegetation coverage and plant diversity (Fig. S1), which means soil conditions are not suitable for vegetation growth (He and Richards 2015; Li et al. 2018). In turn, these changes in soil C and root shoot ratio can limit the growth of plant and soil biotic communities, and then decrease the soil quality index indirectly.

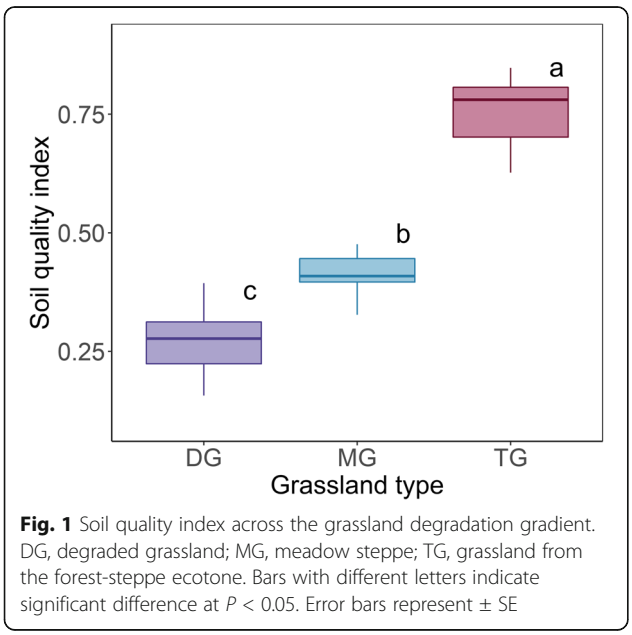

Fig. 1 Soil quality index across the grassland degradation gradient. DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Bars with different letters indicate significant difference at $P < 0.05$. Error bars represent ± SE

Effects of grassland degradation on soil biotic community

In our study, grassland degradation also significantly affected the soil biotic community. Along the gradient of grassland degradation, the highest abundance and diversity of soil nematodes and microorganisms were found in the TG. As a natural grassland with little disturbance, grassland from the forest-steppe ecotone has higher soil moisture and the most frequent material, energy, and biological flow (Sottile et al. 2015), which may result in higher biodiversity in TG than MG and DG. By contrast, degraded grassland has the lowest abundance and diversity of microorganisms. This may be because excessive human interference, such as overgrazing and the excavation of wild herbs. In the degraded grassland ecosystems, grazing animals can affect soil microorganisms directly through feces and trampling (Mahaming et al. 2009), or indirectly through selectively feeding plants to change soil carbon input (Penner and Frank 2019). All these factors can damage soil structure, and form an environment that is not conducive to soil microbe growth (Zhou et al. 2019). Arbuscular mycorrhizal fungi (AMF) are closely related with plant species and biological fertility (Begum et al. 2019; Coutinho et al. 2019), so the reduction of plant communities may result in the decrease of AMF in degraded grassland. Studies have found that fungi can stabilize the input of soil resources (Waring et al. 2013), and promote soil organic carbon accumulation (Six et al. 2006; Strickland and Rousk 2010). In the present study, the lowest values of fungal PLFA and F/B ratio in degraded grassland may indicate that the soil

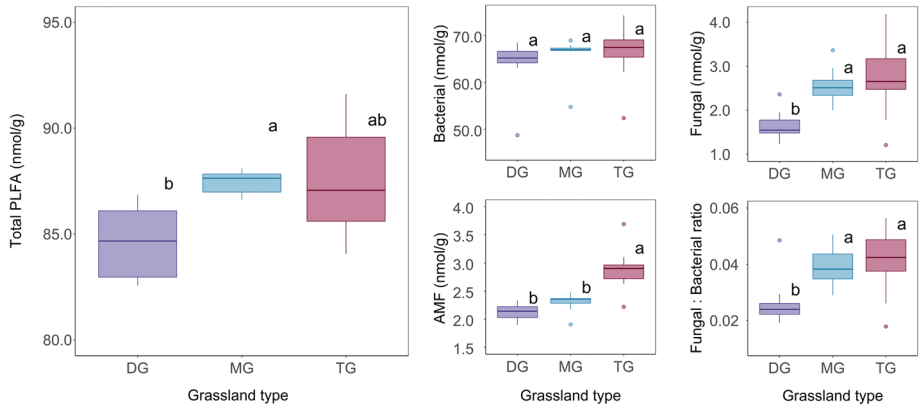

Fig. 2 Changes in soil microbial communities across the grassland degradation gradient. DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Bars with different letters indicate significant difference at $P < 0.05$. Error bars represent ± SE

environment is not sustainable for carbon accumulation and plant growth due to the overgrazing.

Nematodes are one of the most abundant and diverse biological groups in the soil, occupying multiple trophic levels in the soil food web (Thakur et al. 2014; Xiong et al. 2020). The relatively lower abundance and diversity of the nematode community in degraded grassland suggest that grassland degradation has a negative influence on soil nematode community. In degraded grassland ecosystem, continuous overgrazing significantly reduces the diversity of the plant communities, which has an adverse effect on soil nematode communities. On one hand, overgrazing will reduce above- and belowground abundance and diversity due to soil resource depletion (Qi et al. 2011). On the other hand, grazing also increases soil bulk density and reduces air circulation by livestock trampling, which may lead to a decline in omnivorous nematodes in degraded grassland. In addition, a decrease in omnivores-predators may reduce the top-down regulation to the soil food web, resulting in an increase in plant-parasite nematodes in degraded grasslands, and then negatively influence the plant growth and nutrient cycling (Ruan et al. 2012).

Relationship between soil quality index and soil biota

In agreement with our second hypothesis, we found that the dissimilarities in microbial and nematode community composition were closely related to the changes in soil quality, which explained 15–20% of variations in soil biotic communities. Our results suggest that changes in soil quality can alter the composition of soil microbial and nematode communities. Since soil biological properties are sensitive to environmental changes and provide important information about soil functions (Stone et al. 2016), our results reinforce that grassland degradation induced by overgrazing can negatively affect soil quality and soil biodiversity. Although soil biodiversity is important for maintaining ecosystem function and stability, it was often ignored in previous grassland degradation assessments due to its complexity in analysis and

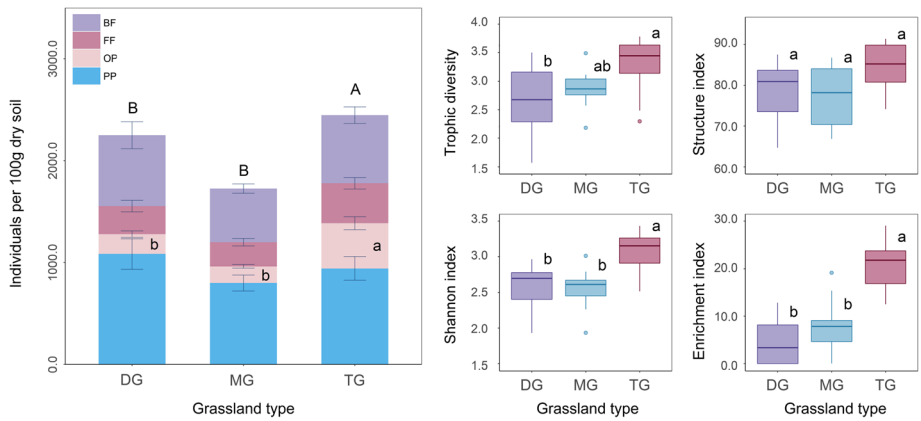

Fig. 3 Changes in soil nematode communities across the grassland degradation gradient. DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Bars with different letters indicate significant difference at $P < 0.05$. Error bars represent ± SE

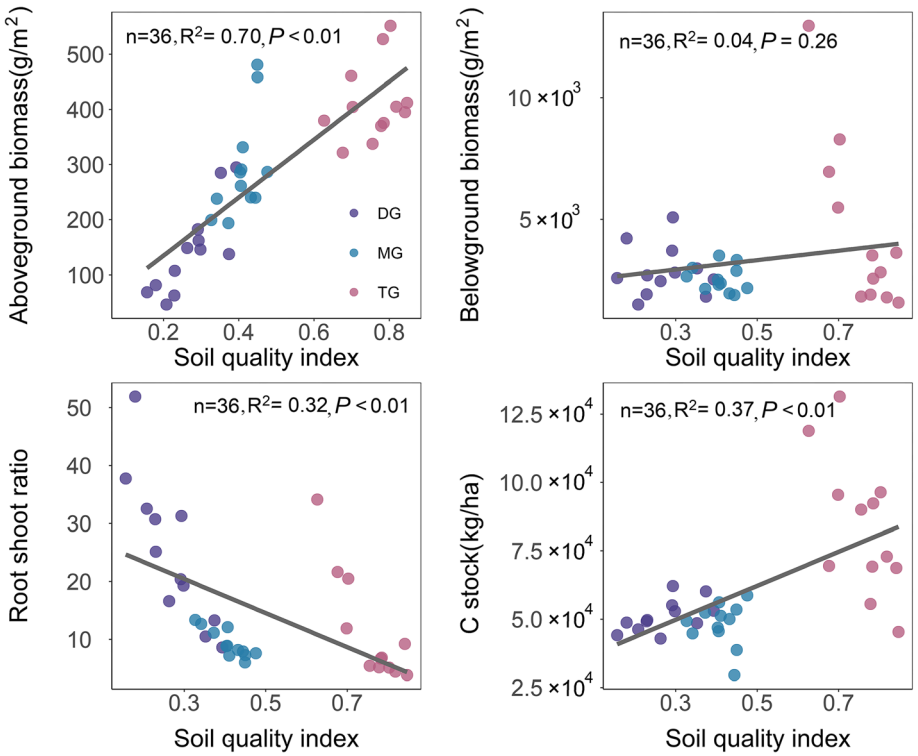

Fig. 4 Correlations between soil quality index and selected soil and plant characteristics

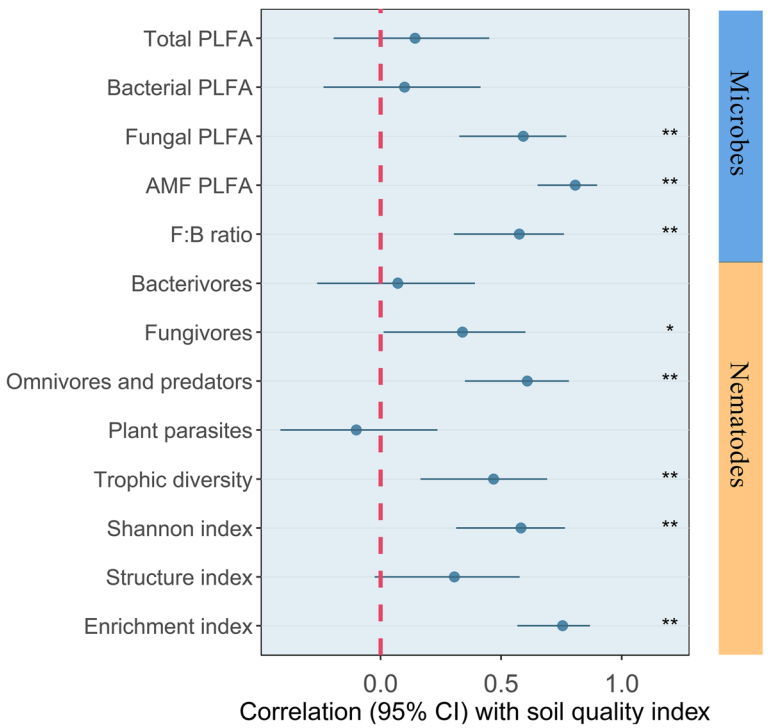

Fig. 5 Pearson correlation analysis between soil quality index and indices of soil microbial and nematode communities

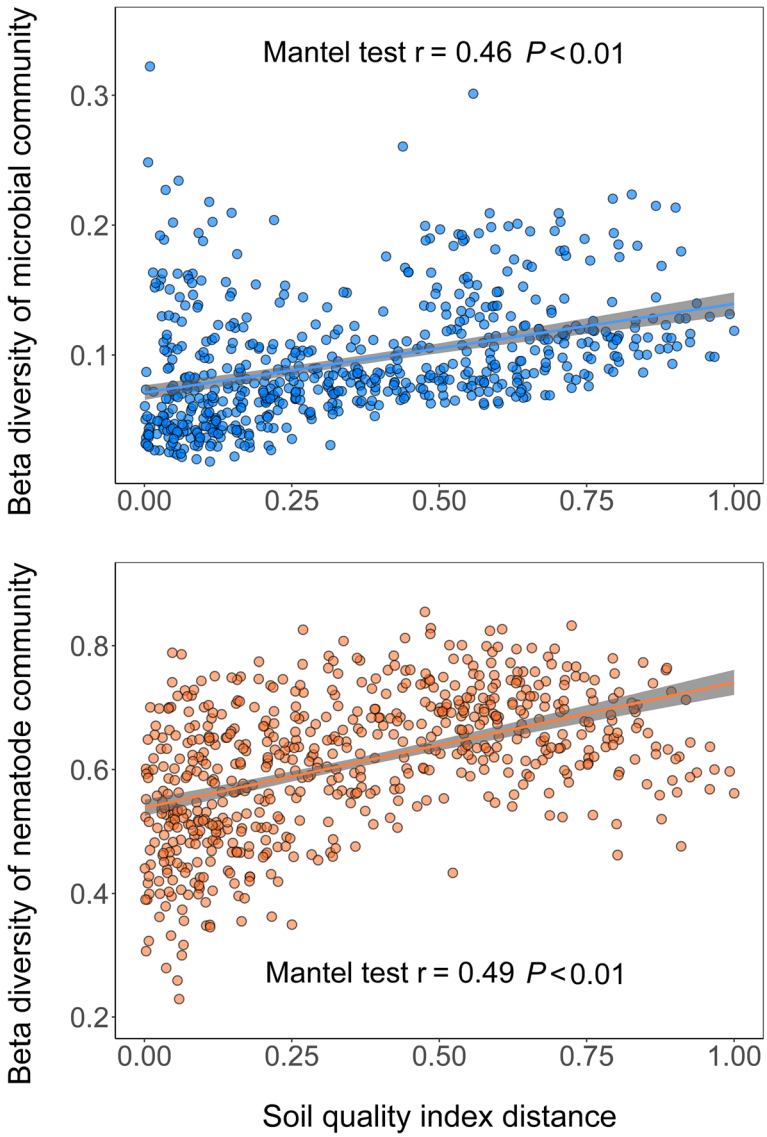

Fig. 6 Correlation between the beta diversity of soil microbial/nematode communities (Bray-Curtis distance) and the soil quality index distance (Euclidean distance) along the grassland degradation gradient (based on n = 36 soil samples)

sampling procedures. With the rapid developments in molecular techniques and bioinformatics, the diversity and composition of soil biota can be measured in a rapid and cost-effective manner (Du et al. 2020). Therefore, including biological properties in soil quality evaluations can provide better assessment of the degree of grassland degradation and their effects on soil ecological functions.

Conclusion

Our research reveals that changes in soil quality induced by grassland degradation are closely related with soil carbon, the root shoot ratio, and soil microbial and nematode communities. In order to accurately assess the degradation, changes in both soil quality and the soil biotic communities should be considered. As one of the key contributors to soil quality, soil carbon restoration should be a priority in order to better restore the ecosystem functions and biodiversity in semi-arid temperate grasslands.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13717-020-00256-3.

Additional file 1: Figure S1. Shannon index and evenness index of plant community along the grassland degradation gradient. DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Bars with different letters indicate significant difference at $P < 0.05$. **Figure S2.** PCA analysis of soil microbial community (left)

and nematode community (right). DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Means ± SE are shown. **Figure S3.** Soil C stock across grassland degradation gradient. DG, degraded grassland; MG, meadow steppe; TG, grassland from the forest-steppe ecotone. Bars with different letters indicate significant difference at $P < 0.05$. Means ± SE are shown. **Table S1.** Results of redundancy analysis (RDA) of soil and plant characteristics on microbial (PLFA) and nematode community composition.

Abbreviations

DG: Degraded grassland; MG: Meadow steppe; TG: The grassland from the forest-steppe ecotone; AMF: Arbuscular mycorrhizal fungi; PLFA: Phospholipid fatty acid; SQI: Soil quality index; PCA: Principal component analysis; MDS: Minimum data set

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Authors' contributions

Qi Li and Zhengwen Wang designed the experiment. Xu Han analyzed the data and wrote the draft together with Yuhui Li. Yuhui Li and Siwei Jiang analyzed the soil and plant properties of all the samples. Qi Li, Yingbin Li, and Xiaofang Du approved the final manuscript. The author(s) read and approved the final manuscript.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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