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Conversion of cropland into agroforestry land versus naturally-restored grassland alters soil macro-faunal diversity and trophic structure in the semi-arid agro-pasture zone of northern China

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Abstract: Restoration of cropland (termed 'Farm') after abandonment including shrubs (termed 'Shrub'), trees (termed 'Tree') and natural grassland (termed 'Grass') has become a routine process aimed to improve land productivity and control desertification. During this restoration process, soil macro-faunal diversity, and trophic structure were investigated at four types of sites (Farm, Shrub, Tree, and Grass) during growing season in the semi-arid agro-pasture zone of northern China. Results indicated that the Staphylinidae family was found to dominate at the Grass, Shrub, and Tree sites, whiles larval Pyralidae individuals were found at the Grass site only. The density of the omnivores (i.e., Formicidae family) was significantly (P<0.05) greater at the Grass site than at the Tree and Farm sites. The total density and richness of predator and phytophages were found to be markedly (P<0.05) greater at the Grass site than at the Farm site. Meanwhile, we found the taxon richness of predators was significantly (P<0.05) higher at the Shrub site than at the Farm and Tree sites. Compared with the Farm and afforested Shrub/Tree sites, the Grass site had greater density, taxon richness, and Shannon index (P<0.05). In conclusion, natural restoration of abandoned croplands toward grassland was an effective strategy relative to artificial afforestation for improvement of soil biological diversity. Moreover, planting shrub is a preferable measure in abandoned croplands for land development in the semi-arid agro-pasture zone of northern China.

Keywords: abandoned cropland; agro-pasture zone; community diversity; land restoration; soil macrofauna

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1 Introduction

In arid and semi-arid agro-pasture zone of northern China, more than half of the pasture area has been cultivated by the economic plants in recent years (Zhao et al., 2007). Such grassland sages

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by cultivation were more susceptible to ecosystem degradation as a result of topsoil erosion, leading to a significant decrease in biodiversity, followed by desertification processes (Su et al., 2004). In order to protect and improve the degradable sandy grassland ecosystems, local government and residents often applied two typical measures as recovery practices: (1) natural restoration of abandoned croplands under exclosure management; and (2) artificial afforestation in abandoned croplands in terms of shrub and/or tree plantations (Thomas et al., 2004; Wang et al., 2010; Liu et al., 2014).

Due to the great importance of restoration practices, many studies were initiated focusing on the effectiveness on soil-vegetation systems by the practices of conversion of cropland to naturally restored grassland and agroforestry system (Zhao et al., 2010; Hu et al., 2016). Since the 1950s, the US government started to initiate land acreage division plan in order to protect soil resources (Ericksen and Collins, 1985). Since 1999, the first practices in China were implemented in Sichuan, Shanxi, and Gansu provinces in order to restore the abandoned croplands to grassland and agroforestry systems (Li, 2002). Regarding the restoration process, the conversion of the abandoned croplands to grassland and agroforestry systems was reported to indicate the changes in plant cover, as well as soil physical and chemical parameters along a time scale (Hou and Zhang, 2002; Yang et al., 2006; Liu, 2009). This ecological process by the conversion of croplands into grassland and agroforestry systems played important implications on the recovery of degraded arid ecosystems and related land management practices (Zhao et al., 2010).

For example, Thomas et al. (2004) found quick recolonization of soil macro-fauna into the former rice fields after abandonment of culture. Liu et al. (2013a) indicated that naturally restored grassland under livestock exclusion could enhance the soil macro-faunal assemblies and improve their biodiversity relative to the cultivated croplands. Takeda and Abe (2001) and Liu et al. (2014) reported that artificially afforested land plantations could provide suitable living conditions that might result in a complex of soil macro-faunal community structure. In total, the abiotic factors modulated by afforested plantations in terms of life forms (i.e., shrubs and trees) could dictate varying spatial and temporal activities of soil animals (Whitford, 2000; Doblas-Miranda et al., 2009; Liu et al., 2013b). However, changes in soil macro-faunal diversity and trophic structure in response to the distinctive conversion practices in the semi-arid agro-pasture zone, northern China, were largely unknown.

Soil fauna is ecologically important in many aspects (Liu et al., 2013b). These organisms can act as pollinators or important components of food chains and nutrient cycles, and they can alter soil structure and fertility in arid and semi-arid regions (Lobry de Bruyn, 1999). Moreover, soil macro-arthropods had little migration ability and relatively small home-range (Dennis, 2003), and were very sensitive to changes in the soil environments (Zhao and Liu, 2013). Any changes in soil environment caused by land management practices could have a significant effect on soil community (Doblas-Miranda et al., 2009; Zhao and Liu, 2013). What's more, the interactions between belowground and aboveground ecosystems could be expected to indicate a considerable influence on community- and ecosystem-level processes during the recovery of degraded arid ecosystems (Wardle et al., 2004). Focusing on such agro-pasture zone of northern China, land management practices frequently occurred, including the cultivation of grassland into croplands, shrub/tree afforestation in the abandoned croplands and allowance of natural restoration of the abandoned croplands (Liu, 2009). Therefore, there was a great need to assess the effects of land management practices regarding the alteration from cropland to agroforestry and grassland on soil faunal community (Zhao et al., 2010).

The aims of this study were (1) to determine soil macro-faunal community composition, density, and diversity together with trophic structure under different types of land management practices regarding the alteration from cropland into an agroforestry system and natural restored grassland; and (2) to determine the relationship between soil macro-faunal community structures and soil properties in the semi-arid agro-pasture zone in northern China. Two hypotheses were given: (1) the alteration from cropland to an agroforestry system and grassland could increase soil macro-faunal activity abundance and diversity; and (2) agroforestry practices by tree/shrub plantations could facilitate more soil macro-faunal diversity relative to naturally restored grassland.

2 Materials and methods

2.1 Study area

The study was conducted at the Naiman Desertification Research Station (42°55′N, 120°42′E; 360 m a.s.l.), Chinese Academy of Sciences, which is located in the southwestern part of Horqin sandy land in Inner Mongolia Autonomous Region, northern China. Crop production (e.g., corn, wheat, and watermelon) was the main land usage of this area during the short growing season (i.e., from May to September). However, large areas of these cultivated grasslands after abandonment have become moderately to seriously desertified (Zhao et al., 2010), since the decrease in productivity was one of the main motives for local farmers to abandon land. In order to protect the soil resources and control desertification timely, local farmers were allowed to restore these abandoned lands naturally by native vegetation, shrubs, and/or trees with nearly half a century (Wang et al., 2010). The main plant species used for these afforestation processes included trees, i.e., *Populus simonii* and *Pinus sylvestris*, and sub-shrubs and shrubs, i.e., *Caragana microphylla*, *Salix gordeivii*, *Periploca sepium*, and *Artemisia halodendron* (Zhao et al., 2010).

The region has a continental, semi-arid climate, with strong winds, dry winters and springs, and comparatively rain-rich summers, followed by short and cool autumns. The mean annual precipitation is 366 mm, of which 70%–80% falls during the summer growing season, and the annual potential evaporation is 1935 mm. The annual mean temperature is 6.8°C, with a maximum mean monthly temperature of 21.9°C in July and a minimum of –14.7°C in January. The annual mean wind velocity ranges from 3.4 to 4.1 m/s. The soils of this region are identified as degraded sandy chestnut soils according to the Chinese soil classification system, and are mostly equivalent to the Orthi-sandic Entisols of sand origin according to the FAO-UNESCO system (Zhao et al., 2007).

2.2 Experimental design

Four land cover types were selected as the study area: (1) two replicate croplands characterized by a maize (*Zea mays*) monoculture for five years were selected as control sites (termed 'Farm'); (2) two nearby replicate abandoned maize croplands allowing natural restoration under exclosure for 16 years, were selected as naturally restored grassland (termed 'Grass'); (3) two nearby replicate abandoned maize croplands afforested by woodlands with *Populus simonii* were selected as artificial agroforestry lands (termed 'Tree'); and (4) two replicate abandoned maize croplands afforested by shrublands with *Periploca sepium* for 20 years were selected as artificial agroforestry lands (termed 'Shrub'). Each type of the four study sites comprised a land area of 0.5–3.0 hm^2. The basic information on vegetation characteristics was given in Table 1.

Table 1 Information of vegetation characteristics at each site

Site	Density (individuals/m^2)	Height (m)	Cover (%)	Plant species and others
Farm	7.3±0.5	1.77±0.10	80–90	Monoculture (*Zea mays*); line spacing is 1.0 m, and row spacing is 0.5 m
Shrub	1.3±0.2	0.75±0.11	30–40	*Allium mongolicum*, *Setaria viridis*, *Pennisetum centrasiaticum*, and *Corispermum macrocarpum*; herbaceous height is 0.15 (±0.06) m and herbaceous density is 76 (±3) individuals/m^2
Tree	0.6±0.1	25.00±4.00	60–70	Few grasses
Grass	40.0±7.0	0.34±0.07	30–40	*Cleistogenes squarrosa*, *Setaria viridis*, *Phragmites australis*, *Salsola collina*, *Artemisia scoparia*, and *Chenopodium glaucum*

Note: Farm, cropland; Tree, afforested plantation by trees; Shrub, afforested plantation by shrubs; Grass, naturally restored grassland from the abandoned croplands. Mean±SE.

From late July to early August in 2009, five sampling points were chosen randomly at each replicate site, and one quadrat (1 m×1 m) was placed at the center of each sampling point. This sampling period in summer represented the growing season that could harbor greatest plant biomass (Luo et al., 2016) and activity abundances of soil arthropods (Zhao et al., 2014). In each quadrat, we excavated a 30 cm×30 cm×30 cm (length×width×depth) soil sample and recovered all macro-organisms by hand-sorting to investigate soil macro-faunal community structure. In addition, we collected an additional soil sample from the 0–30 cm depth using a cylindrical 200-cm^3 stainless steel soil auger for the analysis of soil physical-chemical properties. Each soil composite sample was obtained by mixing five subsamples collected from five locations in each quadrat. There were 80 samples collected for the soil arthropod community and soil abiotic analysis for each site (2 samples×5 quadrats×2 replicate sites×4 land managements).

2.3 Data collection

Samples of soil macro-fauna were stored in 75% alcohol in the field and brought back to the laboratory for identification at the order and/or family level according to the keys of Yin (2001) and Zheng and Gui (1999). The soil macro-fauna was classified into taxonomical groups (i.e., order and/or family) on the basis of morphological features under a binocular magnifying glass (40×). We classified the obtained taxonomic assembly into four throphic groups including predators (Pr), phytophagies (Ph), saprophages (Sa), and omnivores (Om) based on their feeding lifestyle as indicated by Doblas-Miranda et al. (2007).

Soil samples for physical-chemical properties were brought back to the laboratory and passed through a 2-mm sieve to remove plant parts and other debris. Part of each sieved sample (ca. 5 g) was oven-dried in order to determine soil water content (%). The other part of each sieved sample (ca. 20 g) was air-dried to determine selected chemical properties. Soil pH and electrical conductivity (EC, µs/cm) were determined in 1:1 (v/v) soil water solution and in 1:5 (v/v) soil water aqueous extract, respectively. Soil organic carbon (SOC, g/kg) was measured by the $K_2Cr_2O_7$-H_2SO_4 oxidation method of Walkley and Black (1934), and soil total nitrogen (TN, g/kg) was measured by the Kjeldahl procedure (UDK 140 Automatic Steam Distilling Unit, Automatic Titroline 96, Italy). In each quadrat, soil temperature (ST, °C) at 30 cm depth was determined during the experimental period by a portable thermometer with conductivity wires (Sato KeiryokiMfg Co. Ltd., Japan). The soil properties at each site were included in Table 2.

Table 2 Soil properties at each studied site

Site	SWC (%)	ST (°C)	pH	EC (µs/cm)	SOC (g/kg)	TN (g/kg)
Farm	2.37±0.23^b	24.10±0.30^b	7.76±0.04^a	33.33±11.00^a	2.16±0.12^b	0.16±0.01^c
Shrub	4.97±0.01^a	26.10±0.07^a	7.33±0.01^b	34.56±7.05^a	2.29±0.02^b	0.21±0.02^b
Tree	2.27±0.01^b	23.34±0.11^c	8.00±0.02^a	16.78±3.40^a	1.02±0.01^c	0.08±0.01^d
Grass	1.39±0.04^c	24.48±0.02^b	7.82±0.15^a	32.33±4.67^a	2.56±0.03^a	0.25±0.04^a

Note: Values with different lowercase letters in the column are significantly different at $P<0.05$ level. Farm, cropland; Tree, afforested plantation by trees; Shrub, afforested plantation by shrubs; Grass, naturally restored grassland from the abandoned croplands. ST, soil temperature; SWC, soil water content; TN, total nitrogen; SOC, soil organic carbon; EC, electrical conductivity. Mean±SE.

2.4 Data analysis

Within each replicate, the specimen contents from the five sampling points were pooled together as one sample for two reasons: (1) no significant differences in soil macro-faunal density were observed among the five points; and (2) enriching the data used for multivariate analysis of variance. In addition, the adult and larval groups were separately recorded because of their different roles played in soil ecosystems (Swift et al., 1979). The density of each taxonomic group was determined for each site, and the total density (individuals/m^2), taxonomic richness (the total number of taxonomic groups recorded per square meter) and Shannon index (H) were calculated.

$$H = -\sum P_i \log_2 P_i, \tag{1}$$

$$P_i = x_i / \sum x_i, \tag{2}$$

where x_i is the number of individuals in the group category i, and P_i is the proportion of the total number of individuals belonging to the group category i.

Redundancy analysis (RDA) was used to examine the main abiotic factors (ST, SWC, pH, EC, SOC and TN) affecting the distribution of individual faunal groups (Leps and Smilauer, 2003). Data were first analyzed by detrended correspondence analysis (DCA) using version 4.5 of CANOCO software (Microcomputer Power, Ithaca, NY), which suggested RDA as an appropriate approach for further analysis (length of gradient <4 for soil macro-faunal communities). We used RDA to correlate each faunal group with the environmental variables by selecting the linear combinations of environmental variables that gave the smallest residual sum of squares (Liu et al., 2016). Monte Carlo permutation procedures (499 permutations under reduced model) were carried out for significance (P<0.05) testing of the selected soil properties.

All statistical analyses were carried out using version 15.0 of SPSS for Windows (SPSS Inc., Chicago, IL). A post-hoc test with multiple comparisons (Fisher's Least Significant Difference) and analysis of variance (ANOVA) was used to to clarify statistical differences among sites. Before applying parametric tests, we tested normality for homogeneity of variances. For all tests, statistically significant differences were assigned to P<0.05 level.

3 Results

3.1 Composition and density of taxonomical groups of soil macro-faunal community

A total of 45 taxonomic groups from 8 orders and 39 families of a soil macro-faunal community were collected at the sampling sites during the study period (Table 3). There were 11, 23, 10, and 35 taxonomic groups observed at the Farm, Shrub, Tree, and Grass sites, respectively. The overall soil macro-faunal assemblage was dominated in terms of density by the family Staphylinidae and larval Melolonthidae (17.72% of Coleoptera and 15.02% of the total community, respectively), as well as the family Formicidae (Hymenoptera, 21.92%), which together made up 54.66% of the total number of individuals. There were 19/45 taxonomic groups encompassing the number of individuals exceeding 1% of the total. However, the other 26 taxonomic groups made up only 11.41% of the totals.

Table 3 Density distribution (individuals/m^2) of taxonomic groups of a soil macro-faunal community at each site

Taxa	Trophic structure	Farm	Shrub	Tree	Grass	F value
Theridiidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	0.0±0.0	1.0
Linyphiidae	Pr	0.0±0.0	0.0±0.0	0.0±0.0	2.0±0.0	–
Araneidae	Pr	0.0±0.0	2.0±1.0	1.5±1.5	0.5±0.5	1.0
Lycosidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	0.5±0.5	0.7
Oxyopidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	2.5±1.5	2.3
Thomisidae	Pr	0.0±0.0	1.0±1.0	0.0±0.0	2.0±0.0	3.7
Gnaphosidae	Pr	0.5±0.5	0.5±0.5	0.0±0.0	1.5±0.5	2.1
Philodromidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	1.0±1.0	0.7
Salticidae	Pr	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Labiduridae	Pr	1.5±1.5	0.0±0.0	0.0±0.0	0.0±0.0	1.0
Gryllotalpidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Gryllidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Cicadellidae	Ph	0.0±0.0	0.5±0.5	0.0±0.0	0.0±0.0	1.0
Rhopalidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Anthocoridae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	1.0±1.0	1.0
Lygaeidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	2.0±1.0	4.0
Cydnidae	Ph	0.0±0.0	0.5±0.5	0.0±0.0	1.5±0.5	4.0
Miridae	Ph	0.0±0.0	1.0±0.0	0.0±0.0	2.0±0.0	–

To be continued

Continued

Taxa	Trophic structure	Farm	Shrub	Tree	Grass	F value
Reduviidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	0.0±0.0	1.0
Pentatomidae	Ph	0.0±0.0	1.0±1.0	0.0±0.0	0.0±0.0	1.0
Adult Carabidae	Pr	3.0±0.0	0.5±0.5	0.0±0.0	1.0±1.0	5.5
Adult Staphylinidae	Pr	0.0±0.0	0.5±0.5	0.5±0.5	28.5±18.5	2.3
Adult Pselaphidae	Ph	1.5±0.5	0.0±0.0	0.0±0.0	1.0±1.0	1.8
Adult Aphodiidae	Ph	2.5±1.5	0.0±0.0	0.0±0.0	1.5±1.5	1.3
Adult Elateridae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Adult Teneberionidae	Ph	0.5±0.5	0.5±0.5	1.0±1.0	1.5±1.5	0.2
Adult Curculionidae	Ph	0.0±0.0	0.0±0.0	0.5±0.5	0.5±0.5	0.7
Adult Chrysomelidae	Ph	0.0±0.0	0.5±0.5	0.0±0.0	0.0±0.0	1.0
Adult Coccinellidae	Pr	0.0±0.0	1.0±1.0	0.0±0.0	0.0±0.0	1.0
Larval Carabidae	Pr	0.0±0.0	0.5±0.5	0.0±0.0	0.5±0.5	0.7
Larval Melolonthidae	Ph	2.0±1.0	4.0±3.0	4.5±2.5	14.5±9.5	1.2
Larval Rutelidae	Ph	0.5±0.5	0.0±0.0	0.0±0.0	0.0±0.0	1.0
Larval Elateridae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Larval Coccinellidae	Pr	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Larval Buprestidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	–
Larval Teneberionidae	Ph	0.5±0.5^{b}	1.5±0.5^{ab}	0.5±0.5^{b}	4.5±0.5^{a}	14.3*
Larval Curculionidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Larval Meloidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	1.0±1.0	1.0
Larval Asilidae	Sa	1.0±0.0	2.0±1.0	2.0±2.0	3.0±0.0	0.5
Larval Therevidae	Sa	0.0±0.0	0.0±0.0	1.0±1.0	0.0±0.0	1.0
Adult Noctuidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0
Larval Noctuidae	Ph	0.0±0.0	0.0±0.0	0.5±0.5	1.5±1.5	0.8
Larval Pyralidae	Ph	0.0±0.0^{b}	0.0±0.0^{b}	0.0±0.0^{b}	3.5±0.5^{a}	49.0**
Larval Plutellidae	Ph	0.0±0.0	0.5±0.5	0.0±0.0	0.0±0.0	1.0
Formicidae	Om	3.5±0.5^{b}	11.0±1.0^{ab}	1.5±0.5^{b}	20.5±5.5^{a}	9.4*
Tenthredinidae	Ph	0.0±0.0	0.0±0.0	0.0±0.0	0.5±0.5	1.0

Note: Farm, cropland; Tree, afforested plantation using trees; Shrub, afforested plantation using shrubs; Grass, naturally restored grassland from the abandoned croplands; Pr, predator; Ph, phytophagy; Sa, saprophagy; Om, omnivory; "–" means default. * and ** mean significances at P<0.05 and P<0.01 levels, respectively. Different lowercase letters with the same row are significantly different at P<0.05 level among different managements. Mean±SE.

Within soil macro-faunal assemblage, a remarkably greater density of the Staphylinidae family was found at the Grass site relative to the Shrub and Tree sites, with no individuals collected at the Farm site (Table 3). A considerably greater density of larval Melolonthidae was found at the Grass site compared with the Tree site and Farm site. The density of the Formicidae family was significantly (P<0.05) greater at the Grass site compared with the Tree and Farm sites, with the intermediate value at the Shrub site. A similar pattern was followed by the density of larval Tenebrionidae with the order of Grass>Shrub>Farm=Tree. There were a great number of larval Pyralidae individuals only found at the Grass site.

3.2 Taxon density and richness of functional groups of soil macro-faunal community

One taxonomic group (i.e., family Formicidae) was identified as omnivores so that we obtained the same result to that mentioned above. Two taxonomic groups (i.e., larval Asilidae and larval Therevidae) were identified as saprophages, with 1, 2, 3, 3 individuals observed at the Farm site, Shrub, Tree, and Grass sites, respectively. There were no significant (P>0.05) differences observed in the density and taxon richness of saprophages among the four sites, i.e., Farm, Shrub, Tree, and Grass sites.

Compared to the Farm site, total predator and phytophages density were found to be markedly (P<0.05) greater at the Grass site, while there were no significant (P>0.05) differences among the Farm, Shrub, and Tree sites (Fig. 1). Likewise, compared to the Farm site, the taxon richness of phytophages was found to be markedly (P<0.05) greater at the Grass site, while there were no significant (P>0.05) differences among the Farm, Shrub, and Tree sites. However, the taxon richness of predators was found to be markedly (P<0.05) greater at the Grass and Shrub sites compared to the Farm and Tree sites, while there were no significant (P>0.05) differences between the latter two sites.

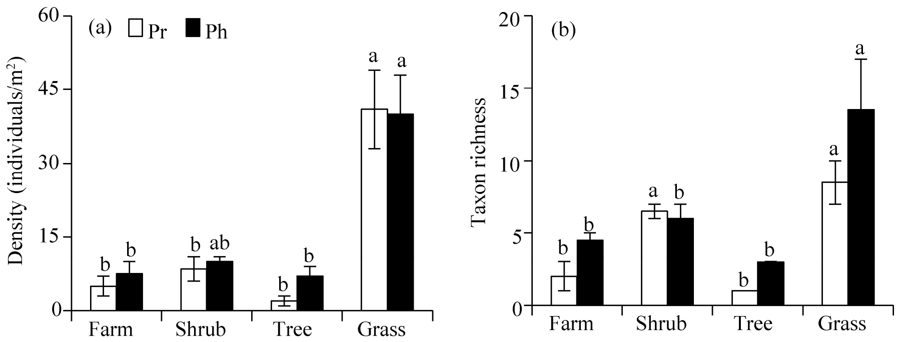

Fig. 1 Taxon density (a) and richness (b) of predator (Pr) and phytophagy (Ph) of a soil macro-faunal community at each site in the semi-arid agro-pasture zone of northern China. Farm, cropland; Tree, afforested plantation using trees; Shrub, afforested plantation using shrubs; Grass, naturally restored grassland from the abandoned croplands. Different lowercase letters are significantly different at P<0.05 level among different managements. Bars indicate standard errors.

3.3 Community indices of soil macro-faunal community

There was a significant (P<0.05) effect of the alteration of cropland into agroforestry and grass sites on soil macro-faunal density and diversity indices (Fig. 2). It was found that the grass site markedly harbored (P<0.05) greater density, taxon richness, and Shannon index compared to the Farm and Shrub sites. However, there were no significant (P>0.05) differences of these three community indices among the Farm, Shrub and Tree sites.

3.4 Contribution of soil properties to soil macro-faunal community structure

RDA was carried out to determine the main factors affecting soil macro-faunal community structure in conversion of cropland into agroforestry land and grassland (Fig. 3). Axes 1 and 2 accounted for 70.1% and 23.9% of the overall variance within the faunal group data, respectively, i.e., a total of 94.0% of the total variance. The cumulative species-environment relation for axes 1 and 2 was 96.3%, indicating that these axes accounting for the bulk of the variance in the faunal group data could be attributed to soil physical-chemical properties. Species-environment correlations for both axes were above 0.98%, indicating that the faunal group data were strongly correlated with environmental parameters. Monte-Carlo significance tests revealed that both the first axis (F=4.69, P=0.04) and all axes (F=17.02, P=0.02) combined, which explained a significant amount of the variation within the obtained data.

Figure 3 illustrated the values and the interaction between the variables by using the length of the arrow to indicate how much variance could be explained by a factor. The direction of the arrows for individual environmental factors indicated an increasing concentration of that factor. Cumulative canonical coefficients and interrelated correlations regarding soil properties for axes 1 and 2 indicated that total soil nitrogen (r=0.647, P<0.01), organic carbon (r=0.522, P<0.05), and soil pH (r=0.508, P<0.05) had the greatest influence on faunal community structure (Fig. 3). It was suggested that the variability in soil macro-faunal density explained in the first and second axes was due to the effects of soil total soil nitrogen, organic carbon, and soil pH.

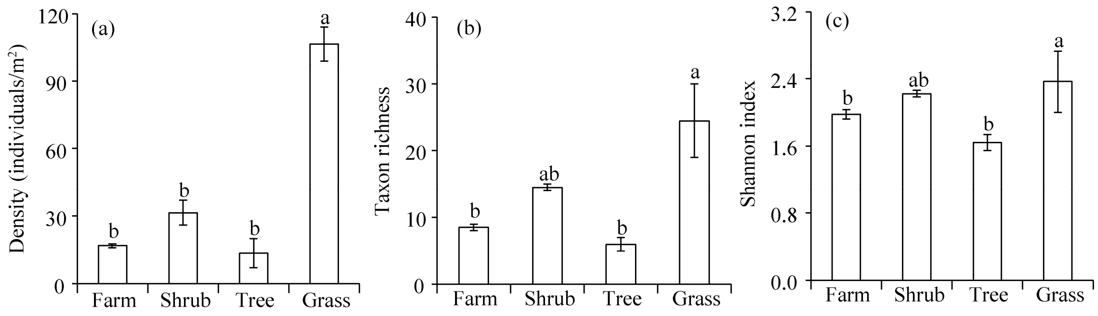

Fig. 2 Total density (a), taxon richness (b), and Shannon index (c) of a soil macro-faunal community at each site in semi-arid agro-pasture zone in Inner Mongolia, northern China. Different lowercase letters are significantly different at $P<0.05$ level among different managements. Farm, cropland; Tree, afforested plantation by trees; Shrub, afforested plantation by shrubs; Grass, naturally restored grassland from the abandoned croplands. Bars indicate standard errors.

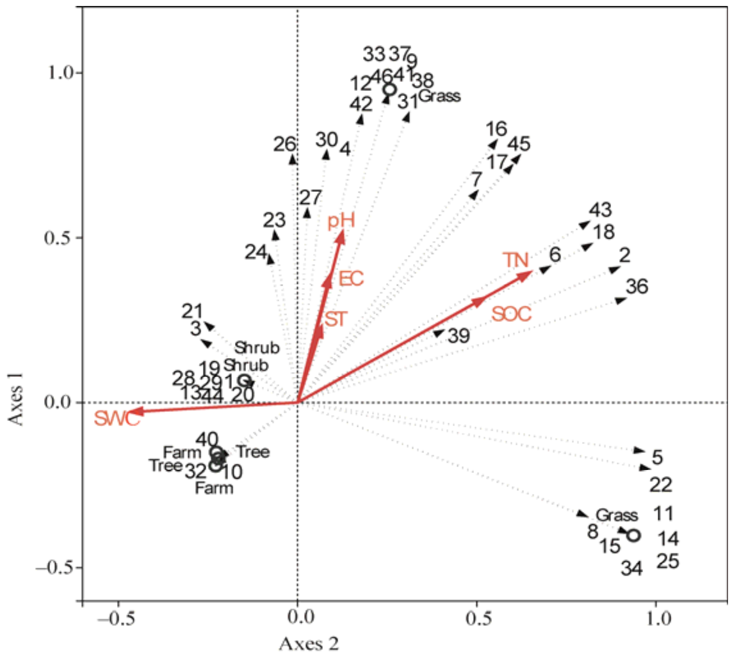

Fig. 3 Biplot of the first two redundancy analysis axes for showing the association of soil macro-faunal community composition with environmental variables. Farm, cropland; Tree, afforested plantation by trees; Shrub, afforested plantation by shrubs; Grass, naturally restored grassland from the abandoned croplands; ST, soil temperature; SWC, soil water content; TN, total nitrogen; SOC, soil organic carbon; EC, electrical conductivity. The numbers close to up-triangles refer to taxonomical groups: 1, Theridiidae; 2, Linyphiidae; 3, Araneidae; 4, Lycosidae; 5, Oxyopidae; 6, Thomisidae; 7, Gnaphosidae; 8, Philodromidae; 9, Salticidae; 10, Labiduridae; 11, Gryllotalpidae; 12, Gryllidae; 13, Cicadellidae; 14, Rhopalidae; 15, Anthocoridae; 16, Lygaeidae; 17, Cydnidae; 18, Miridae; 19, Reduviidae; 20, Pentatomidae; 21, adult Carabidae; 22, adult Staphylinidae; 23, adult Pselaphidae; 24, adult Aphodiidae; 25, adult Elateridae; 26, adult Teneberionidae; 27, adult Curculionidae; 28, adult Chrysomelidae; 29, adult Coccinellidae; 30, larval Carabidae; 31, larval Melolonthidae; 32, larval Rutelidae; 33, larval Elateridae; 34, larval Coccinellidae; 35, larval Buprestidae; 36, larval Teneberionidae; 37, larval Curculionidae; 38, larval Meloidae; 39, larval Asilidae; 40, larval Therevidae; 41, adult Noctuidae; 42, larval Noctuidae; 43, larval Pyralidae; 44, larval Plutellidae; 45, Formicidae; 46, Tenthredinidae.

4 Discussion

In arid and semi-arid agro-pasture zone in northern China, management practices regarding the restoration of cropland into agroforestry land and grassland were largely recognized by the local government and residents, with the hope that such land practices would improve the restoration of degraded ecosystems and reverse desertification processes for land development (Ma, 2003; Zhao et al., 2010). Under these management practices, changes in environmental conditions were expected to exert a strong influence on soil arthropod composition and density distribution (Callaham et al., 2006; Zhao and Liu, 2013). In the present study, a great number of the Staphylinidae family were found at the Grass, Shrub, and Tree sites, but some larval Pyralidae individuals were found at the Grass site only. Moreover, a considerably greater number of larval Melolonthidae, Tenebrionidae, and Formicidae families were found at the Grass site. These findings were similar to Liu et al. (2013a, 2014) who reported diverse and specific taxa at the Grass sites under grazing exclusion by naturally restoration compared with Farm and/or Shrub sites. As confirmed, the biplot of the redundant analysis (RDA) showed that these four families (i.e., larval Pyralidae, larval Melolonthidae, larval Tenebrionidae, and Formicidae family) preferred naturally restored grassland from the abandoned croplands.

These family-specific responses to the microhabitat preferences could be used as reliable bio-indicators of environmental change generated by habitat changes as a result of land use alterations as showed by Heino and Soininen (2007) and Vieira et al. (2012). These changes obtained in the number of larval Pyralidae, larval Melolonthidae, larval Tenebrionidae, and the Formicidae family at the Grass site was found to be significantly correlated with the diverse food resources provided by the recovery of vegetation cover and herbaceous diversity, similar to the finding of Liu et al. (2014). In addition, this finding was probably explained by that the Grass site could offer more niche space relative to mono microhabitats at the Farm site, thus diversifying the living conditions for these specific taxa according to Tilman's resource completion theory (Tilman, 1981).

The conversion of cropland into agroforestry land and grassland affected trophic-group composition, reflected in the changes of resources in each habitat (Wardhaugh et al., 2012). The greater predator density and taxon richness at the Grass site were determined by the density and richness of phytophages arthropods, which were known to be potential prey and were strongly related to the altered abiotic conditions, as shown by Liu et al. (2015b). Zhao and Liu (2013) and Liu et al. (2016) found that afforested shrubland resulted in diverse herbaceous vegetation and improved soil properties, which became an attractive niche enhancing the diversity of predator-dwelling families. Similarly, the greatest omnivores (i.e., Formicidae family) observed at the Grass site was found to be correlated with the recovery of vegetation cover and herbaceous diversity as indicated by Liu et al. (2014).

The taxon richness and Shannon index were found to shed light on the obtained shifts in the taxonomic and trophic composition of a soil macro-faunal community following the conversion of cropland into afforested plantation and naturally restored grassland. This finding was inconsistent with our first hypothesis and with the findings of Thomas et al. (2004), evidencing the greater species richness in recent ex-rice fields (2 years) compared with the natural grassland. However, this was consistent with the findings of previous studies on other ecosystems where human-induced changes in soil pH, soil moisture, and nutrients, together with resource availability played important roles in structuring soil faunal communities (Huhta and Hanninen, 2001; Byrne et al., 2008; Hanel, 2010). Multivariate analysis revealed that changes in community structure were largely mediated by changes in environmental parameters (i.e., soil organic carbon and total nitrogen content, in addition to herbaceous vegetation). The obtained results were able to estimate 94% of arthropod community shifts, where the soil physical-chemical variables (soil temperature, soil water content, total nitrogen, organic carbon content, soil electrical conductivity, and pH) remained constant, similar to the findings of Li et al. (2014). Moreover, our results obtained from the correlation analysis further elucidated that soil organic carbon, total nitrogen content, and soil pH were the most important factors determining the distribution of soil macro-fauna.

However, there were no significant differences in total density and diversity indices between afforested (i.e., the Shrub and Tree sites) and the cultivated sites (i.e., the Farm site). This result was in contrast to the first hypothesis stating that the alteration from cropland into agroforestry land could facilitate more soil macro-faunal diversity. Yet it was in contrast to the findings of Liu et al. (2015a) who found a greater contribution of the manually afforested shrubland to ground-dwelling arthropod diversity relative to the naturally restored grassland. It was suggested that there was limited ecological effectiveness of afforested plantation on soil macro-faunal density and diversity relative to naturally restored management from the abandoned croplands, resulting in dissimilarity with the second hypothesis.

In general, a growing number of empirical studies demonstrated the high price of wealth and labor forces through the artificial afforested practices for restoration of the abandoned croplands in desertified regions (Sun et al., 2004; Zhao et al., 2009). These results, therefore, implied that naturally restored practice converted from the abandoned croplands under exclosure was an effective and optional strategy for soil biological diversity conservation though it needed a long-term recovery process in arid and semi-arid agro-pasture zone of northern China (Zhao et al., 2009; Zida et al., 2011). Regarding the great taxon richness of predators observed at the Shrub site, shrubs could be preferable to trees by afforestation in the abandoned croplands for artificial agroforestry practices. There was an 'arthropod island' of shrub cover, which facilitated soil arthropods beneath shrub canopy (Zhao and Liu, 2013). Canepuccia et al. (2009) and Doblas-Miranda et al. (2009) elucidated the importance of plant (biotic) and soil (abiotic) interplay as key factors in determining the distribution of a soil active arthropod community in shrubland.

5 Conclusions

Our study provided insights into the consequences of the land management practices on soil macro-faunal and soil physical-chemical characteristics. We found that the conversion of cropland to afforested plantation and naturally restored grassland resulted in major changes in arthropod activity, taxonomic and trophic structure. Meanwhile, the naturally restored grassland facilitated the taxon density and richness of functional groups of soil macro-faunal community and was an effective and optional strategy for biological diversity conservation relative to artificial afforested practices in the abandoned croplands. However, there was a limited ecological effect of the artificial afforested practices on soil macro-faunal community structure, despite the artificial shrubland practices being, to some extent, beneficial for the improvement of arthropod predator diversity and the related trophic structure. Specifically, shrubs could be preferable relative to trees by afforestation in the abandoned croplands for desertification control and recovery of a desertified grassland ecosystem in the arid and semi-arid agro-pasture transition zone in northern China.

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