Are soil biological properties and microbial community structure altered by organic farm management?

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Abstract

Environmental conditions and farm management practices have a considerable impact on soil biota, affecting nutrient cycling processes and ecosystem functioning. Understanding how management practices influence soil fertility and agricultural productivity is essential to improve the sustainability of agroecosystems. The effect of farming history on microbial soil properties was assessed by analysing soil samples from two organic and conventionally managed sites. $C_{\text{mic}}$ and $N_{\text{mic}}$, enzyme activities, bacterial community composition (PCR-DGGE) and total numbers of fungi and bacteria (soil dilution plating) were determined. Results suggested that organic farming practices did not have a clear positive effect on soil microbial biomass and activity; distinct differences in bacterial community composition were detected by PCR-DGGE but not by soil dilution plating. Findings indicate that practices commonly associated with conventional farming (application of mineral fertilisers or pesticides) have a less pronounced effect on the soil microbial community than other management techniques (e.g. manure application and crop rotation).

Introduction

Soil biota plays an important role in maintaining soil fertility and productivity and improving the functioning of the soil ecosystem. Studying the response of the microbial community to agricultural disturbances is vital to our understanding on how management practices contribute to sustaining fertility and productivity to improve soil management systems (Wardle et al. 1999). The effect of different management regimes and perturbations on the soil microbial community, e.g. crop rotations, manure applications and tillage, has been studied in a wide range of soil and management systems, incl. conventional, low-input and organic farming. Most research suggests that organic practices have a positive, stimulating influence on the soil microbial community by increasing microbial biomass, enhancing diversity and improving soil functions like nutrient cycling (e.g. Watson et al. 2002). In comparison, there is little evidence of negative effects of mineral fertiliser and pesticide usage on soil organic matter, microbial diversity and activity (Fraser et al. 1988). This suggests that recognized beneficial management practices (e.g. green manuring, crop rotations, conservation tillage) have a bigger impact on the soil microbial community than the land-use system itself.

Materials and methods

Adjacent organic and conventionally managed sites of the same soil type (Udic Ustochrept, USDA) with similar fertility levels were chosen within the cropping farm at Lincoln University, New Zealand (43°38’S; 172°27’E) to compare soils with differing management histories with regard to soil biological properties and microbial community composition, and to identify fungal species that are indicative of the management system. The sites had been farmed under contrasting organic (ORG) and conventional (CON) management systems for 26 and over 100 years, respectively. ORG, previously been under a low-input 6-year rotation, was under a mixed herb-ley for 3 years at the time of sampling. The site had never received fertiliser, compost or manure, had not been grazed

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or subjected to inversion ploughing. CON had been commercially managed under an 8-year crop rotation and had been under pasture for 2 years at the time of sampling. During the rotation, residues were incorporated to a depth of 15 cm by ploughing. During the 8-year rotation, a total of 70 kg N and 16 kg P were applied per ha and yr. Top soil samples (0-15 cm) were collected in January, March and June 2002, sieved (4 mm) and stored at 4°C. All analyses were carried out in triplicate: microbial biomass C (C_{mic}) and N (N_{mic}) (Sparling and West 1988), arginine deaminase activity (Alef and Kleiner 1987) (ADA), fluorescein diacetate hydrolysis (Adam and Duncan 2001) (FDA), total C and N (C_{tot}, N_{tot}). PCR-DGGE was performed on 16S rDNA fragments of triplicate DNA extracts using eubacterial primers F984GC and R1378; thermal cycling conditions were as described by Heuer et al. (1997). From each soil sample, spread plates were prepared in triplicate on four different media: Czapek Dox agar (CDA); Nutrient agar (NA); Trichoderma selective medium (TSM); King’s medium B (KB). After incubation, cfu g⁻¹ dry soil were estimated for bacteria and fungi. Selected fungal colonies were subcultured and identified. All numerical data were analysed by general linear model analysis of variance using GenStat on total or log_{10} transformed values where appropriate. Samples were considered significantly different when p<0.05 and least significant differences (LSD_{0.05}) were calculated.

Table 1. Mean values of three sampling dates in 2002 and levels of significance for soil properties in ORG and CON topsoil samples (0-15 cm). ***, p<0.001; **, p<0.01; NS, not significant.

<table>
<thead>
<tr>
<th>Soil property</th>
<th>ORG</th>
<th>CON</th>
<th>Significance</th>
</tr>
</thead>
<tbody>
<tr>
<td>C_{mic} (µg g⁻¹)</td>
<td>494</td>
<td>596</td>
<td>***</td>
</tr>
<tr>
<td>N_{mic} (µg g⁻¹)</td>
<td>50.1</td>
<td>47.6</td>
<td>NS</td>
</tr>
<tr>
<td>ADA (µg g⁻¹ h⁻¹)</td>
<td>2.86</td>
<td>1.91</td>
<td>***</td>
</tr>
<tr>
<td>FDA (µg g⁻¹ h⁻¹)</td>
<td>115</td>
<td>123</td>
<td>NS</td>
</tr>
<tr>
<td>C_{tot} (%)</td>
<td>2.77</td>
<td>2.93</td>
<td>**</td>
</tr>
<tr>
<td>N_{tot} (%)</td>
<td>0.242</td>
<td>0.243</td>
<td>NS</td>
</tr>
</tbody>
</table>

Results

ADA was significantly higher in ORG, while C_{mic}, C_{org} and microbial quotient were significantly greater in CON at all sampling dates. FDA and N_{mic} were significantly higher in CON in April and June, respectively; however, the differences were not significant when assessing overall trends (Table 1). Seasonal variation was similar for both soils. DGGE profiles of the bacterial communities revealed similar numbers of bands in both soils, while the banding patterns were distinctly different. Significantly higher numbers of fungi were recovered from CON on CDA (p<0.001) and TSM (p=0.036), while differences for bacteria were not statistically significant. The absolute differences in microorganism numbers between the two sites were minor (e.g. fungi on CDA: 1.8x10^5 cfu g⁻¹ (ORG), 2.4x10^5 (CON)) and likely to be of little practical significance with regard to soil ecology and function.

Characterisation of selected fungal isolates did not show major differences between the two soils although seasonal variations could be observed. From both soils, the following species were isolated: *Penicillium, Cladosporium, Gliocladium, Trichoderma, Mortierella, Botrytis, Paecilomyces, Coelomycete, Fusarium, Chrysosporium, Phoma, Alternaria, and Mucor*. While *Penicillium* and *Trichoderma* were most frequently isolated, no particular fungal species occurred predominantly in one soil. The small and inconsistent numbers of isolates suggests a random pattern of occurrence.
Discussion

The results suggest that past organic management did not have a major positive effect on soil microbial biomass and activity. The higher $C_{mic}$ observed in CON samples were in accordance with our expectations, as ORG was a low-input area while CON had been grazed, cultivated and fertilised regularly. Crop rotations and fertilisation have a positive influence on the soil microbial biomass through greater return in crop residues. The overall similar levels of FDA observed for the soils in this study are most likely linked to inherent soil properties such as soil type and long-term management practices (cf. Dick 1997) that might affect chemical soil properties. The slightly higher FDA activity in CON is consistent with higher levels measured in other soils receiving mineral fertilisers and seems to be a positive response to repeated inorganic fertilisation.

Soil dilution plating proved unsuitable for identifying key species indicative of the farm management system. Despite some differences in total numbers, no bacterial or fungal species were repeatedly isolated from either soil in large numbers. These findings are inconsistent with previous studies where organic management resulted in higher bacterial counts in soils (Fraser et al. 1988). However, most positive effects on microbial numbers in organically farmed soils are due to high organic matter amendments which did not occur in this study. In our study, microbial counts correspond to soil biological properties, which showed small differences. It is likely that the lower microbial numbers in ORG and the general lack of significant differences result from the fact that the two sites were providing comparable conditions for the microbial populations due to comparable chemical and physical soil properties, similar plant cover and both being in a restorative phase. This supports the theory that microbial numbers in soils are mostly influenced by changes in the soil environment and management techniques that cause such changes (Fraser et al. 1988). While the cfu assay suggested similarly sized and structured bacterial populations in the two soils, PCR-DGGE revealed clear differences between ORG and CON indicating distinctly different eubacterial communities. In contrast, the number of bands (i.e. species richness) was similar in both profiles suggesting a comparable number of species in both soils, despite significant differences in microbial biomass. This implies differences in species evenness, which is also suggested by the different intensities of the bands. The data showed how the various methods assess different characteristics of the soil biota. Microbial community composition was affected by the longer-term management, while the fraction assessed by soil dilution plating as well as microbial biomass and activity seemed to be influenced by inherent soil properties or management practices that were similar on the two sites.

Conclusions

Management practices such as manure application or crop rotations have a greater influence on microbial biomass size, activity and community structure and outweigh mineral fertiliser and pesticide usage. Thus differences observed in organic and conventionally managed soils should not necessarily be considered system effects, but be assessed as a collection of different management techniques. FDA seems an unreliable measure of microbial activity and soil quality due to linkages with inherent soil properties and mineral N. The relationship between microbial diversity and activity is not clear-cut and key fungal species indicative of one farming system could not be identified.
Acknowledgments
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References