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Effects of land use intensity on dissolved organic carbon properties and microbial community structure

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ABSTRACT

In the last three decades there has been a major shift in China's agriculture with the conversion from cereal fields to vegetable production, however little is known about the impact of this land use change on labile soil carbon and microbial community structure. We conducted a study to characterize dissolved organic carbon (DOC) and soil microbial community by comparing greenhouse vegetable fields with contrasting management intensity and adjacent cereal fields (wheat–maize rotation) in Shouguang and Quzhou in North China. Compared with cereal fields, greenhouse vegetable cultivation increased soil organic carbon (SOC) and total nitrogen (TN), while it decreased the soil pH, particularly at the high-intensity site. The DOC concentration was significantly higher in greenhouse vegetable fields than in cereal fields, whereas DOC composition differed between greenhouse vegetable fields and cereal fields only at high management intensity. Chemical fractionation indicated that DOC from greenhouse vegetable fields with high management intensity was less decomposed than DOC from cereal fields, because the percentage of hydrophobic acid (HOA) as DOC was higher in vegetable fields. Vegetable production significantly changed the microbial community structure in comparison to cereal fields: high-intensity management increased total bacteria, G (+) bacteria and fungi, while low-intensity decreased fungi and increased bacteria-to-fungi ratio. The main factor affecting microbial community structure was soil pH in this study, accounting for 24% of the differences.

1. Introduction

Land use changes represent the most substantial human alteration of ecosystems, drastically affecting soil chemical, physical and biological characteristics [1]. In the North China plain, the main land use was cereal cropping with wheat–maize rotation. Since the 1980s, however, farmers have been encouraged to convert cereal fields to vegetable production because of increased consumer demand. As a result, vegetable production has developed rapidly, and today China is the world leader in vegetable production: 18.4 million ha are dedicated solely to vegetable production, accounting for 11.6% of the national cropland area [2] and about 1.0% of total harvested area globally [3].

Compared with cereals, vegetable cultivation requires more intensive management and larger inputs of nutrients and irrigation [4]. This is especially true for greenhouse vegetable production in North China, which is characterized by very intensive management in terms of fertilization, tillage and irrigation [5,6]. Furthermore, inputs of carbon (C) and nitrogen (N) have not always increased proportionately in response to land use conversion, e.g. in some agricultural production areas in China the conversion from cereal fields (wheat–maize rotation) to greenhouse vegetable production have led to 4.9 fold increases of soil N inputs and 1.9 fold increases of soil C [7], and this combined with tillage and irrigation is likely to affect C and N cycling [8,9]. For example, a previous study showed that conversion from cereal to vegetable cultivation led to higher soil organic carbon (SOC) and total nitrogen (TN), especially under higher management intensity [7], as well as to higher concentrations of labile C forms such as dissolved organic carbon (DOC) [8]. However, it remains to be determined how DOC composition responds to land use type conversion from wheat–maize rotation to greenhouse vegetable fields.

Dissolved organic carbon represents only a small proportion of SOC but is considered to be a key indicator of soil quality due to its rapid response to land use and management practices [10].

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Previous studies showed that management practices can affect on DOC properties, e.g. long-term manure input increased the aromaticity of DOC [11]. Similarly, dissolved organic matter in degraded peatlands had a higher specific absorption at 285 nm and a higher humification index than those of intact peatlands (low intensity land use) [12].

Land use changes and management practices are also key factors affecting soil microbial communities, via changes in soil properties such as pH, moisture, temperature [13–16], nutrient availability [17,18] and SOC composition [19,20]. However, it is unclear how microbial communities are affected by changing to greenhouse vegetable production.

Dissolved organic carbon is the primary energy source for microorganisms and affects their activity and abundance in the soil [10,21]. Numerous studies have reported a positive relationship between microbial activity (CO_2 production) and DOC concentration [11,22,23]. The components of DOC, however, differ in decomposability. This makes DOC an important factor affecting microbial activity and community structure [12], but the effects may strongly depend on DOC composition. For example, hydrophobic acids, rich in aromatic structures, are difficult to decompose for microorganisms [12,24,25].

Significant acidification has taken place in vegetable fields in China due to the high N fertilizer input, intensive cropping cycles and irrigation which enhances removal of bases [8,26–28]. Nonetheless, the interactive effect of pH and DOC concentration or DOC properties on microbial communities remains to be determined under these intensively managed greenhouse vegetable soils.

The paired greenhouse vegetable and adjacent cereal (wheat–maize rotation) soils at two research sites, in North China were sampled in this study. The objectives of this study were 1) to assess the response of the soil microbial community structure and DOC properties to conversion from cereal fields to greenhouse vegetable fields, and 2) to evaluate which soil properties (SOC, TN, DOC properties and pH) are the main drivers of microbial community structure.

2. Materials and methods

2.1. Study sites

The two study sites have been described in detail previously [7]. Briefly, two greenhouse vegetable production areas in North China, differing in management intensity in terms of C and N input and tillage frequency, were selected: Quzhou in Hebei province with low management intensity (C input from manure, 3053 kg C ha^{-1}; N input from manure and inorganic N fertilizer, 670 kg N ha^{-1}, tillage, 1–2 times), and Shouguang in Shandong province with high management intensity (C input from manure, 9548 kg C ha^{-1}; N input from manure and inorganic N fertilizer: 2178 kg N ha^{-1}; tillage, 2 times). These sites were compared to adjacent cereal fields under the wheat–maize rotation, which had a similar level of management intensity at both sites (C input from cereal residues: 6330–6866 kg C ha^{-1}; N input from inorganic N fertilizer and cereal residues, 444–553 kg N ha^{-1}; tillage, once before wheat).

Both regions have a monsoon climate of the semi-humid temperate zone with only small differences in mean annual temperature (Quzhou: 13.1 °C; Shouguang: 12.7 °C) and precipitation (Quzhou: 556 mm; Shouguang: 594 mm). The soil type is a Fluvo-aquic Ochri-Aquic Cambisols at both sites.

2.2. Soil sampling

In spring 2008 (growing season for both greenhouse vegetable and wheat–maize rotation), three representative greenhouse vegetable fields with adjacent (50 m) cereal (wheat–maize rotation) fields were selected at Quzhou and Shouguang. The greenhouse vegetable fields were established 7–11 years before the study, whereas cereals have been cultivated for more than 30 years [7]. Soil samples were obtained from each field by collecting 12 randomly selected cores (30 mm diameter; 0–30 cm deep) and mixed to give one composite sample per field. Plant roots and leaves were carefully removed by hand. Samples were stored at field moisture content at 4 °C in airtight polypropylene bags and transported to the laboratory immediately. The samples were divided into several parts. One part was stored at −80 °C for microbial community analysis. Another part of soil was stored at 4 °C and DOC was extracted within one week. The extracted DOC solution was stored at −20 °C until analysis. Another part of the soil sample was air dried at room temperature and used for SOC, TN, and soil pH measurements.

2.3. Soil chemical analyses

Soil texture was determined by the pipette method [29]. Soil pH was measured in 1:2.5 (w/v) soil slurries, where 10 g (<2 mm) of air-dried soil was added to 25 ml of deionized water and the pH was measured after 30 min. SOC and TN contents were determined by dry combustion using a Vario MACRO C/N elemental analyzer (Elementar Corp., Germany).

DOC was extracted from the field-moist soil samples (equivalent to 20 g oven-dried soil) with 0.5 mol L^{-1} K_2SO_4 (soil/solution ratio of 1:5 w/v) for 1 h [30]. The extract was then passed through a 0.45 μm membrane filter and analyzed for total oxidizable C (Shimadzu Corp., Japan).

2.4. DOC fractionation

The determination of chemical composition of DOC was a modification of the procedure described by [31], which is based on the adsorption to nonionic resin (Amberlite XAD-8) and separates the DOC into hydrophilic components and hydrophobic components: Acids, neutrals and bases.

Hydrophobic bases (HOB): The filtered DOC sample was pumped through an XAD-8 column at a flow rate not exceeding 10 bed volumes h^{-1}. Following the sample, 0.3 bed volumes of distilled water rinse were pumped into the XAD-8 column. The influent and effluent tubing were then reversed, and the hydrophobic bases were backflush eluted with 0.3 bed volume of 0.1 M HCl, followed by 1.5 bed volumes of 0.01 M HCl.

Hydrophilic components (HIM, which includes hydrophilic bases (HIB), hydrophilic acids (HIA) and hydrophilic neutrals (HIN)): The effluent from the XAD-8 column was acidified to pH 2 with HCl and recycled through the XAD-8 column at 10 bed volumes h^{-1} or less. The non-sorbed portion of the sample was rinsed from the resin by 5 bed volumes of 0.01 M HCl.

Hydrophobic acids (HOA): Hydrophobic acids were desorbed by backflush elution with 0.3 bed volume of 0.1 M NaOH, followed by 5 bed volumes of distilled water. Hydrophobic neutral (HON): The XAD-8 column was pumped dry after the elution of the hydrophobic acid fraction. The XAD-8 beads were allowed to dry at room temperature for 15 h and then extracted with anhydrous methanol and distilled water in a Soxhlet extractor.

2.5. Microbial community structure

Soil microbial community structure was determined using phospholipids fatty acid (PLFA) analysis. The method was adapted from [32,33]. Fatty acids were extracted with a one-phase

Table 1
Soil organic carbon (SOC), total nitrogen (TN), pH and C:N ratio in low and high intensity vegetable (V) and adjacent cereal (C) fields.

Site	Land use	SOC (g kg^{-1})	TN (g kg^{-1})	C:N	pH (H_2O)	DOC (mg C kg^{-1})
Quzhou	C	7.48 ± 0.35 b	0.91 ± 0.13 b	8.22 ± 1.05 a	8.23 ± 0.01 a	47.7 ± 2.41 b
	V	8.23 ± 0.46 b	0.97 ± 0.05 b	8.48 ± 0.29 a	8.01 ± 0.06 a	67.8 ± 3.67 ab
Shouguang	C	7.50 ± 0.83 b	0.76 ± 0.08 b	9.87 ± 0.27 a	8.15 ± 0.08 a	47.6 ± 8.09 b
	V	13.1 ± 1.16 a	1.63 ± 0.08 a	8.03 ± 0.14 a	6.85 ± 0.47 b	85.9 ± 11.4 a

Standard errors of the means ($n = 3$) are presented as ± values.
C: Cereal field (wheat–maize rotation); V: Greenhouse vegetable field.
Means followed by different letters are significantly different at $p < 0.05$ within same column.

extraction mixture containing chloroform:methanol:phosphate buffer (1:2:0.8 vol/vol/vol). Five grams of frozen soil were extracted with 19 ml of the solvent in a shaker for 2 h. After centrifugation for 10 min at 2500 rpm, the supernatant was decanted. The soil was then vortexed and re-extracted for 1 h with an additional 9.5 ml of extractant. Supernatant from the second extraction was added to the first. Then samples were shaken with 7 ml phosphate buffer and 8 ml $CHCl_3$ and the phases allowed to separate overnight. The $CHCl_3$ layer was decanted and dried under N_2 at 30 °C. Phospholipids were separated from neutral and glycolipids on solid phase extraction columns (SPE-Si, Supelco, Inc., USA). The column was conditioned with 6 ml $CHCl_3$, followed by 6 ml acetone, 3 ml methanol and dried under N_2 at 30 °C. The samples were then subjected to mild alkaline methanolysis by dissolving in 1 ml 1:1 MeOH:toluene and 1 ml 0.2 M KOH, and heating at 35 °C for 15 min. Two ml of H_2O and 0.3 ml of 1.0 M acetic acid were added. The resulting fatty acid methyl esters were extracted with 2 × 2 ml aliquots of hexane. Hexane aliquots were combined and dried under N_2 at room temperature. Samples were then re-dissolved in hexane containing 19:0 as an internal standard and analyzed using a gas chromatograph (N6890, Agilent) equipped with MIDI peak identification software (Version 4.5; MIDI Inc., Newark, DE).

The abundance of individual fatty acids is expressed on a soil dry weight basis. The PLFAs 18:2ω6, 9c were taken to indicate fungal biomass [23]. i15:0, a15:0, 15:0, i16:0, 16:1ω7c, i17:0, a17:0, cy17:0, 18:1ω7c, cy19:0ω8c were chosen to represent bacterial biomass [33], of which i15:0, a15:0, i16:0, i17:0, a17:0 are markers for Gram-positive bacteria [34].

2.6. Statistical analysis

The soil chemical proprieties and concentrations of individual fatty acids among different land-use types were compared by using one-way ANOVA analyses with SAS (SAS Inc., 1996). Differences of $p < 0.05$ were considered to be statistically significant using the LSD test.

The PLFA data were log $(x + 1)$ transformed to focus attention on patterns of the whole community by giving rare fatty acids similar weighting as common fatty acids. Log transformed PLFA patterns were analyzed by Primer-E software (Primer-E Ltd, Plymouth Marine Laboratory, Plymouth, UK). Non-metric multi-dimensional scaling (MDS) was based on all detected PLFAs. Like principle component analysis, multi-dimensional scaling (MDS) is a multivariate analysis. The reliability of the two-dimensional MDS plots is indicated by the stress value. Stress values ≤0.2 indicate that the ordination was a good reflection of overall community structure [35]. Significant differences in microbial community structure between treatments were determined by PERMANOVA. Soil chemical and biological characteristics explaining the observed patterns were determined by the DistLM procedure in Primer. The procedure was also used to assess the contribution of the different fatty acids to the observed patterns.

3. Results

3.1. Soil organic C, total N and soil pH

Conversion from cereal fields to greenhouse vegetable fields increased SOC and TN contents. Compared with cereal fields, SOC and TN increased by 10% and 6.6% in greenhouse vegetable fields in Quzhou with low management intensity, while in Shouguang with high intensity SOC and TN increased by 75% and 114% (Table 1). Compared with cereal fields, the soil pH in the greenhouse vegetable fields in Shouguang with high intensity management was significantly lower (1.3 units) (Table 1).

3.1.1. DOC concentration and chemical composition

The DOC concentration was significantly higher under greenhouse vegetable fields than under cereal fields at both sites,

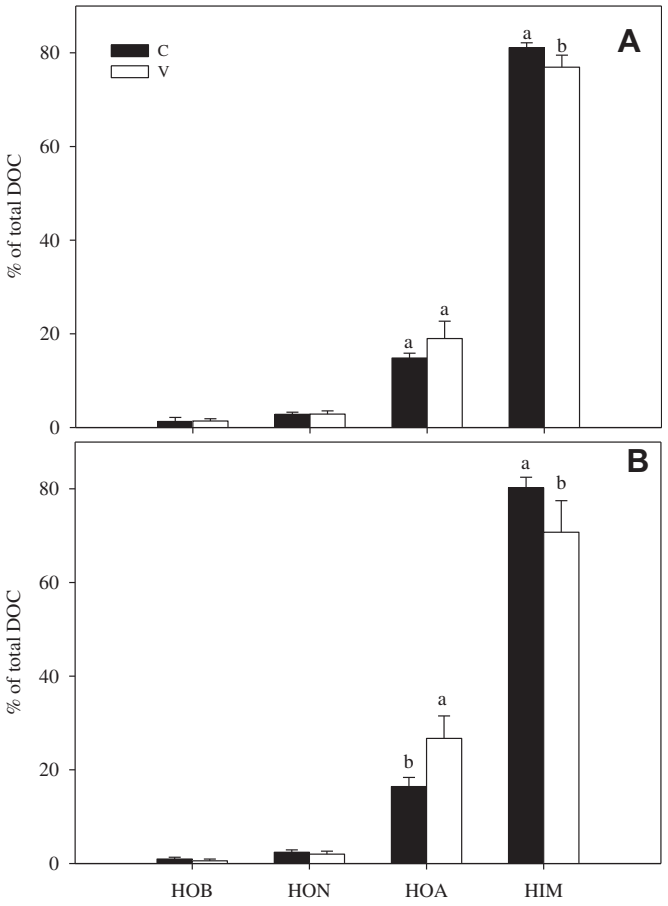

Fig. 1. DOC fractions in low- (A) and high- (B) intensity vegetable fields (V) and adjacent cereal (C) fields. Percentage of the total DOC (mean and SE, $n = 3$) in hydrophobic bases (HOB), hydrophobic neutrals (HON), hydrophobic acids (HOA) and hydrophilic components (HIM) is presented. Means followed by different letters are significantly different ($p < 0.05$) between land use within each site.

particularly with high management intensity (Table 1). Land use type and management intensity affected not only DOC concentration, but also its chemical composition (Fig. 1). The relative abundance of the DOC fractions decreased in the order of HIM > HOA > HON > HOB across land use types and sites. The hydrophobic components (including HOA, HOB and HON) accounted for 17–38% of the total DOC, with no difference between cereal fields and greenhouse vegetable fields at both sites (Fig. 1).

The hydrophilic component was the largest fraction of total DOC (ranging from 62.3 to 83.4%) and its proportion was lower with high-intensity greenhouse vegetable management compared to those in the adjacent cereals. HOA was the major hydrophobic component and its percentages were higher in the high-intensity greenhouse vegetable fields than in the adjacent cereal fields, whereas there were no differences between cereal fields and low-intensity greenhouse vegetable fields (Fig. 1A).

3.2. Microbial community structure

There were 32 individual PLFAs identified in this study and total average PLFAs concentrations at two sites ranged from 43.2 to 68.8 nmol g^{-1} (Table 2). High intensity management in greenhouse vegetable fields (at Shouguang) significantly increased total PLFAs concentration compared to cereal fields (Table 2).

The PLFA signature groups also changed markedly. Conversion from cereal fields to vegetable fields significantly increased total bacterial PLFAs (Table 3). PLFAs concentrations indicating the G (+) bacteria (i15:0, a15:0, i16:0, i17:0, a17:0) and fungi (18:2ω6, 9c) were significantly higher in the high-intensity vegetable fields compared with the cereal fields (Tables 2 and 3). The concentrations of some individual PLFAs concentrations indicating G (−) bacterial groups (16:1ω7c and 18:1ω7c) were also highest in the high-intensity vegetable fields (Table 2). The ratio of bacterial to fungal PLFAs was greatest with low-intensity greenhouse vegetable management (Table 3).

In our study, the stress value of the MDS plot was 0.1, indicating that the ordination was a good reflection of overall microbial community structure (Fig. 2). In the plot, each symbol represents a microbial community. Three fatty acids contributed most to the patterns, namely the G (+) fatty acid a15:0 (36%) and the two G (−) fatty acids 16:1ω7c and 10Me 18:0 (together 15%). The vectors in Fig. 2 indicate the environmental that contributed most to the differences in community structure based on PERMANOVA analysis which showed that microbial community structure was significantly affected by site, land use type and interactions between site and land use type, with land use type being the most important. Significant differences in microbial community structure between cereal fields and greenhouse vegetable fields were detected at both sites. The community structure in cereal fields at the two sites was similar, while there were significant differences between high- and low-intensity vegetable management. Among the different soil properties, only soil pH had a significant effect on community composition, explaining 24% of the PLFA patterns (Fig. 2).

4. Discussion

This study showed that high-intensity greenhouse vegetable cultivation alters the soil pH, DOC composition and microbial

Table 2
Concentration of individual PLFAs determined in low and high intensity vegetable (V) and adjacent cereal (C) fields.

PLFA	PLFA concentration (nmol g^{-1})			
	Lower intensity of vegetable cultivation (Quzhou)		Higher intensity of vegetable cultivation (Shouguang)	
	C	V	C	V
i14:0	0.55	0.75	0.62	0.69
14:1ω5c	0.56 ab	1.71 a	0.42 b	0.97 ab
14:0	0.39	0.78	0.39	0.64
i15:1	0.07	0.41	0.03	0.41
i15:0	0.13 b	0.81 b	0.11 b	3.78 a
a15:0	0.20 bc	1.03 b	0.14 c	2.74 a
15:0	0.10 b	0.62 a	0.11 b	0.36 ab
i15:0(3OH)	1.26	2.32	1.38	1.41
15:0(2OH)	1.66	0.02	1.18	1.08
i16:1	0.20	0.20	0.60	0.34
i16:0	0.62 b	0.73 b	0.66 b	1.85 a
a16:0	1.53	0.68	1.57	2.48
16:0	3.27 ab	4.84 ab	2.76 b	6.88 a
16:1ω7c	1.11 b	1.40 b	1.13 b	2.23 a
16:1ω5c	1.12 b	1.01 b	1.24 b	2.29 a
10Me16:0	2.33 b	2.13 b	1.89 b	5.32 a
16:1(2OH)	0.40	0.51	0.53	0.42
a17:1	2.70	1.31	2.68	3.04
i17:0	1.00 b	1.43 ab	1.12 ab	1.75 a
a17:0	3.26 a	1.53 b	3.18 a	4.09 a
17:1ω7c	0.57 ab	0.85 ab	1.18 a	0.96 b
cy17:0	1.62	1.97	1.67	1.37
i18:0	0.96 ab	0.80 c	1.41 a	0.57 bc
18: 2ω6,9c	3.57 b	2.36 c	3.42 b	5.24 a
18: 1ω9c	1.23 b	1.41 b	1.55 b	2.54 a
18:1ω7c	1.89 b	1.77 b	2.06 b	3.06 a
18:0	2.19	3.02	2.58	3.11
10Me18:0	1.61	1.65	0.64	2.61
18:1(2OH)	2.01	0.00	2.17	1.04
cy19:0ω8c	2.99 ab	2.20 b	4.13 a	3.27 ab
18:3ω6c (6,9,12)	1.76	1.96	2.35	1.37
20:0	0.79	2.69	2.66	1.87
Total PLFAs	43.2	44.1	46.9	68.8

C: Cereal field (wheat–maize rotation); V: Greenhouse vegetable field.
Means followed by different letters are significantly different at $p < 0.05$ within same row.

Table 3
Concentrations of bacterial, fungal and G (+) PLFA, ratios of bacterial:fungal PLFA and G (+):total PLFA in vegetable (V) and cereal (C) fields at two sites of North China.

	Lower intensity vegetable cultivation		Higher intensity vegetable cultivation	
	C	V	C	V
Bacterial PLFAs (nmol g^{-1})	12.8 ± 2.14 b	13.5 ± 2.56 b	14.1 ± 1.20 b	24.5 ± 2.33 a
Fungal PLFAs (nmol g^{-1})	3.37 ± 0.25 b	2.36 ± 0.04 c	3.42 ± 0.08 b	5.24 ± 0.36 a
Ratio bacterial:fungal	3.55 ± 0.34 b	5.70 ± 1.03 a	4.12 ± 0.42 ab	4.66 ± 0.17 ab
Gram (+) bacterial PLFAs (nmol g^{-1})	5.21 ± 0.32 b	5.53 ± 1.46 b	4.96 ± 0.65 b	14.2 ± 1.45 a
Ratio G (+):total PLFAs	0.12 ± 0.01 b	0.12 ± 0.02 b	0.11 ± 0.01 b	0.21 ± 0.01 a

Standard errors of the means ($n = 3$) are presented as ± values.
C: Cereal field (wheat–maize rotation); V: Greenhouse vegetable field.
Means followed by different lower-case letters are significantly ($p < 0.05$) different within same row.

community structure compared to cereal cultivation. Furthermore, the significant correlation between microbial community structure and soil pH indicated that the microbial community structure was to a large extent determined by soil pH.

Despite the frequent tillage, which favors decomposition of organic matter, SOC and TN were highest at high-intensity greenhouse vegetable management. This can be explained by the high application rates of farmyard manure used in this system. The finding that high rates of fertilizer addition can lower the pH (Table 1) has been shown previously and was mainly explained by N addition [8,26–28].

The higher DOC concentration under vegetable cultivation can be explained by at least three factors. Firstly, high application rates of manures and slurry increase DOC concentration [36]. Secondly, as the DOC correlates with total SOC [37,38], the observed higher SOC content under vegetables led to higher DOC. In agreement with other studies, we also found that DOC has a positive relationship with SOC (data not shown) suggesting the importance of SOM as the main DOC source. Finally, lower pH values may lead to higher DOC content. This is due to lower Ca^{2+} concentrations in the soil and the higher solubility of organic compounds at low pH.

Intensive greenhouse vegetable management also affected DOC composition: the percentage of HOA was higher with intensive vegetable management than under cereals. HOA is rich in aromatic structures and complex molecules and therefore, difficult to decompose [12,25]. The higher proportion of HOA under intensive greenhouse vegetable management is probably derived from manures and slurries. Further, more intensive microbial decomposition of the other fractions, especially HIM, which are easily available than HOA, may contribute to the relative increase of HOA. Similarly, Marschner [23] found that management practices such as long-term manure input increased the aromaticity of DOC.

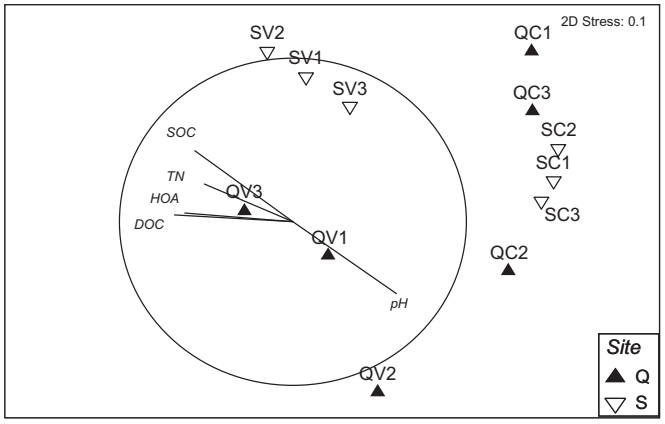

Fig. 2. MDS plots of PLFA patterns based on Bray–Curtis similarities in vegetable (V) and cereal (C) fields at two sites of North China Plain. C: Cereal field (wheat–maize rotation); V: Greenhouse vegetable field. Q: Quzhou, lower intensity vegetable management; S: Shouguang, higher intensity vegetable management.

The high input of nutrients with high-intensity vegetable management may also explain the increased abundance of bacteria [23]. Furthermore, high N addition may decrease the C:N ratio of plant residues making them more decomposable for bacteria. The lower pH in the high intensity vegetable soil is unlikely to have contributed to the differences in fungal abundance as it was pH 6.9. Along a continuous soil pH gradient (spanning from pH 4.0 to 8.3), fungal biomass decreased slightly from pH 6 to 8.3 [40]. In this study, concentrations of G (+) markers (i15:0, a15:0, i16:0, i17:0, a17:0) were highest under higher-intensity vegetable management. Previous studies reported that G (+) bacteria are well adapted to soils with low substrate availability [41,42]. We found a higher ratio of iso-to-anteiso 15:0 and 17:0 PLFAs (data not shown) which may indicate environment disturbance in the high-intensity vegetable fields [16]. Conversion of cereal fields to intensive vegetable fields increased the bacteria-to-fungi ratio. Nevertheless, significant difference was only detected at the low-intensity site.

The MDS plots analysis of total PLFA patterns showed that despite the relatively narrow pH range, only soil pH significantly affected microbial community structure in this study. This confirms previous findings [39,41,43] that soil pH is a major factor shaping microbial communities. For example, in a continental survey, soil pH was the most important factor affecting bacterial community structure [14]. Although DOC is the primary energy source for microorganisms and affects their activity and abundance in the soil [10,21], we did not find significant relationship between DOC properties and soil microbial community. It should be noted that soil pH can also strongly influence abiotic factors, such as carbon availability [44]. For example, soil pH had marked effects on soil microbial community and how the community responds to substrate addition [39,45].

5. Conclusions

This study indicated that land use change, particularly to high-intensity management, affects soil chemical and biological properties. High rates of fertilizer and manure application not only increased nutrient and carbon input, but also resulted in soil acidification and changes of DOC composition. This affected soil microbial communities, favoring microbes that are more competitive at high substrate concentrations and adapted to lower soil pH. While the impact of high-intensity greenhouse vegetable management on soil functioning was not directly assessed here, the accumulation of aromatic compounds in the DOC may suggest a lack of microbial species capable of decomposing these compounds. Thus, further studies are needed to assess the capacity of microbial species for degradation of aromatic compounds in these intensively managed arable soils.

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