ELSEVIER

Soil Biology & Biochemistry 36 (2004) 1785–1792

Soil Biology & Biochemistry

www.elsevier.com/locate/soilbio

Microbial and biochemical soil quality indicators and their potential for differentiating areas under contrasting agricultural management regimes

Gary D. Bending[a,*], Mary K. Turner[a], Francis Rayns[b], Marie-Claude Marx[c], Martin Wood[c]

[a]*Warwick HRI, University of Warwick, Wellesbourne, Warwick CV35 9EF, UK*
[b]*Henry Doubleday Research Association, Ryton-on-Dunsmore, Coventry CV8 3LG UK*
[c]*Department of Soil Science, University of Reading, Reading RG6 6DW UK*

Received 30 September 2003; received in revised form 24 March 2004; accepted 8 April 2004

Abstract

The aim of this study was to examine interrelationships between functional biochemical and microbial indicators of soil quality, and their suitability to differentiate areas under contrasting agricultural management regimes. The study included five 0.8 ha areas on a sandy-loam soil which had received contrasting fertility and cropping regimes over a 5 year period. These were organically managed vegetable, vegetable–cereal and arable rotations, an organically managed grass clover ley, and a conventional cereal rotation. The organic areas had been converted from conventional cereal production 5 years prior to the start of the study. All of the biochemical analyses, including light fraction organic matter (LFOM) C and N, labile organic N (LON), dissolved organic N and water-soluble carbohydrates showed significant differences between the areas, although the nature of the relationships between the areas varied between the different parameters, and were not related to differences in total soil organic matter content. The clearest differences were seen in LFOM C and N and LON, which were higher in the organic arable area relative to the other areas. In the case of the biological parameters, there were differences between the areas for biomass-N, ATP, chitin content, and the ratios of ATP: biomass and basal respiration: biomass. For these parameters, the precise relationships between the areas varied. However, relative to the conventionally managed area, areas under organic management generally had lower biomass-N and higher ATP contents. Arbuscular mycorrhizal fungus colonization potential was extremely low in the conventional area relative to the organic areas. Further, metabolic diversity and microbial community level physiological profiles, determined by analysis of microbial community metabolism using Biolog GN plates and the activities of eight key nutrient cycling enzymes, grouped the organic areas together, but separated them from the conventional area. We conclude that microbial parameters are more effective and consistent indicators of management induced changes to soil quality than biochemical parameters, and that a variety of biochemical and microbial analyses should be used when considering the impact of management on soil quality.
© 2004 Elsevier Ltd. All rights reserved.

Keywords: Soil quality; Light fraction organic matter; Arbuscular mycorrhizal fungus; Enzymes; Metabolic diversity

1. Introduction

A number of frameworks have been produced to provide quantitative estimates of soil quality. Several of these frameworks rate soil quality by assessing key soil functions, each of which is quantified using physical, biochemical and microbial parameters. These systems have shown the potential to differentiate soil quality in areas receiving contrasting agricultural management regimes (Glover et al., 2000; Reganold et al., 2001). The parameters used in the existing rating methods are largely focussed on properties which change slowly with time, such as C, N and P content, limiting their usefulness for detecting early management induced changes to soil quality. Those rating systems which do include a microbial component focus on biomass-C and N, the value of which for defining the status of microbial processes, and the characteristics of soil microbial communities, is limited.

In the case of biochemical indicators, soil organic matter (SOM) is typically used as a measure of soil quality. However, SOM has a number of pools with different functional roles in soil, and which could provide a measure of subtle, or early effects of management on soil quality. In terms of nutrient supply, dissolved organic N (DON), labile

* Corresponding author. Tel.: +44-1789-470382; fax: +44-1789-470552.
E-mail address: gary.bending@hri.ac.uk (G.D. Bending).

0038-0717/$ - see front matter © 2004 Elsevier Ltd. All rights reserved.
doi:10.1016/j.soilbio.2004.04.035

organic nitrogen (LON) and light fraction organic matter (LFOM) respond more rapidly to management than SOM content (Biederbeck et al., 1994; Janzen et al., 1992) and are considered to be important for governing patterns of N mineralization in many soils (Bonde and Rosswall, 1987; Janzen et al., 1992; Sierra, 1996). Carbohydrates play a role in aggregation of soil particles, which is a key determinant of many soil structural properties (Oades, 1984).

A variety of microbial parameters have the potential for use as diagnostic indicators of soil quality. Measurement of the status and activities of specific microbial communities contributing to soil processes has the potential to provide particularly rapid and sensitive means of characterising changes to soil quality. Although the value of biomass measurements as an indicator of soil quality is unclear, when used in conjunction with respiration to give a metabolic quotient, it has been used to provide information on changes to the structure and functioning of soil microbial communities (Wardle and Ghani, 1995). The size and diversity of specific functional microbial groups, such as arbuscular mycorrhizal fungi and nitrifying bacteria communities also have potential to characterise the effects of management on the sustainability of soil (Chang et al., 2001; Helgason et al., 1998). Additionally, the metabolic characteristics and diversity of soil microbial communities are known to be sensitive to management (Bending et al., 2000; Marx et al., 2001), and may also provide information on the status and activity of the microbial community as well as the resilience of the community to stress.

While there are many reports of the dynamics of such functional, biochemical and microbial parameters in soil, including the impacts of management, most studies have taken the parameters in isolation, and widely contrasting timescales in studies using different indicators makes comparisons between studies difficult. Additionally, many of the studies using such indicators have been made across different soil types, soil that has been under contrasting long-term management, or different habitats. Much less is known of the relative value of such indicators for differentiating areas under different management on the same soil type, or for providing information on changes to soil quality in the short-term. The aim of the present study was to compare the relative value of functional, biochemical and microbial parameters with traditional measures of soil quality for differentiating areas under contrasting management regimes.

2. Materials and methods

2.1. Study site

The study site was located on the farm at HRI-Wellesbourne, Warwickshire, UK. The site is on sandy-loam soil with 73% sand, 12% silt and 14% clay. Full soil characteristics are described by Whitfield (1974). Five 0.8 ha areas with different management regimes were selected for investigation (Table 1). Areas A, B, C and D were located in Hunts Mill field, which was converted to organic management in 1995/96. Prior to conversion, the field had been in conventional cereal production for over 20 years. Area A had a 23-month grass clover ley on conversion, followed by three cereal crops, which were interspersed with clover fertility-building crops, and a final potato crop. Area B received a 30-month grass clover ley on conversion, followed by an organic vegetable rotation. Area C had a 6-month vetch fertility-building crop on conversion, followed by an organic vegetable–cereal rotation. Area D had been under a mown grass clover ley since conversion began. Area E was taken from within Deep Slade field, which is adjacent to Hunts Mill. Area E had been under conventional cereal production for over 20 years prior to the study. Until conversion of Hunts Mill, the two fields had been under the same conventionally managed cereal rotation. The site has no livestock, and green waste compost had been applied to the fertility-building phase of the areas within Hunts Mill in accordance with the Code of Good Agricultural Practice (UKROFS, 2001).

2.2. Sampling strategy

Sampling was done in the first week of May 2001. In the case of areas B and C, each 0.8 ha area was divided into six strips which had each received different vegetable crop sequences. For sampling, each strip was divided into four equal area sub-strips (16 × 20 m). Across each sub-strip, 20 cores were taken from 0 to 15 cm depth using a 2.5 cm auger. In areas A, D and E, each area had received a uniform management. Each area was divided into six sub-areas, from each of which 20 cores were taken from 0 to 15 cm depth. Cores from each sub-strip or sub-area were pooled and passed through a 3 mm sieve prior to use. Soil samples were analysed for a variety of biochemical and biological parameters.

2.3. Biochemical analyses

Total organic matter C and N were determined using an automated C/N analyser (CN-2000, Leco Corporation, Michigan, USA). LFOM was separated using a 1.7 g cm^{-3} solution of NaI according to Strickland and Sollins (1987), and its C and N content determined using the C/N analyser. Water-soluble carbohydrates (WS-Carb) were extracted by incubation of soil in a boiling water bath for 16 h (Brink et al., 1960), and measured using a phenol–H_2SO_4 assay (Dubois et al., 1956). Soil mineral-N was extracted using 0.5 M K_2SO_4, and NH_4^+–N and NO_3^-–N measured using the indolphenol blue assay and by HPLC, respectively (Bending et al., 1998). LON was determined by subtracting initial mineral-N content from mineral-N accumulated following a 2 week incubation of

Table 1
Management regimes over the 6 years prior to sampling

Area	Rotation type	Crop sequence						
		1996	1997	1998	1999	2000	2001
A	Organic arable	Grass-red clover ley	Grass-red clover ley/ winter wheat [a]	Spring wheat [a]/ white clover	Spring wheat [a]/ white clover	Potatoes	Fallow
B	Organic vegetables	Conventional winter wheat/Grass-red clover ley	Grass-red clover ley	Grass-red clover ley	Potatoes/cabbage	Vegetables [b]	Vegetables [b]
C	Organic vegetable-cereal	Conventional winter wheat/vetch	Vetch/spring barley [a]	Clover/vegetables [b]	Spring barley [a]/clover	Potatoes/cabbage	Fallow
D	Organic ley	Grass-red clover ley	Grass-red clover ley	Grass-red clover ley	Grass-red clover ley	Grass-red clover ley	Grass-red clover ley
E	Conventional cereal	Conventional cereals	Conventional cereals	Conventional cereals	Conventional cereals	Conventional cereals	Conventional cereals

[a] Undersown with white clover.
[b] Onion, carrot, leek.

200 g portions of soil at 15 °C in an aerobic incubation chamber (Bending et al., 2000). DON was determined by subtracting mineral-N from the total N content of 0.5 M K_2SO_4 extracts, as determined by alkaline persulphate oxidation (Cabrera and Beare, 1993).

2.4. Microbial analyses

For the biological analyses, 135 g samples of soil were moistened to 60% water holding capacity and incubated at 15 °C for 14 days as described above. Microbial biomass-N was measured using the chloroform fumigation-extraction technique (Joergensen and Brookes, 1990), followed by alkaline persulphate oxidation for determination of total N. Microbial biomass-C was derived from biomass-N using the equation 'biomass-C = 21 × N released by fumigation' (Amato and Ladd, 1988). Microbial basal respiration was determined by measuring CO_2 evolution from 20 g portions of soil incubated at 25 °C for an hour, using an infra red gas analyser (ADC, Hoddesdon, UK). Microbial ATP was extracted in 0.1 M Tris–EDTA buffer (pH 7.8) and ATP measured using an Enliten ATP assay kit (Promega, Southampton, UK).

Arbuscular mycorrhizal fungus (AMF) colonization potential was measured using an *Allium cepa* (onion) bioassay. Onion seedlings (two per pot) were grown in 200 g portions of soil (moistened to 60% WHC) under controlled glasshouse conditions (max/min temperatures 25 and 15 °C, respectively) for 14 weeks. Two pots were set-up for each soil sample. At harvest, roots were removed, washed and stained in aniline blue according to Grace and Stribley (1991). The % root length of each seedling colonized by AMF was determined by measuring the length of 20 × 1 cm root lengths showing evidence of AMF mycelium, arbuscules or spores.

Microbial community metabolism and metabolic diversity were determined by enzyme analysis and by measuring metabolism of the Biolog culturable microbial community. The activities of eight key enzymes involved in soil C, N, P and S dynamics were determined using a microplate fluorimetric assay (Marx et al., 2001). The metabolic profile of microbes culturable in Biolog GN microplates was determined according to Bending et al. (2000). For the enzyme and Biolog analyses, community level physiological profiles (CLPPs) were determined using canonical variate analysis (CVA). For the enzyme analysis, four samples were chosen randomly from each of areas A, D and E, and 26 samples were chosen randomly from across areas B and C. In the case of the Biolog analysis, within areas B and C, soil from sub-strips from within each strip were pooled, so that a total of six samples were analysed from each area, together with six from each of areas A, D and E. For enzyme and Biolog data, Shannon's diversity index was determined according to Zak et al. (1994).

Table 2
Biochemical quality in areas under contrasting management

Area	Total soil organic-C (mg g^{-1})	Total soil organic-N (mg g^{-1})	LFOM-C (μg g^{-1})	LFOM-N (μg g^{-1})	Mineral-N (μg g^{-1})	Labile organic-N (μg g^{-1})	Dissolved organic-N (μg g^{-1})	WS-Carb (μg g^{-1})
A	12.26^{a}	0.99^{a}	1087^{a}	42.8^{a}	7.91^{a}	6.71^{a}	7.42^{a}	5.07^{ab}
B	10.97^{ab}	0.88^{ab}	581^{b}	18.4^{b}	7.56^{a}	4.36^{b}	2.19^{b}	4.78^{ab}
C	9.85^{b}	0.78^{b}	680^{b}	25.1^{c}	8.60^{a}	5.15^{ab}	6.26^{a}	4.44^{a}
D	10.74^{ab}	0.88^{ab}	710^{b}	18.5^{b}	8.36^{a}	6.33^{ab}	6.52^{a}	5.58^{b}
E	11.47^{ab}	0.79^{b}	684^{b}	20.2^{bc}	11.57^{b}	6.17^{ab}	6.14^{a}	5.01^{ab}
LSD ($P = 0.05$)	2.28	0.17	185	5.8	1.52	2.14	2.7	1.14
	***	***	***	***	***	*	***	*

Significance of main effects (***, $P < 0.001$; **, $P < 0.01$; *, $P < 0.05$). Areas which have different letters are significantly different ($P < 0.05$). All parameters reflect amount per g^{-1} dw of soil.

2.5. Analytical design and statistical analysis

The program GENSTAT (Version 5.3, Lawes Agricultural Trust, Rothamsted Experimental Station) was used to determine significance of differences between the areas, and to perform the CVA analysis.

3. Results

3.1. Biochemical analyses

There were significant differences between the areas for all of the biochemical quality parameters (Table 2). The only significant differences in SOM C and N content were between areas A and C. In the case of LFOM C and N, area A had higher contents than all of the other areas. Mineral-N content was higher in area E than the other areas. DON was lower in area B relative to the other areas, while the only significant difference in LON was between areas B and A. WS-Carb was higher in area D relative to area C.

3.2. Biological analyses

There were significant differences between the areas with respect to biomass-N, ATP, chitin and the ATP and respiration: biomass ratios, but not microbial respiration (Table 3). Biomass-N was higher in area E than the other areas except A. ATP was lower in area E relative to the other areas except B. Chitin was higher in area D relative to the other areas except A. Respiration: biomass-C was higher in areas B and C relative to the other areas. ATP: biomass-C was higher in area C relative to the other areas. Management had a significant effect on AMF colonization potential (Table 4). Although there were no significant differences in AMF root colonization potential between the organic areas, AMF inoculum potential was very low in area E, with the % of the onion test crop root length colonized representing less than 1% of that colonized in area A.

There were significant differences between the areas in the activities of *N*-acetyl-β glucosaminidase, acid phosphatase, and leucine peptidase (Table 5). For *N*-acetyl-β glucosaminidase and acid phosphatase, activities in area A were higher than in the other areas except D. For leucine peptidase, activity was lower in area C than the other areas.

Both Biolog and enzyme derived metabolic diversity showed significant differences between the areas (Table 6). In the case of Biolog data, Shannon's diversity index was lower in area E relative to the other areas, and higher in area B relative to all areas except C. There were no differences between areas A, C and D. Since all enzymes were found in all samples, diversity recorded in the enzyme analysis reflects only the 'evenness' or distribution of enzyme activity. Enzyme diversity was higher in area E relative to the other areas, while diversity in area B was higher than areas A, C and D, which were not different from each other.

Table 3
Microbial biomass characteristics in areas under contrasting management

Area	Biomass-N (μg g^{-1} soil)	Basal respiration (μl CO_2 g^{-1} h^{-1})	Log ATP (ng g^{-1} soil)	Chitin (μg g^{-1} soil)	Respiration: biomass-C	ATP: biomass-C
A	$21.3^{a,c}$	91.6^{a}	3.27^{a}	11.62^{ac}	0.81^{a}	0.36^{a}
B	16.7^{ab}	77.8^{a}	2.88^{ab}	7.85^{b}	2.22^{b}	0.53^{ab}
C	13.0^{b}	96.6^{a}	3.24^{a}	8.97^{b}	4.14^{c}	1.06^{b}
D	14.8^{ab}	89.9^{a}	3.20^{a}	12.18^{c}	0.98^{a}	0.41^{a}
E	25.4^{c}	98.2^{a}	2.05^{b}	9.53^{ab}	0.62^{a}	0.06^{a}
LSD ($P = 0.05$)	7.8	48.4	0.88	2.2	0.95	0.54
	***	NS	*	***	***	*

Significance of main effects (***, $P < 0.001$; **, $P < 0.01$; *, $P < 0.05$; NS, not significant). Areas which have different letters are significantly different ($P < 0.05$). Parameters reflect amount per g^{-1} dw of soil.

Table 4
Arbuscular mycorrhiza inoculum potential in areas under contrasting management

Area	% root length colonized by AMF
A	18.9 (25.6)[a]
B	12.9 (19.0)[a]
C	16.7 (22.5)[a]
D	21.4 (26.2)[a]
E	0.2 (1.7)[b]
LSD ($P = 0.05$)	(10.4)
	***

Significance of main effect (***, $P < 0.001$). Areas which have different letters are significantly different ($P < 0.05$). Figures in brackets represent angular transformed data, to which LSD and ANOVA relate.

CVA of the Biolog metabolism data showed that CLPP of areas A, C and D were similar (Fig. 1). However, CLPP in area B and E were clearly separated from the other areas, and from each other. For the enzyme data, CLPP of areas A, B, C and D were clustered together, although there were significant differences between area C and areas B and D (Fig. 2). However, CLPP of area E soil was clearly separated from the other areas.

4. Discussion

All of the biochemical quality parameters showed differences between the areas. However, the precise relationships between the areas varied between the different parameters. This could reflect the varied origins of the different parameters, and the contrasting effects of management on each parameter. There were few consistent differences between the organic rotations and the grassland or conventional cereal areas.

LFOM and DON were the only biochemical parameters which highlighted clear differences between one area and all of the others. In the case of LFOM C and N, amounts were over 50 and 70% higher in area A relative to the other areas. LFOM primarily represents partially degraded plant litter inputs, together with microbial and faunal debris/tissues (Golchin et al., 1994). LFOM has a high C and N content relative to the bulk SOM, and is considered a moderately labile OM pool, with amounts determining patterns of N mineralization, making it a valuable indicator of soil fertility (Janzen et al., 1992; Sierra, 1996).

Amounts of crop residue inputs which accumulate as LFOM depend on the quality of the input, with those possessing high lignocellulose contents favouring LFOM formation (Bending et al., 1998). Changes to LFOM have been shown to occur within 3 years of the imposition of changes in management (Liang et al., 1998), and to vary according to the phase of a 6-year rotation (Janzen et al., 1992), with changes controlled by the type of material incorporated as well as the amount. In addition to fertility-building crops, area A received primarily low quality cereal residues over the 6 years following conversion, in contrast to the other organic areas, which had higher quality vegetable or grass inputs. This could have contributed to increased quantities of LFOM C and N in area A relative to the other organic areas (Bending et al., 1998). However, the conventionally managed area E had cereals over the same period, yet also had a lower LFOM content than area A. Differences in management of the cereal crops, including the diversity of residues incorporated, tillage, fertilizer regimes and undersowing could have contributed to increased stabilisation of cereal residues in the organic area.

DON originates from newly incorporated organic matter as well as humified OM and the plant rhizosphere (Kalbitz et al., 2000). Many environmental properties affect DON dynamics, and the pool can show seasonal fluctuation reflecting the influence of temperature and moisture content on formation and degradation of DON. However, the size of the DON pool is considered to be more stable than that of mineral-N (Murphy et al., 2000). In our study, DON was a similar size to the soil mineral-N pool, and was highly correlated with LON ($r = 0.73$, $P < 0.001$), which could indicate that DON was a key source of LON. The amount of dissolved organic matter is influenced by the nature of OM inputs to soil, and Lundquist et al. (1999) found that organic

Table 5
Soil enzyme activities in areas under contrasting management

Area	Enzyme activity (nmol MUB/AMC min^{-1} g^{-1} dw soil)							
	cbio	gal	nag	glu	aph	sul	xyl	lep
A	3.27[a]	2.84[a]	5.00[a]	12.75[a]	27.2[a]	1.44[a]	2.54[a]	3.30[a]
B	3.11[a]	2.29[a]	3.79[b]	11.21[a]	19.89[bc]	1.16[a]	2.07[a]	4.09[b]
C	3.11[a]	2.2[a]	4.11[b]	10.03[a]	21.70[b]	1.22[a]	2.16[a]	2.70[c]
D	2.82[a]	2.4[a]	4.27[ab]	12.23[a]	23.56[ab]	1.44[a]	2.53[a]	3.64[ab]
E	3.23[a]	2.27[a]	4.02[b]	10.93[a]	15.89[c]	1.19[a]	2.11[a]	3.73[ab]
LSD ($P = 0.05$)	0.63	0.67	0.76	3.00	4.51	0.30	0.52	0.60
	NS	NS	***	NS	***	NS	NS	***

Significance of main effect (***, $P < 0.001$; NS, not significant). Areas which have different letters are significantly different ($P < 0.05$). MUB, 4-methylumbeliferone; AMC, 7-amino-4-methyl coumarin; cbio, Cellobiohydrolase; gal, Galactosidase; nag, *N*-acetyl-β glucosaminidase; glu, β-glucosidase; aph, Acid phosphatase; sul, Sulphatase; xyl, Xylosidase; lep, Leucine peptidase.

Table 6
Metabolic diversity in areas under contrasting management

Area	Shannon's diversity index	
	Biolog data	Enzyme data
A	4.19[a]	1.60[a]
B	4.27[b]	1.67[b]
C	4.24[ab]	1.62[a]
D	4.20[a]	1.62[a]
E	4.06[c]	1.74[c]
LSD ($P = 0.05$)	0.06	0.04
	***	***

Significance of main effects (***, $P < 0.001$). All enzymes were detected in all samples, so that diversity reflects only evenness of enzyme activity.

management increased dissolved organic C content. However, in our study, area B, which received an organic vegetable rotation, had significantly lower amounts of DON than the other areas. This area also had the lowest amounts of LON and mineral-N, which could be indicative of N limitation, one of the key factors limiting productivity in organic farming, which can arise following growth of high-N demanding organic vegetable crops (Watson et al., 2002).

Area E had a larger biomass content and less ATP than most of the organic areas. However, there were few differences between the organic areas with respect to these properties. Other studies have found higher biomass-N contents in soil under long-term organic relative to conventional management (Lundquist et al., 1999). However, biomass-N can be readily affected by a range of environmental factors, and can fluctuate widely over the course of the year (Rice et al., 1996). Since biomass reflects the populations of highly diverse microbial groups, it is difficult to interpret the implications of changes or differences in biomass-N.

There were clear differences in the ratio of respiration: biomass (the metabolic quotient (qCO_2)) between

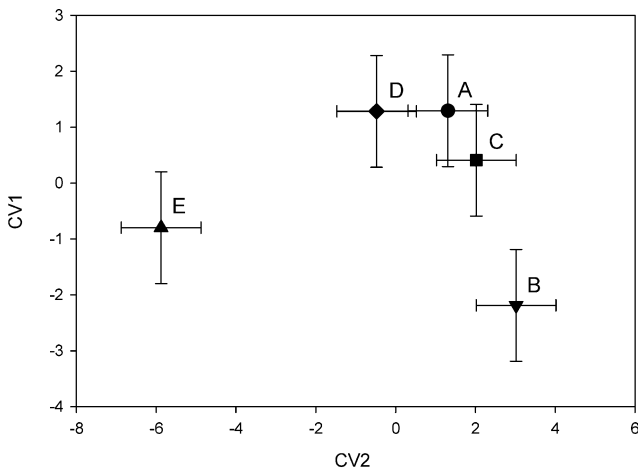


Fig. 1. Canonical variate analysis ordination plot of community level physiological profile for Biolog analysis. CV1 and CV2 accounted for 74.9 and 13.4% of the variability, respectively. Bars represent 95% confidence limits (●, area A; ▼, area B; ■, area C; ◆, area D; ▲, area E).

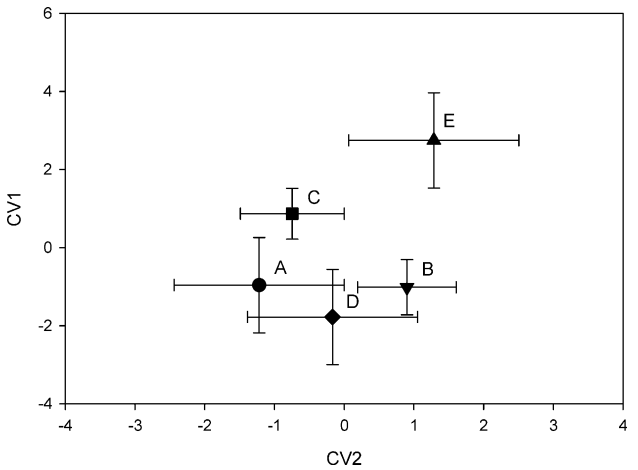


Fig. 2. Canonical variate analysis ordination plot of community level physiological profile for enzyme analysis. CV1 and CV2 accounted for 59.5 and 25.9% of the variability, respectively. Bars represent 95% confidence limits (●, area A; ▼, area B; ■, area C; ◆, area D; ▲, area E).

the organic vegetable rotations (areas B and C) and the other areas. However, there was no difference in qCO_2 between the conventional area E and areas A and D. qCO_2 has often been used to assess the physiological status of the soil community. Stress can reduce qCO_2 (e.g. Chander and Brookes, 1991) an effect attributed to reduced efficiency of conversion of substrate to biomass-C, or a shift in the structure of microbial communities between R strategists, with high growth rates and low yields of biomass, and K strategists, which have constant population sizes and higher biomass yield efficiencies (Insam et al., 1996).

Change in soil management can result in change to qCO_2. Anderson and Domsch (1990) showed that crop rotation favoured lower qCO_2 relative to monocultures while Lundquist et al. (1999) found higher qCO_2 in organic relative to conventional soil. Organic matter additions can also result in increased qCO_2 (Ocio and Brookes, 1990). Further, Wardle and Ghani (1995) suggested that the effect of fertiliser and manure applications on qCO_2 depends on the nutrient status of the soil, with applications enhancing qCO_2 in non-nutrient stressed situations, with the opposite true under nutrient stress. Wardle and Ghani (1995) suggested that the difficulty in ascribing differences in qCO_2 to disturbance and stress limit the usefulness of qCO_2 as a diagnostic indicator of soil quality. However, it clearly does have potential when used in conjunction with other biochemical and microbial analyses.

There were clear differences between the areas in the colonization potential of AMF. While there were no differences between the organically managed areas, area E had very low AMF colonization potential. Communities of AMF are highly influenced by management, and may be reduced by mineral fertilizer application, cultivation and pesticides (Kurle and Pfleger, 1994). AMF communities are diverse, with great differences between species and strains in habitat and functional interactions with their host.

These characteristics, together with the obligate symbiotic nature of AMF, and susceptibility to perturbation make AMF important potential indicators of soil fertility in sustainable agricultural systems. Mader et al. (2002) reported less inoculum of AMF in conventional relative to organic systems. Further, diversity of AMF communities has been shown to be substantially reduced in conventional relative to semi-natural habitats (Helgason et al., 1998).

There were differences in activities of *N*-acetyl-β-glucosaminidase, acid phosphatase and leucine peptidase across the areas, although the differences were not consistent, with *N*-acetyl-β-glucosamine and acid phosphatase highest in area A relative to all the other areas with the exception of area D, and leucine peptidase highest in area B relative to most other areas. Correlation analysis revealed that with the exception of a weak relationship with β-glucosidase, activity of leucine peptidase was not correlated with the other enzymes, although activities of all the other enzymes were interrelated (data not shown). These results indicate that factors influencing leucine peptidase activity are different to those controlling activities of the other enzymes. Soil enzyme activities control rates of soil nutrient cycling processes, and could be valuable indicators of soil functional diversity (Bending et al., 2002). Our data suggests that the enzymes tested vary in their sensitivity to management, and that there could be scope to use a limited number of soil enzymes to provide information on functional diversity.

CVA of enzyme and Biolog data revealed differences between the areas. Although the precise separation of the areas was different, both methods clustered together areas A, C and D, with area B separated from these areas in the Biolog but not the enzyme analysis. Both analyses separated area E from the other areas. The separation of area E from the other areas was also apparent from the metabolic diversity data. While there were no clear differences in diversity between areas A, B, C and D, area E was clearly different from all the other areas, with lower diversity recorded in the Biolog plates. In the case of enzyme data, all the enzymes were present in all areas, so that the diversity index reflects evenness or distribution of activity across the enzyme types. The results indicated that there was greater evenness in area E relative to the other areas, which with the exception of area B, were similar to each other.

Metabolism in Biolog plates reflects potential of the culturable portion of the microbial community to respond to substrates, while enzyme analyses reflect the status of microbial metabolism in situ. However, our results indicate that enzyme and Biolog analyses gave broad agreement when comparing metabolism and metabolic diversity across the areas. Further, Bending et al. (2002) showed that Biolog and enzyme analyses gave similar results when considering the impacts of crop residue inputs on the metabolism and metabolic diversity of soil communities. The conventionally managed area E was consistently separated from the other areas by the metabolism analyses. Similarly, Mader et al. (2002) found that Shannon diversity index in Biolog GN plates was greater in organic relative to conventionally managed systems, and that there were also differences in activities of soil enzymes. Using the same field plots described in the current study, Bending et al. (2000) showed that Biolog metabolism and diversity diverged in field plots exposed to contrasting crop rotations after 16 months or less, with the changes occurring before changes to labile OM fractions were apparent, indicating the technique could be a useful early indicator of change.

The quality of an agricultural soil is a measure of its capacity to sustain crop productivity while preserving environmental quality. Glover et al. (2000) rated soil characteristics contributing to soil quality according to their positive or negative contribution to four soil functions, involving accommodation and movement of water, resistance to degradation and capacity to sustain crop growth and productivity. The quality characteristics were rated as 1. 'More is better', in which higher levels are beneficial 2. 'Less is better', in which lower levels are beneficial, or 3. 'Optimum', in which increasing amounts have a benefit until an optimal point is reached, after which further increases have a negative effect.

According to Glover et al. (2000), organic matter and biomass reflect 'more is better' properties, increases of which would be associated with improved soil quality. Microbial metabolic diversity may reflect the range of substrates metabolised by a community and its resistance to stress while AMF are key contributors to plant nutrient uptake in low input situations. Metabolic diversity and AMF inoculum potential also therefore reflect 'more is better' properties. The differences in biochemical and microbial properties between the treatments in our study indicate that the organic management practices imposed had improved soil quality relative to the conventional site. However, the implications of the size of the change in soil quality for crop productivity and the environment are not clear.

5. Conclusions

Overall, our results demonstrate that biochemical and biological parameters can provide contrasting indications of soil quality. While the biochemical parameters highlighted differences between the areas, there was no consistent separation of the different areas, and no clear differences in any of the parameters tested between the organic and conventional areas. However, the microbial analyses generally highlighted differences in the size, structure and functioning of the microbial communities between conventionally managed and organic areas. The results indicate that microbial parameters could be more effective and consistent indicators of management induced changes to soil quality than biochemical parameters, and highlight the need to consider a wide variety of both biochemical and microbial analyses when comparing the impacts of management on soil quality.

Acknowledgements

We thank the Department for Environment, Food and Rural Affairs for funding, Lorna Jackson for help with sampling and Dr Julie Jones for statistical analysis and advice.

References

Amato, M., Ladd, J.N., 1988. Assay for microbial biomass based on ninhydrin-reactive nitrogen in extracts of fumigated soils. Soil Biology & Biochemistry 20, 107–114.

Anderson, T.H., Domsch, K.H., 1990. Application of eco-physiological quotients (qCO_2 and qD) on microbial biomasses from soils of different cropping histories. Soil Biology & Biochemistry 22, 251–255.

Bending, G.D., Turner, M.K., Burns, I.G., 1998. Fate of nitrogen from crop residues as affected by biochemical quality and the microbial biomass. Soil Biology & Biochemistry 30, 2055–2065.

Bending, G.D., Putland, C., Rayns, F., 2000. Changes in microbial community metabolism and labile organic matter fractions as early indicators of the impact of management on soil biological quality. Biology and Fertility of Soils 31, 78–84.

Bending, G.D., Turner, M.K., Jones, J.E., 2002. Interactions between crop residue and soil organic matter quality and the functional diversity of soil microbial communities. Soil Biology & Biochemistry 34, 1073–1082.

Biederbeck, V.O., Janzen, H.H., Campbell, C.A., Zentner, R.P., 1994. Labile organic matter as influenced by cropping practices in an arid environment. Soil Biology & Biochemistry 26, 1647–1656.

Bonde, T.A., Rosswall, T., 1987. Seasonal variation of potentially mineralizable nitrogen in four cropping systems. Soil Science Society of America Journal 51, 1508–1514.

Brink, R.H., Dubach, P., Lynch, D.L., 1960. Measurement of carbohydrates in soil hydrolyzates with anthrone. Soil Science 89, 157–166.

Cabrera, M.L., Beare, M.H., 1993. Alkaline persulphate oxidation for determining total nitrogen in microbial biomass extracts. Soil Science Society of America Journal 57, 1007–1012.

Chander, K., Brookes, P.C., 1991. Microbial biomass dynamics during the decomposition of glucose and maize in metal contaminated and non-contaminated soils. Soil Biology & Biochemistry 23, 917–925.

Chang, Y.J., Hussain, A.K.M.A., Stephen, J.R., Mullen, M.D., White, D.C., Peacock, A., 2001. Impact of herbicides on the abundance and structure of indigenous beta-subgroup ammonia-oxidizer communities in soil microcosms. Environmental Toxicology and Chemistry 20, 2462–2468.

Dubois, M., Gilles, K.A., Hamilton, J.K., Hofman, G., Smith, F., 1956. Colorimetric method for the determination of sugars. Analytical Chemistry 28, 350–355.

Glover, J.D., Reganold, J.P., Andrews, P.K., 2000. Systematic method for rating soil quality of conventional, organic, and integrated apple orchards in Washington state. Agriculture Ecosystems and Environment 80, 29–45.

Golchin, A., Oades, J.M., Skjemstad, J.O., Clarke, P., 1994. Study of free and occluded particulate organic matter in soils by solid state ^{13}C CP/MAS NMR spectroscopy and scanning electron microscope. Australian Journal of Soil Research 32, 285–309.

Grace, C., Stribley, D.P., 1991. A safer procedure for routine staining of vesicular-arbuscular mycorrhizal fungi. Mycological Research 95, 1160–1162.

Helgason, T., Daniell, T.J., Husband, R., Fitter, A.H., Young, J.P.W., 1998. Ploughing up the wood-wide web? Nature 394, 431.

Insam, H., Hutchinson, T.C., Reber, H.H., 1996. Effects of heavy metal stress on the metabolic quotient of the soil microflora. Soil Biology & Biochemistry 28, 691–694.

Janzen, H.H., Campbell, C.A., Brandt, S.A., Lafond, G.P., Townley-Smith, L., 1992. Light fraction organic matter in soils from long term crop sequences. Soil Science Society of America Journal 56, 1799–1806.

Joergensen, R.G., Brookes, P.C., 1990. Ninhydrin reactive measurements of microbial biomass in 0.5 M K_2SO_4 soil extracts. Soil Biology & Biochemistry 22, 1023–1027.

Kalbitz, K., Solinger, S., Park, J.H., Michalzik, B., Matzner, E., 2000. Controls on the dynamics of dissolved organic matter in soils: a review. Soil Science 165, 277–304.

Kurle, J.E., Pfleger, F.L., 1994. The effects of cultural practices and pesticides on VAM fungi. In: Pfleger, F.L., Linderman, R.G. (Eds.), Mycorrhizae and Plant Health. APS Press, St Paul, Minnesota, USA, pp. 101–131.

Liang, B.C., MacKenzie, A.F., Schnitzer, M., Monreal, C.M., Voroney, P.R., Beyaert, R.P., 1998. Management-induced change in labile soil organic matter under continuous corn in eastern Canada. Biology and Fertility of Soils 26, 88–94.

Lundquist, E.J., Jackson, L.E., Scow, K.M., Hsu, C., 1999. Changes in microbial biomass and community composition, and soil carbon and nitrogen pools after incorporation of rye into three California agricultural soils. Soil Biology & Biochemistry 31, 221–236.

Mader, P., Fliessbach, A., Dubois, D., Gunst, L., Fried, P., Niggli, U., 2002. Soil fertility and biodiversity in organic farming. Science 296, 1694–1697.

Marx, M.C., Wood, M., Jarvis, S.C., 2001. A microplate fluorimetric assay for the study of enzyme diversity in soils. Soil Biology & Biochemistry 33, 1633–1640.

Murphy, D.V., Macdonald, A.J., Stockdale, E.A., Goulding, K.W.T., Fortune, S., Gaunt, J.L., Poulton, P.R., Wakefield, J.A., Webster, C.P., Wilmer, W.S., 2000. Soluble organic nitrogen in agricultural soils. Biology and Fertility of Soils 30, 374–387.

Oades, J.M., 1984. Soil organic matter and structural stability: mechanisms and implications for management. Plant and Soil 76, 319–337.

Ocio, J.A., Brookes, P.C., 1990. An evaluation of methods for measuring the microbial biomass in soils following recent additions of wheat straw and the characterization of the biomass that develops. Soil Biology & Biochemistry 22, 685–694.

Reganold, J.P., Glover, J.D., Andrews, P.K., Hinman, H.R., 2001. Sustainability of three apple production systems. Nature 410, 926–930.

Rice, C.W., Moorman, T.B., Beare, M., 1996. Role of microbial biomass carbon and nitrogen in soil quality. In: Doran, J.W., Jones, A.J. (Eds.), Methods for Assessing Soil Quality. SSSA Special Publication 49. Soil Science Society of America Inc., Wisconsin, USA, pp. 203–215.

Sierra, J., 1996. Nitrogen mineralization and its error of estimation under field conditions related to the light fraction soil organic matter. Australian Journal of Soil Research 34, 755–767.

Strickland, T.C., Sollins, P., 1987. Improved method for separating light- and heavy-fraction organic material from soil. Soil Science Society of America Journal 51, 1390–1393.

UKROFS, 2001. UKROFS Standards for Organic Agriculture. Department for Environment Food and Rural Affairs, London.

Wardle, D.A., Ghani, A., 1995. A critique of the microbial metabolic quotient (qCO_2) as a bioindicator of disturbance and ecosystem development. Soil Biology & Biochemistry 27, 1601–1610.

Watson, C.A., Atkinson, D., Gosling, P., Jackson, L.R., Rayns, F.W., 2002. Managing soil fertility in organic farming systems. Soil Use and Management 18, 239–247.

Whitfield, W.AD., 1974. The soils of the National Vegetable research Station, Wellesbourne. Report of the National Vegetable Research Station for 1973, pp. 21-30.

Zak, J.C., Willig, M.R., Moorhead, D.L., Wildman, H.G., 1994. Functional diversity of microbial communities: a quantitative approach. Soil Biology & Biochemistry 26, 1101–1108.