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Sustaining Soil Biological Functions in Organic Systems

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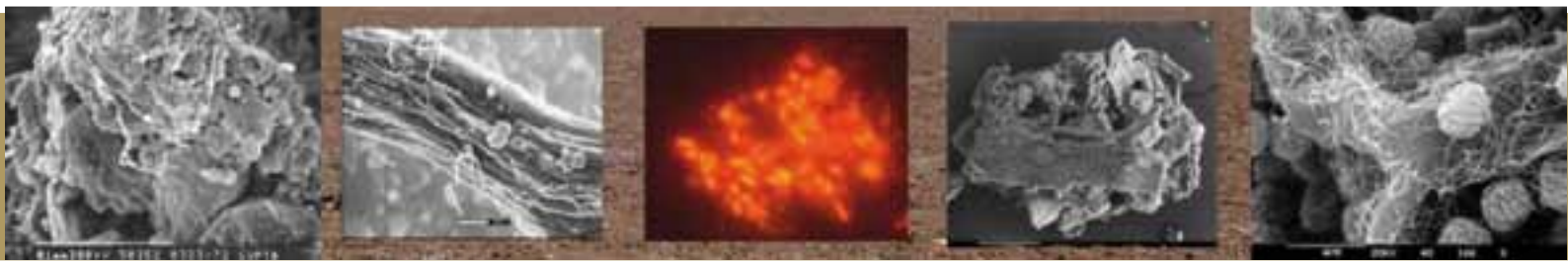

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Sustaining Soil Biological Functions in Organic Systems

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Foreword

Although the organic farming industry in Australia has a long history, broad acre organic agricultural farming is still not widely accepted as a sustainable alternative for production, nutritional and environmental benefits. There is a general perception that organic farming practices would automatically result in enhanced soil microbial diversity resulting in improved biological processes. Results from overseas research are at times contradictory and there has been limited evaluation of soil biological status or organic farming systems under Australian conditions. Since production under organic farming systems is heavily dependent upon optimum functioning of soil biota, it is essential to know the status of biological health in order to develop successful nutrient and plant health management systems.

This report provides information from one of the few comprehensive assessments of the diversity and functional capability of soil microbial communities under broad acre organic farming systems in the southern Australian agricultural region. The use of soils from farmers' fields for all the biological property assessments makes the results of this study more relevant to the field environment and in a farming system context. Results reported clearly show the importance of using a polyphasic approach to the proper assessment of soil biological health relevant to nutrient cycling, plant health and overall catabolic potential under organic farming systems and allows comparison with neighbouring conventional farms.

The project also evaluated a range of soil biological measurements for their suitability to provide relevant and consistent information on specific soil biological properties. These may assist RIRDC in prioritising future research investment relevant to organic farming industry. It will also provide some preliminary guidelines for organic farmers in terms of how to approach nutrient cycling and plant health related management aspects.

This project was funded from RIRDC core funds which are provided by the Australian Government, and by CSIRO Entomology.

This report is an addition to RIRDC's diverse range of over 2000 research publications and it forms part of our Organics Research and Development Program, which aims to facilitate the organic industry's capacity to meet rapidly increasing demand, domestically and globally.

Most of RIRDC's publications are available for viewing, free downloading or purchasing online at www.rirdc.gov.au. Purchases can also be made by phoning 1300 634 313.

Peter O'Brien
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About the Author

Dr. Gupta, the principal investigator, has more than 15 years experience in soil-microbe-plant interaction research both in field experimentation and controlled environment investigations. He brings valuable knowledge on methodology and strong scientific rigour to the project. He has been a key research member of the Mallee Sustainable Farming Project since its inception and his research through MSF-Project identified the potential for improving soil microbial functions through farming system management resulting in a number of production, economic and environmental benefits. His reviews to the GRDC Soil Biology Initiative and MLA formed the basis for many of the projects developed through these programs during the last 6 years. Dr. Gupta has also made significant contributions to producing non-scientific publications useful for farmers, educational institutions and Landcare organisations (e.g. Life in Soil and Farming systems).

Acknowledgments

Financial support for this project was provided by the RIRDC and CSIRO Entomology. The project supervisor expresses his sincere appreciation to Mr. Chris McDonough, Mr. Charlton Jeisman, Rural solutions SA), Ms. Emma Leonard (AgriKnowHow, Urania, SA) and Dr. John Kirkegaard (CSIRO Plant industry, Canberra) for their help with the identification of suitable farms and soil sampling. All the work in this project was conducted using soil samples from farmer fields in SA, Victoria and NSW. The project team extends their appreciation to all the farmers for allowing samples to be taken from their farms and time spent in discussions related to background history and other relevant details of their farming system. Mr. Marcus Hicks was the technical officer at CSIRO Entomology who was responsible for most of the laboratory analysis.

Abbreviations

MB	microbial biomass
MA	microbial activity
DGGE	denaturing gradient gel electrophoresis
AO	ammonia oxidizing microorganisms
CB	cellulolytic bacteria
CF	cellulolytic fungi
PCR	polymerase chain reaction
*amo*A	gene that encodes for ammonia monooxygenase enzyme involved in the nitrification process
*nif*H	a marker gene that encodes for nitrogenase reductase involved in the nitrogen fixation process
RON / RofN	rate of nitrification
SIR	substrate induced respiration
Min_N	N mineralization potential
Min_C	C mineralization potential

Contents

Tables

Figures

Executive Summary

What the report is about

In this scoping project, we present initial science-based information on the status of soil biological health under broad acre-organic farming systems in the southern Australian rainfed agricultural region.

The report contains quantitative information about the levels of key functional groups of soil microbiota essential for nutrient supply, disease suppression and overall soil resource quality after exposure to organic farming practices for more than 3 years and compared to a neighbouring conventional farm. Currently there is very little such information available for these systems.

Who is the report targeted at?

There is a perception that soil biodiversity under Australian organic farming systems is higher than conventional farming but there is a very limited knowledge base. In this scoping project, we obtained initial scientific information on the status of key functional groups of soil microflora and associated functions essential for nutrient management and plant health. This report provides 'science behind the belief' for the various perceived biological benefits from organic systems in broad acre agriculture using a system based approach.

This project is specifically designed for the Australian organic farming industry, in particular the broadacre farming industry. However flow-on benefits on regulators of soil biological functions may be useful for the general agricultural industry. Since most of the crop requirement for essential nutrients under organic farming has to be met from the actions of soil biological processes, a better understanding of the dynamics of soil microbiota would help manage these better and harness greater benefits. We provide the 'science behind the belief' for greater levels of biological functions in organic systems. This scoping study provides RIRDC with methodology which will be a foundation for describing or assessing soil biological status in organic farming systems and for future investment in farming system based research. As this is a one year scoping study it is unrealistic to define the magnitude of expected benefits, economic or otherwise.

Background

Soil biota regulate a number of processes in agroecosystems and maintenance of the functional biodiversity is not only critical for productivity but is also essential for maintenance of ecosystem health. Soil microbial diversity is a key to its functional capability and resilience. Unlike conventional farming systems, plant health and production in organic farming systems mainly depend on a healthy soil biota and optimum functioning of biological processes. A healthy soil biota is not only essential for sustainable crop productivity but also for maintaining ecosystem health.

Knowledge on the status of soil microbial communities and functions in Australian organic farming systems is very limited. In this scoping project, we present science-based information on the status of key functional groups of soil microflora and associated functions essential for nutrient management and plant health. A greater understanding of the soil biological health and biological capacity of organic farming systems will not only help determine their role in areas of key challenge for Australian organic agriculture (e.g. nutrient management, disease control) but also would assist in the development of best practice organic farming techniques.

Aims/objectives

The broad acre organic farming industry and RDC's aiming to develop management practices for the long-term sustainability of organic farming systems will directly benefit from this research.

Biological functions in soils are a product of the diverse group of microbial communities and these are limited by environmental and soil constraints. Long-term sustainability of crop productivity in organic farming systems, with no modern agrochemical inputs, depends upon the optimal functioning of soil microbiota communities. Specific objectives of this study were to:

- Quantify the composition and/or activity of key functional groups of soil microbiota involved in carbon and nutrient turnover and disease suppression in Australian organic farming systems.
- Determine the capacity of microbial functions in organic systems to support crop nutrient requirements, discover the disease suppression potential and identify relationships, if any, with soil physical and chemical properties.

In addition, the underlying aim was to evaluate a polyphasic (integrated) approach for its suitability for use in assessing the status of soil biological health under organic farming systems.

Methods used

We used soil samples collected from fields that have been farmed organically (with reliable records of history for at least five years) to quantify the composition and/or activity of key functional groups of soil microbial communities. A direct comparison between organic and conventional farming systems on fields does have limitations because fields are not idealised systems i.e. multifactor differences make it difficult to ascertain simple relationships. Organic and conventional systems overlap in a number of management practices, except for fertilizer and biocide use and tillage, thus making our study a system based comparison with multiple regulating factors.

Using a polyphasic approach incorporating a diverse array of DNA and traditional microbiological methods, we determined, for soils from organic farms and neighbouring conventional farms:

- the genetic and catabolic diversity of soil microflora
- population level of key functional groups
- levels of biological processes involved in N and P mineralization.

Since carbon inputs and turnover is one of the key underlying factors differing between the two systems we tried to relate the results from these systems in terms of management practices that can affect C inputs and turnover.

Results/key findings

The results arising from this research were as follows:

1. Methodology to describe soil biological status (Objective 1)
   1.1. The use of a polyphasic approach that integrated diversity and activity related measurements provided a detailed description of soil microbial communities which allowed effective differentiation of soil biological status in organic farming systems compared to that under a neighbouring conventional farming system.

2. Diversity and functional capability of soil microbial communities (Objective 2)
   2.1. The genetic diversity of soil bacteria and fungal communities under organic farming systems was significantly different to that under conventional farming systems but soil type also had a significant effect. Genetic richness of soil bacteria was generally higher in organic farm soils whereas the richness of soil fungi was variable. Soils from no-till systems exhibited greater richness of soil fungi.
   2.2. Community level physiological profiling of soil microbial communities showed significant effects of farming system, soil type and season. Catabolic potential was generally higher in red-brown earth soils and lowest in Mallee sands. The effects of the farming system in use on catabolic diversity varied with soil type and season. Catabolic potential significantly reduced from pre-sowing to in-crop sampling probably due to the lack of available carbon in soil.
   2.3. Microbial biomass (MB) C and N and microbial activity levels were generally higher in organic farming soils compared to the conventional no-till soils. Soil type had greater effect on MB levels than the farming system. In the Mallee sands, MB levels reduced significantly from pre-sowing to anthesis sampling.
   2.4. No consistent trends were observed in the populations of cellulolytic bacteria and fungi between soils from organic and conventional farming systems.
   2.5. Both populations and activity of nitrifying microorganisms were generally higher in soils from organic farming systems at pre-sowing compared to in-crop samples, but the differences didn't persist in the in-crop soil samples.
   2.6. Activity of phosphatase enzymes was lower in the organic farm soils compared to no-till soils from Loxton and Ardrossan in SA. Application of rock phosphate to the organic farm at James town resulted in higher levels of phosphatase enzymes.
   2.7. Differences in the levels of soilborne pathogen inocula between organic and conventional farming soils varied with pathogen type, e.g. *Rhizoctonia solani* AG8 inoculum was lower where as the levels of *Pythium* spp. were higher in organic farm soils compared to conventional farm soils. There were no consistent and significant differences in the disease suppression potential against Rhizoctonia bare patch disease.
   2.8. Populations of *Trichoderma* group B species were generally lower in the organic farm soils compared to conventional no-till soils.

3. Relevance of changes in soil biological properties under organic farming systems (Objective 2)
   3.1. N mineralization potential of soils from both organic and conventional farms was significantly and positively related to levels of MB and soil organic C. N mineralization potential was also positively correlated with bacterial diversity, rate of nitrification and soil respiration.
   3.2. Although soils from organic farms showed higher levels of MB and activity prior to sowing, the lack of large and persistent differences in MB and soil biological processes involved in N and P cycling suggest that nutrient availability could become a limiting factor to productivity unless improvements in biological inputs can be achieved. This relationship could not be tested in this project due to last year's drought induced reduction in grains yields.
   3.3. The presence of higher inoculum levels for some soilborne pathogens, combined with lower levels of beneficial fungi such as *Trichoderma* species, suggest that organic farming systems analysed in this study may not support high levels of biological disease suppression. Our observation of no measurable improvements to disease suppressive potential supports this hypothesis.

4. Additional findings (Objectives 1 and 2)
   4.1. Recent developments in DNA based and microbiological methods facilitate the detailed analysis of genetic and functional diversity of soil microbial communities relevant to nutrient cycling and plant health related functions.

4.2. Community level physiological profiling of microbial communities based on C-substrate utilization provided a catabolic diversity based description which helped give a better assessment of the effect of farming system, soil type and season.
4.3. There is a significant difference in the rate of nitrification per unit population of nitrifying microorganisms between pre-sowing and in-crop samples and the exact reasons for this seasonal effect are unknown.
4.4. The effect of organic farming systems on soil biological status is influenced by soil type and environmental variation. Although important differences in specific soil biological properties do exist between organic and conventional farming systems, due to the variation in soil type and environmental factors, it is be difficult to arrive at generalized universal conclusions.

Implications for stakeholders

There is a general belief in the organic industry that the practice of organic farming in broad acre agriculture will automatically improve the diversity and functional capability of soil biota. Until now it has been difficult to confirm or disagree with this belief due to the lack of information from systematic and detailed evaluation of the soil microbial communities under organic farming systems.

Results reported here clearly show that an enhanced soil microbial community and biological processes, relative to conventional systems, may not be a definitive feature of all organic systems. It is necessary to provide adequate levels of C inputs to meet the energy demand by the microbial communities in order to maintain or improve biological activities relevant to nutrient mineralization and plant health.

Under organic farming, a greater diversity of plant types (crops and weeds) in the pasture-crop rotation and the use of repeated cultivations for weed control may be promoting the build up of soilborne pathogen inocula. This suggests that regular monitoring for relevant pathogens should be done. Despite a small increase in the genetic diversity of soil bacteria, the reduction in populations of beneficial fungi such as *Trichoderma* spp. may contribute to the lack of improvements in disease suppressive potential. The increased use of cultivation in organic farming systems can cause a decline in soil organic C levels in the Mallee resulting in the loss of soil biological benefits and suggesting the need for an alternative approach that reduces the number of cultivations.

This study will also benefit policy makers. For a proper assessment of the status of soil biological health under organic farming systems, an integrated polyphasic approach involving assessment of diversity and functional capability of microbial communities should be used. Recent developments in DNA and microbiological methods facilitate detailed assessment of microbial dynamics. The inherent lower soil organic matter levels in Australian broad acre agricultural soils means it is essential to improve soil biological status under organic farming systems in order to maintain the biological processes needed for nutrient supply and plant health. The use of intensive cultivation regimes as part of organic farming systems may work against the build up of soil biological capability and organic matter levels.

Although all organic systems follow some fundamental principles, individual farms may differ in terms of management techniques making it difficult to generalise observations from one farm to another across different regions. Simple assessments of individual organisms may provide conflicting evidence about whether organic farming is enhancing soil biota community.

Recommendations

For RIRDC and other Research and Development Corporations, the main recommendation from this one year study is that there is an urgent need for future investment in a wide scale analysis of organic farming systems for their soil biological status. The belief that there is enhanced soil community on

organic farms may be only partially true. In soil types with low organic matter levels and in rainfed systems, there is an immediate need for a complete assessment of soil biological status. This is necessary for successful soil quality management and long-term sustainability of organic farming systems as part of the broad acre agricultural industry.

The role of cultivation and grazing in reducing the amounts of *Trichoderma* DNA and the lack of development of disease suppressive potential against soilborne pathogens in organic systems need urgent attention if their impact on production and sustainability of broad acre organic farming in Australia is to be addressed. Finally, future research should be a more targeted investigation of the effects of individual factors, such as tillage or soil type, on soil biological health in organic systems.

It is useful for growers to know that, contrary to popular belief, the practice of organic farming may not automatically result in increased diversity and functional capability of microbial communities. It may therefore be necessary to regularly assess key biological properties or microbial groups in order to properly harness benefits from biological activities and not mine the soil reservoir. There is a need to increase C inputs from crop residues and reduce disturbance as a (weed) management tool in order to improve the biological benefits under broad acre organic farming systems.

1. Introduction

Soil biota regulate a number of processes in agroecosystems and maintenance of the functional biodiversity is not only critical for productivity but is also essential for maintenance of ecosystem health. A number of studies worldwide have shown that management practices in agricultural systems can be modified to promote the benefits from soil biological activities without compromising productivity and ecosystem health.

It is suggested that soil microbial diversity is a key to the functional capability and resilience of the soil ecosystem, in particular its ability to respond to changing climate and rainfall. In most southern Australian agricultural soils carbon availability dictates the levels of microbial populations and associated soil biological processes (Dalal et al., 2004; and Gupta et al. 2008).

Unlike conventional farming systems, plant health and production in organic farming systems mainly depend on a healthy soil biota and optimum functioning of biological processes. A reduction in the overall C inputs in organic systems may result in reduced populations of soil microbiota and most importantly a decline in the benefits from soil biological processes. In the low fertility Australian soils, contributions from biological processes are significant, e.g. 20 to 50 % of annual crop N requirement in southern Australian soils (Roget and Gupta, 2004).

Results from the Mallee Sustainable Farming (MSF) Project demonstrated that improved microbial functions due to increased C inputs in the new farming systems in the Mallee region have resulted in:

1. increased nutrient efficiency
2. increased suppression of soil-borne disease
3. increased stability of soil aggregates and
4. reduced persistence of agrochemicals.

Results from and MSF core trial at Waikerie suggest that changes in quantity and quality of C inputs through farming systems would result in signature changes in microbial community composition (Gupta and Roget, 2006, unpublished [www.msfp.org]). Results from overseas research on the influence of organic farming systems on microbial community structure are variable (Mader et al., 2002; Widmer et al., 2006). For example, while the effects of Biodynamic and Bioorganic farming systems on microbial biomass were significant, differences in bacterial community structure between organic and conventional farming systems were weak compared to the effects of crop type (Widmer et al., 2006). Poveda et al. (2006) found limited effects of soil organisms on plant growth in organic systems but more pronounced effects of soil organisms on aphid and pathogen infection in wheat crops compared to conventional farming systems.

Cultivation is generally used as a management tool for weed control in organic farming systems and Wu et al. (2007) reported that land management practices that disturb or disrupt soil fungal communities will significantly reduce their diversity. The implication of such effects on soilborne pathogens or beneficial fungi is not known.

Currently knowledge on the status of soil microbial communities and functions in Australian organic farming systems is very limited. In this scoping project, we present information, from a system based analysis, on the status of key functional groups of soil microflora and associated functions essential for nutrient management and plant health. A greater understanding of the soil biological health and biological capacity of organic farming systems will not only help determine their role in areas of key challenge for Australian organic agriculture (e.g. nutrient management, disease control) but also would assist in the development of best practice organic farming techniques in which soil biota 'work for us' i.e. meet the needs of the growing crop.

Traditionally the effects of farming system practices on soil biological properties are evaluated using individual parameter assessments. The aim of this project was to provide 'science behind the belief' on the various perceived biological benefits from organic systems in different cropping regions using an integrated polyphasic system based approach.

2. Objectives

Biological functions in soils are a product of the diversity of microbial populations and their activity as limited by environmental and soil constraints. Crop productivity in organic farming systems, with no modern agrochemical inputs, depends upon the optimal functioning of soil microbial communities.

Our aims were to:

1. Quantify the composition and/or activity of key functional groups of soil microbiota involved in carbon and nutrient turnover and disease suppression in Australian organic farming systems.

2. Determine the capacity of microbial functions in organic systems to support crop nutrient requirements, disease suppression potential and identify relationships, if any, with soil physical and chemical properties.

In addition, the underlying aim of this one year scoping project was to evaluate the suitability of an integrated polyphasic approach to describe and assess the soil biological status in organic farming systems (Appendix 1). The general trend of a lower level of crop productivity in organic farming systems suggests reduced amounts of carbon inputs through crop residue and lower levels of biological activity, in particular in the low-fertility Southern Australian agricultural soils. However, with no modern agrichemical inputs these systems may be supporting a higher level of microbial diversity (functional diversity). In this project we acquired scientific evidence testing these hypotheses.

3. Methodology

Sites

We utilized fields that have been farmed organically, with reliable history for at least five years, to quantify the composition and/or activity of key functional groups of soil microbiota. Identification of some of the suitable farmer fields (in SA, Victoria and NSW) was done in consultation with various organic farming industry bodies such as NASAA, agronomists in State Departments of Agriculture (e.g. Mr. Chris McDonough, Mr. Charlton Jeisman, Rural solutions SA) and other researchers (John Kirkegaard, CSIRO PI, Canberra). Details of the field samples are given in the Tables 1 and 2.

Soil sampling methodology

Surface (0-10cm) soil samples were collected from paddocks that have come out of the pasture phase and undergone the fallowing operations prior to seeding an annual cereal crop. Details of farms that were sampled for laboratory analyses are given in Tables 1 and 2. Since the sampling is done on a farm paddock, and not in an experimental plot, for each farming system surface (0-10 cm) soil samples were collected from a minimum of 4 representative zones (i.e. replicates) to account for field level spatial variability. Samples were collected at 4 points (i.e. replications) on a ~150 transect.

At each point, surface soil was collected using a soil corer from 6-8 places to give a total of ~5 kg of soil. This combined sample represented one replication resulting in 4 samples per field. The procedure was repeated on a nearby (similar soil type) conventional (no-till or cultivated) farm for comparison. For ‘in-crop’ sampling, soils were collected from areas close to crop rows.

We collected samples at two times i.e. prior to sowing and ‘in-crop’ sampling at close to anthesis, with the aim of linking the biological status of the soil to functions relevant for plant growth and performance. Previous research done as part of the MSF project showed that biological measurements of microbial biomass, N supply potential, plant pathogen inoculum levels at the time of sowing reflect the nutritional and disease potential status of the soil.

The key aspect of this project is the measurement of the biological properties at times relevant to crop production and environmentally significant periods. We used an integrated approach where laboratory based measurements were complemented with ‘*intact’* soil core measurements. Surface (0-10 cm) soil samples collected from fields twice a year were transported to Adelaide laboratories for various analyses.

Information about crop yields, management practices and general farming system operations was obtained from farmers’ records and limited analysis was done within the project (funding restrictions). Crop yields during this project year were severely affected by the drought and restricted our efforts to relate results from nutrient mineralization analyses to crop nutrient uptake. We used the information on crop performances during the last 3-5 years and the management practices implemented on each paddock (cultivation, grazing etc.) to interpret the data obtained and their relevance to the overall assessment of the farming system.

Laboratory analyses

Soil samples were analysed for a combination of population and functional analyses.

1. Diversity parameters

- Metabolic profiles of microbial community (C substrate utilization profiles, Campbell et al., 2003; Widmer et al., 2006)
- Functional gene properties related to N mineralization (nitrification-*amoA*, Stephan et al., 1999) and N-fixation (*nifH*, , Rosch et al., 2003)
- Genetic diversity of soil bacteria and fungi (16S rDNA-DGGE and 18r DNA-DGGE)

Carbon substrate utilization profiles of soil microbial communities were determined using the Microresp® method modified with specific carbon substrates selected for Australian soils (Campbell et al. 2003; Gupta et al., 2007). As part of the MSF project, this method was standardized for Australian soils in our laboratory (Gupta, V.V.S.R., unpublished).

Unlike some culture based methods, the 96-well plate 'Microresp' method that was used to measure the carbon substrate utilization profile of a soil microbial community directly utilizes the whole soil samples thus allowing the response of the entire microbial community to be measured. Since the quality and quantity of C inputs regulate the diversity and overall activity of soil microbial communities in the low organic matter Australian soils, this measurement can provide very useful and meaningful information about the ability of different farming systems to support a viable microbial community.

Diversity of bacteria and fungi (DGGE) and quantification of functional communities

DGGE analysis was used to analyse diversity of bacteria and fungi population in the soils collected prior to sowing in 2007 from different farming system treatments. Subsamples of DNA extracted by SARDI-RDTS for root disease testing were used for the DGGE analyses (bacteria and fungi populations) and quantification of functional populations (ammonia oxidizing –amoA and nitrogen fixing-nifH populations).

The bacterial and fungal population diversity in above soil samples was determined through the analysis of 16S and 18S ribosomal DNA gene diversity. All rDNA samples were PCR amplified using an Eppendorf Mastercycler under conditions specific to bacteria and fungal communities. The primers used for bacteria and fungal diversity were F968-GC and R1401 (Duineveld et al., 1998) and ITS 1F-GC and ITS 2 (Gardes and Bruns, 1993; Wakelin et al., 2007), respectively. A 40-bp GC clamp (Ferris et al. 1996) was added to the 5' end of all forward primers to prevent complete strand dissociation during DGGE. PCR amplification products were initially analysed on a perpendicular DGGE polyacrylamide gel (consisting of 8% acrylamide/bis) with broad denaturing gradient range (20-80%), to determine the optimum concentrations of denaturants (urea and formamide). The final denaturant gradient gel electrophoresis was performed on a Ingeny phorU system (Ingeny International), bacterial (45-70%) and fungal (30-60%) formamide:urea denaturing gradient overlayed with a 0% stacking gel, 8% acrylamide:bis-acrylamide, run at 110V for 16 h.

It was then stained with SYBR Gold (Molecular Probes) for 30 min and rinsed in water for 20 min. and visualised with a Dark Reader light box (Clare Chemical Inc.) and photographed using an Olympus E500 SLR digital camera. Bands were picked manually as the software was unable to distinguish between bands and the dark stained background of each lane.

Dendograms for bacterial and fungal communities were constructed using unweighted bands and Ward's method for clustering.

Real-time PCR was used to quantify levels of functional genes encoding key enzymes used in the nitrogen fixation (nifH) and nitrification (amoA) processes. PCR was conducted using the Stratagene Mx3000P qPCR system with PCR primers synthesised by Geneworks Pty Ltd. Nitrogenase reductase (nifH) gene fragments were amplified using primers described by Rösch et al. (2002), and the ammonia monooxygenase (amoA) gene was amplified using primers described by Stephen et al. (1999), modified from Rotthauwe et al. (1997). Each 25 µl PCR reaction contained 1 × QuantiTect SYBR Green master mix (Qiagen Inc.), 10 mM of each primer and 4 µl of template DNA. For amplification of AmoA genes, 0.8 % BSA (Promega Inc) was also included in each reaction.

PCR amplification was initiated by a hot start incubation of 15 min at 95°C. For amplification of nifH fragments, this was followed by 40 cycles of 94°C for 45 s, 55°C for 60 s and 72°C for 45 s, with a final elongation step of 5 min at 72°C. The same protocol was used for amoA amplification, except annealing was at 60°C for 45 s. Dissociation curves were conducted at the end of real-time PCR to verify product specificity.

A standard curve was generated using serial dilutions of DNA extracted from a soil obtained from Streaky Bay (Eyre Peninsula, South Australia), that was known to contain relatively high levels of *nifH* and amoA genes. Amplification was adjusted to background fluorescence of ROX reference dye, and CT values were calculated from a software determined baseline. The CT value is the value at which the increase in amplification of DNA becomes exponential. Results were expressed either as the CT value, or as a relative quantity present in each sample; this was relative to the quantity present in DNA from the Streaky Bay sample which was, by definition, a quantity of 1 unit.

For quantification of DNA in the in-crop samples from Pinnaroo and Cootamundra, standard curves containing known copies of either the nifH or amoA genes were generated. NifH and amoA genes were amplified using genomic DNA isolated from pure cultures of *Azospirillum* and *Nitrosomonas*, respectively. PCR products were then inserted into the pGEM-T Easy vector (Promega Inc.) according to the manufacturer's instructions. Plasmid DNA, containing the inserted gene, was isolated using the Wizard® Plus SV Miniprep DNA Purification system (Promega Inc.) and quantified using a NanoDrop spectrophotometer.

The copy numbers of each gene per ng of plasmid DNA were then calculated, and tenfold serial dilutions of plasmid DNA were made for each gene. For all samples, the CT value was compared with the CT values of the standard curve, and from this the number of copies of each gene per PCR reaction was calculated.

2. Population levels of key functional groups of microorganisms

Populations of cellulolytic bacteria and fungi and nitrifying bacteria were determined using most-probable-number methods (Gupta and Roper, 1994, Weaver et al., 1994).

3. Metabolic status of microbiota (Gupta et al. 1994; Alef and Nannipieri, 1995):

Soil samples from pre-sowing and 'in crop' sampling were analysed for their levels of microbial biomass C and N, substrate induced respiration (SIR) and Potential C and N mineralization using methods described by Gupta et al. (1994) and Alef and Nannipieri (1995). Briefly, chloroform fumigation-direct extraction methods were used to measure the

amount of microbial biomass (Gupta et al., 1994a). Short term incubation methods (laboratory based) were used to measure the level of microbial activity and mineralization potentials of nitrogen (Gupta et al. 1994b). The metabolic status of microorganisms was determined using a substrate induced respiration method (standardized in our laboratory).

4. Rates of key biological processes involved in nutrient cycling

- Rate of nitrification (modified method of Bottemley et al., 2004)
- Nitrogen fixation by free-living N fixing microorganisms – Our efforts to use the 'in situ - acetylene reduction assay (Roper, 1983) to measure the N-fixing potential was not successful due to lack of sufficient rainfall and the dry soil conditions. Therefore we used the results from the DNA analysis of *nifH* populations to discuss the potential of FLN microorganisms.
- N mineralization – Nitrogen mineralization potential was measured using laboratory incubation methods with disturbed soil samples (all the soils from both sampling times) and 'intact soil cores' (three farming systems on Mallee soils near Loxton).
- Activity of phosphatases (acid and alkaline phosphatase) (Alef and Nannipieri, 1995)

Soilborne diseases are an important constraint to broadacre agriculture in Australia. We analysed the soil samples from organic and conventional farms for the inoculum levels of important soilborne pathogens through the SARDI-Root Disease Testing Service. This service utilises DNA techniques to measure the levels of specific soilborne fungal and plant parasitic nematodes. Samples were also analysed for populations of *Trichoderma* spp, a beneficial soil fungus.
(http://www.sardi.sa.gov.au:82/dhtml/ss/section.php?sectID=740&tempID=47).

Phenotype based diversity measurements, if done properly, are useful tools for studying the overall diversity of soil microorganisms, however such data must be supplemented with information on the functional capabilities of the organisms in order to make a meaningful interpretation of their significance to crop productivity and soil system health. Using current technology, detailed phenotypic based diversity measurements are expensive and time consuming. We therefore used an approach where, by measuring the functional diversity and/or actual functional measurements (e.g. nitrification, N mineralization), we can make better interpretations of changes in soil microbial properties and link them to plant essential functions. Recently developed molecular methods provide an opportunity to directly measure some of the functional gene properties (e.g. *amoA* for nitrification).

When these are combined with direct measurements of functions they provide a powerful tool to determine the contribution of soil biological processes to plant essential functions. Using the pre-sowing samples, we measured the populations of nitrifying microorganisms using culture based and DNA methods and the rate of nitrification as a measure of the function. Detailed discussion of this methodological comparison is given for the Mallee soils. Due to the limited budget allocated in this project, we were unable to make such comparisons for other processes i.e. free-living nitrogen fixation and disease suppression.

A direct comparison between organic and conventional farming systems based on farm fields does have limitations because the fields are not idealised experimental systems i.e. multifactor differences make it difficult to ascertain simple relationships. Organic and conventional systems overlap in a number of management practices, but not for fertilizer and biocide use and tillage, thus making our study a system based comparison with multiple regulating factors.

Although all organic systems may follow some fundamental principles, the nature of organic farming is such that individual farms may differ in terms of management techniques making it difficult to generalise across different regions. Since carbon inputs and turnover are key underlying differences between the two systems, we tried to relate the results from these systems in terms of management practices that can affect C inputs and turnover.

Since the project was done in direct collaboration with farmers all the results and their interpretation was made available to them through talks and distribution material. For example, results from the three Mallee farms near Loxton were presented to the three farmers in the presence of the agronomist from Rural Solutions SA and the relevance of the data to their respective farming system discussed.

Statistical analysis

All statistical analyses were done using Genstat (PC/Windows XP; Lawes Agricultural Trust, Rothamsted Experimental Station), ANOVA and regression coefficients were done as per the principals described by Snedecor and Cochran (1980). Multivariate analyses such as Principal Component Analysis (PCA) and Canonical Variate Analysis (CVA) were done using the carbon substrate utilization profile data as per details given in Harch et al. (1997).

4. Results

Sites and soil properties

Soil samples were collected from a total of 13 farm fields (6 organic farming systems, 6 no-till cropping fields and one conventional pasture-crop system) in SA, Vic and NSW. Soil, crop and management details for the different farms are given in Tables 1-3. Soil samples were collected twice during 2007; prior to sowing (8 fields in SA and Vic) and 'in crop' to coincide with anthesis (August-Sept, 2007; 11 fields, SA, Vic and NSW). Soil samples from conventional cropping systems were collected with the aim of comparing the soil biology on an organic farm to that on a conventionally cropped farm on a similar soil type and located close to the organic farm.

Details in the Tables 1 and 2 clearly show that management practices used on organic farms varied between farms; therefore generalizations across organic farms can only be made with caution. Soil type at the three farms near Loxton, SA is alkaline calcareous loamy sand with generally low organic C levels; 0.36%, 0.46% and 0.57% in soils from the organic, no-till and conventional systems, respectively. Data on soil organic C levels reflect the amount of crop residues returned to the soil and the effects of cultivations done in each of the farming system.

The organic farming system with multiple cultivations and lower amounts of crop residues resulted in lowest soil organic C level. The higher level of organic C in the conventional cultivated system compared to no-till system can be attributed to C inputs from the previous seasons pasture. It is well established that well managed pastures that produce a proper amount of dry matter (in response to rainfall received) generally result in increased soil organic C levels. During the last decade, inadequate nutrition and inappropriate herbicide use have resulted in poor pasture growth and resultant dry matter production in the southern Australian rainfed cropping region.

Soils at other farms sampled range from sandy loam (Pinaroo and Ardrossan, SA) to red brown earth (James town, SA and Cootamundra,NSW). Unlike the Mallee organic farm, pastures on other farms supported >2 t per ha of dry matter production suggesting C inputs similar to that in intensive cropping systems. Grazing or cutting for hay was common in all organic farms and pastures; stubble grazing was not practiced on all conventional farms. Stubble grazing was common on no-till farms near Pinaroo and Jamestown in SA.

Since crop residues are the main source of C for biological activity, removal of crop residues through grazing or hay baling will have implications for biological properties irrespective of the farming system. More frequent dry seasons and poor crop/pasture growth during the last 3-4 years would have also forced farmers towards heavy grazing thereby reducing the C inputs to the soil. Another distinct difference between organic farms and conventional farms is the number of cultivations, e.g. weed control in the organic system is mainly performed by cultivation where as herbicide use for weed management is a general practice in the modern conventional broad acre agricultural system.

Biological properties in Mallee soils

Microbial biomass (MB) levels in the Mallee soils ranged from 150 to 224 µg C/g in pre-sowing samples and 119 – 373 µg C/g in 'in crop' soil samples (Table 2). MB carbon accounted for 3 to 6% of soil organic C with the lowest value in 'in crop' samples from organic farms. The amount of N in soil microbial biomass is considered to reflect the N

supply potential of the soil. Microbial biomass N levels in pre-sowing samples were not different between organic and no-till soils (25.0 and 22 kg N / ha, respectively) but MB-N values were significantly reduced in the 'in-crop' organic farm samples in contrast to no-till and cultivated systems.

Soilborne pathogen levels

All the soil samples collected prior to sowing were analysed for the levels of important soilborne fungal and nematode pathogens by the SARDI-Root Disease Testing Service.

Results shown in Table 10 indicate that the levels of plant parasitic nematodes such as *Pratylenchus neglectus, P. thornei* and Cereal Cyst nematodes were either low or below detection limit in all the soils irrespective of the differences in farming systems. The level of the fungal pathogen *Gaumannomyces graminis* var. *tritici (Ggt)*, causal agent of Take-All disease was also low in all soils, although levels were slightly higher in soils under organic systems. Rhizoctonia bare patch is one of the most significant soilborne diseases affecting productivity in wheat and barley in the most of the broad acre cropping regions in southern Australia. Results in this survey showed low levels of *Rhizoctonia solani* AG8 inoculum in soil collected prior to sowing in soils from SA, Vic and NSW with no trend between farming systems observed.

The exception to this was the soils from Pinaroo and Loxton which indicated significantly higher levels of *R. solani* inoculum in soils under no-till compared to organic systems. *Rhizoctonia solani* fungus forms hyphal networks in soil to access C and nutrient sources in the heterogeneous Australian soil environment. The reduced disturbance in the no-till system is in contrast with regular cultivations, to combat weeds, in the organic system. Therefore no-till systems combined with stubble retention favour the establishment of fungal hyphal networks including those by *R. solani*.

Results for the Pinaroo no-till soil indicate a very high level of *R. solani* inoculum signifying the early stages of a no-till-intensive cereal system. Roget (1995) reported a significant increase in the incidence of soilborne diseases in the early years after the implementation of reduced till and stubble retention practices. Inoculum levels for the common root rot (*Bipolaris*) were generally higher in soils under organic farming systems probably due to the presence of wide ranging grass hosts in the pasture phase. The level of *Pythium* spp was higher in heavier soils (Cootamundra and Jamestown) than in sandy soils reflecting the effect of soil texture on soil fungi. Soil analysis by services such as those provided by RDTS can provide a snap shot of the status of pathogenic soil biota giving farmers the option of modifying management practices e.g. rotation etc to reduce losses due to soil borne diseases.

However this analysis only provides information on the level of inoculum and its relevance in terms of actual disease incidence and potential losses depends upon the seasonal conditions including response of the crop grown. The training program available through SARDI utilises knowledge from 20 or more years of research on the field pathology and plant-pathogen interaction in the interpretation of *Ggt* inoculum data combined with paddock history and seasonal conditions in terms of potential losses from the occurrence of Take-all disease. However, such information is not available in terms of disease risk for proper and reliable interpretation of other fungal pathogens levels, e.g. Common root rot, *Pythium* spp. and Rhizoctonia solani etc . The influence of pastures on common root rot and Take-all fungi is more evident from the pathogen levels in the pastures near Ardrossen, SA.

The soil under organic pasture had higher levels of *Bipolaris* compared to that in the fertilized pasture soil. Neate (1994), in his review, indicated that *Pythium* inoculum levels may be higher in soils under annual pastures than under wheat or lupins and this supports our

observations. Wildermuth and McNamara (1991) reported that disease levels of common root rot were not significantly different between rotation treatments i.e. continuous wheat vs. rotational system. Although our results showed some differences in the common root rot inoculum levels, it should be emphasized that the presence of pathogen inoculum alone may not result in disease incidence in the crop. The presence of varietal differences within the cultivars of wheat, triticale and oats in Australia provides opportunity to incorporate them in the rotation and reduce the impacts on productivity.

Overall these analyses suggest that soilborne pathogen levels reflect more on the crop rotation and tillage. The presence of wide ranging plant types in the pasture phase of organic systems could contribute to the higher inoculum levels of some soilborne pathogenic fungi, e.g. common root rot and *Pythium* spp., compared to the conventional cropping system.

Soilborne diseases are one of the major bottlenecks to broadacre farming in southern Australia, therefore management decisions that consider pathogen inoculum levels would be more likely to reduce the disease impacts on productivity and long-term sustainability. Since chemical (fungicide) use is not practiced under organic farming systems, soil analysis to determine the level of pathogen inoculum would be a valuable tool in decision making. In addition, the organic and conventional systems differ in terms of host, pathogen and general microbial community therefore testing for specific pathogen/host combination under specific farming system is required to properly manage the impacts of soilborne diseases.

Populations of Trichoderma spp.

The soil fungus *Trichoderma* includes a number of species associated with a variety of beneficial functions. These free-living fungi have been recognised as plant symbionts, endophytes and parasites of other fungi, and are therefore recommended as biocontrol agents of plant pathogenic fungi. Some species also have the ability to promote plant growth (Harman et al., 2004). In this analysis, the *Trichoderma* spp were grouped in to two groups, e.g. *Trichoderma* A (*T. harzianum, T. aureoviridi, T. inhamatum*) and *Trichoderma* B group (*T. koningii, T. harzianum, T. viridi, T. hamatum*).

Results presented in the Table 7 show that generally the DNA levels for *Trichoderma* A group were very low (<5pg DNA/g soil) in all soils. DNA levels for *Trichoderma* B group ranged from 5 to 650pg DNA / g soil. In general, the levels of *Trichoderma* B group were higher in soils under no-till intensive cropping compared to organic farms, except in the samples from Jamestown in SA where the levels were higher in organic farm soils. The high levels of *Trichoderma* at the Jamestown organic farm could be attributed to the application of a *Trichoderma* inoculant prior to sampling. Both the *Trichoderma* groups were lower in the organic pasture and fertilized pasture soils from Ardrossan, SA. Liu et al. (2008) reported that although the propagule numbers of *Trichoderma* species were higher in soils from conventional farms than organic farms, data were variable depending upon the season resulting in no clear separation based on different management systems. Unlike the no-till sites at Loxton, Pinaroo and Cootamundra, stubble retained at the Jamestown no-till farm was grazed thus resulting in the loss of crop residues that are generally a source of organic matter for soil fungi.

Similarly the low level of *Trichoderma* B in the Loxton-cultivated soils, compared to Loxton-NT soils, could be attributed to stubble grazing and cultivation. Cultivation and grazing may also be responsible for the trend to low levels in organic farm soils. Liu et al. (2008) also suggested that the diversity of *Trichoderma* species may be influenced by a variety of factors including soil texture, crop type and sampling time along with management practices.

Therefore, a clear correlation between specific species and farming system may not be found. In our analysis, both *Trichoderma* A and B group of species include known beneficial *Trichoderma* species and the low levels of *Trichoderma* A group-DNA could be due to sample type and the time of sampling. For example, under conventional no-till systems the stubble with wide C:N ratio (cereal stubble) may be a large component of crop residues compared to pasture residues with narrower C:N ratio. No-till systems are known to promote a fungal-based microfloral community and the composition of soil fungi can differ from that under cultivated systems (Bockus and Shroyer, 1998; Adl, 2003; Stromberger et al., 2007).

In the organic systems, repeated cultivation exposes the protected crop residues to accelerated microbial decomposition where as in the no-till system the protected decomposing crop residues can become a refuge for soil fungi. Overall, results on the levels of *Trichoderma* spp. suggest that the potential for beneficial functions mediated by *Trichoderma* species and the actual benefit under field conditions will depend up on plant type, soil and environmental conditions. Also the interactions between *Trichoderma* spp. and the overall microbial community would impact on the actual benefits from these fungi.

The observation of lower *Trichoderma* DNA in the cultivated organic systems requires a detailed analysis in order to properly interpret its implications in terms of soil biological processes. Liu et al. (2008) concluded that organic farm soils suppressed Southern blight of tomato more because of the higher overall microbial diversity and not because of the propagule number of *Trichoderma* in soils.

Diversity of soil bacterial and fungal populations

Until recently the composition of soil microflora, i.e. bacteria, fungi, was measured using selective media – culture dependant methods. It is now accepted that these methods provide a picture of only a small component of soil microbiota and culture-independent techniques are now routinely used to determine the composition/diversity of microbial communities in soil (Roper and Gupta, 2007). The genotypic composition of bacteria and fungi were done using specific rDNA primers (16S rDNA and ITS primers for bacteria and fungi, respectively) and PCR-DGGE technique.

Results from DGGE gel based profiling for soil samples collected at pre-sowing are shown in Figures 1-4. The number of distinguishable DNA fragments in each sample is considered as an indicator of genetic richness of the specific microbial group (Kuffner et al., 2004; Wu et al., 2007). Overall, 28 separate DNA fragments were observed on the bacterial DGGE gels where as 63 fragments were observed in the fungal DGGE gels. The number of fragments in the 16S rDNA DGGE analysis representing bacterial populations per sample ranged from 17 to 27, lower than those reported from other studies. The choice of PCR primers used and time of sampling are some of the factors that can influence the number of fragments observed using this technique. The individual fragments on a DGGE gel are considered to represent bacterial species/groups with similar genetic signature thus DGGE profile provides a semi quantitative display of microbial diversity.

Although the differences in number of fragments in different samples were small, in general, the number of bands was less in no-till samples (17.5±1.2) compared to organic (21.3±0.5) or cultivated (20.3±0.8) samples. Cultivation exposes organic matter that is otherwise protected and increases the exposure of protected organic matter to soil bacteria, therefore cultivation is generally known to increase populations of various groups of soil bacteria. Organic and cultivated systems had received cultivation prior to our sampling which resulted in increased populations facilitating the detection of more bands. The ITS-rDNA DGGE gels representing fungal populations ranged from 26 to 54 fragments per sample.

The trend with fungal diversity data was different i.e. number of fragments were lowest (22-28) in organic farm samples followed by no-till samples (29-41) and highest in cultivated system (43-60) samples. Dendograms constructed on the relative abundance of specific DNA fragments showed bacterial communities in the cultivated farm samples shared only 23% similarity to those in no-till and organic farms. The differences between organic and no-till systems were less clear, i.e. one of the replicate (replicate 4) from organic farm showed a high degree of similarity with no-till samples. Unlike the bacterial diversity, similarity analysis for fungal communities showed a clear separation between organic farms and the two conventional farms, except for the replicate 4 sample from organic farm which had greater similarity with no-till samples (Figure 2).

Soil Type	**Treatment**	**Bacterial Diversity**	**Fungi Diversity**
		Number of rDNA fragments	
Loxton	Cultivated	20.3	45.5
Loxton	No Till	17.5	36.0
Loxton	Organic	21.3	26.0
Pinaroo	Organic		
James Town	No Till	23.3	43.3
James Town	Organic	27.0	54.0
Ardrossan	Org. Pasture	18.0	43.3
Ardrossan	Fert. Pasture	16.5	37.9
	LSD (P<0.05)	2.2	7.44

Genetic richness based on the number of DNA fragments in DGGE analysis indicated greater differences between samples from different regions (Table shown above). For example, the number of fragments samples from Jamestown farms had higher number of fragments for both bacteria and fungal communities and Ardrossan farms had the lowest number of bacterial DNA fragments. The number of bacterial DNA fragments was higher in organic farm samples at all sites compared to the conventional farms. However the trend was not so clear for the fungal communities i.e. at Loxton, the organic farm showed the lowest fragment number where as they were higher in Jamestown and Ardrossan samples.

Multivariate analysis of abundance and DNA fragments for bacterial communities from all soil samples showed, in general, close similarities for replicate samples from the same site, except for Loxton-Organic 4 and Ardrossan OP1, suggesting that the farming system had a significant influence on the diversity of bacterial communities. However, as there was no general and consistent difference between organic farms and conventional farms, these differences can not be directly attributed to the organic nature of the farming systems. Kuffner et al. (2004) found detectable management induced differences in the community structure of four phylogenetic groups (Eubacteria, Actinomycetes, ammonia-oxidizers and Archaea), however, differences clearer with group specific finger printing (e.g. actinomycetes) than for the total Eubacterial community.

Widmer et al. (2003) found that the strong effect of organic farming systems was in relation to the Farm Yard Manure applications and the effect of farming systems such as bio-dynamic and bio-organic on bacterial populations were relatively weak and non-significant. Wu et al. (2007) found that the composition of soil fungal communities within organic, pasture grass or disk fallow plots were separated into unique clusters and the diversity was significantly reduced following cultivation. Our results also show that genetic diversity of soil fungi

(based on DNA fragments on DGGE gels) was lower in the cultivation dependant organic farms compared to the no-till farms.

Genetic diversity of soil microbial community is known to be influenced by soil type, plant/crop type and disturbance events including tillage and chemical application etc (Mader et al. 2002, Widmer et al., 2006). The organic farming systems we sampled, in general, differ from the conventional agricultural systems in relation to a number of these factors. For example, conventional no-till systems are subjected to a one pass seeding operation combined with chemical control of off-season weeds. Whereas the weed control under the organic farming system is mainly done through repeated cultivations prior to seeding.

In addition, under cultivation dependant control, weeds are allowed to germinate and even grow for a few weeks. Thus soil microorganisms in these situations may be exposed to a greater diversity of plant types than where there is chemical control. Thus our observation of differences in genetic diversity of soil bacteria and fungi between different farming systems i.e. organic vs. conventional farms is not surprising. The importance of these differences in terms of the functional capability is relevant in terms of soil biological health management and decision making at farm level.

Catabolic diversity of microbial communities

Carbon availability is one of the major regulatory factors influencing the diversity, population level and activity of soil microbiota thereby influencing a number of key ecosystem functions in Australian soils. We measured the diversity of the soil microbial community involved in C turnover, based on community level physiological profiling (CLPP) using a C substrate utilization profiling technique for soils. A series of graphs in figures 5 and 6 shows results from multivariate (principle component analysis (PCA) and canonical variate analysis) analysis, for catabolic diversity profiles based on substrate utilization using 22 substrates for selected samples collected at pre-sowing and in-crop for various comparisons i.e. organic vs. conventional systems, pre-sowing vs. in-crop samples.

CLPP analysis based on ‘microresp-soil’ profiles showed significant differences between different sites and farms i.e. carbon substrate utilization patterns were different for different soils (Figures 7-13). Average catabolic potential in the pre-sowing soil samples was influenced by both the farming system type at each location and the soil type. For example, microbial communities from heavier soils (red-brown earth and loams) showed greater utilization of all groups of C sources than those in sandy soils. The trend for average catabolic potential was: Jamestown (red brown earth – 0.498-0.539 µg CO_2-C) > Ardrossan (loam – 0.369-0.413 µg CO_2-C) > Pinnaroo (sandy loam – 0.152µg CO_2-C) > Loxton (Mallee sand – 0.065-0.080 µgCO_2-C) i.e. communities in the heavy textured soils exhibited greater ability to utilize the added C substrates.

Within the red-brown earth soils, in the in-crop soil samples, microbial communities in the Jamestown soils exhibited greater utilization of added substrates compared to those from the Cootamundra site. The effect of the farming system varied from site to site, e.g. average C substrate utilization capacity was higher in conventional farming system soils from Loxton and Ardrossan whereas it was higher in organic farm soils from Jamestown (red-brown earth).

Results also showed that the pattern of use of different C substrates, in general, is different in different soils, e.g. in Jamestown pre-sowing soils, the use of fructose, glucose, sucrose and maltose was higher in organic farm soils where as the use of Aspargine, Glutamine and Aspartic acid we higher in conventional farm soils (Figure 6).

Canonical variate analysis of substrate use data for pre-sowing soils, showed significant discrimination between soil microbial communities under different farming systems e.g. microbial communities from organic, no-till, pasture soils into distinct clusters (Figure 7). Analysis of data for organic farms only showed distinct grouping based on soil type (sandy soils vs. red-brown earth) and cropping system (pasture based vs. cropping based). The extent of discrimination between organic, no-till and cultivated systems in the Mallee soils was small compared to the differences between different sites (Figure 8).

Data in the two graphs shown in Figure 12 indicate clear site based differences in microbial catabolic properties for soils between light textured Mallee sands (Loxton and Pinaroo) and heavier textured (loam) soils from Ardrossen and JamesTown. Results from CVA indicate significant differences in microbial communities under organic farms at different sites.

Canonical variate analysis of C-substrate utilization profiles for 'in crop' samples showed discrimination between organic and conventional farms (Figure 8), site based and system based separation on Mallee (Figure 8) and red-brown earth soils (Figure 9). The discrimination between organic and conventional systems on the red-brown earth soils was associated with the utilization of carbohydrates (Figure 9). In the red-brown earth soil from Jamestown, comparison of data for pre-sowing vs. in-crop samples indicated greater separation for communities in organic samples with no discrimination for no-till samples (Figure 11).

A similar comparison on the Mallee soils showed a reduction in the average catabolic potential (level of C substrate use) in the in-crop soil communities under organic systems whereas an increase was observed for conventional systems. In general, C substrate use was greater for in-crop communities compared to pre-sowing communities, reflecting the influence of more readily available C under the rhizosphere environments compared to pre-crop condition at pre-sowing sampling.

The quality and quantity of above-ground plant biomass have a significant influence on the structure of the underlying microbial community. Plant species can have a major selective influence on the microbial communities in soils through influencing rhizosphere and detritusphere communities (Grayston et al. 1998, Nicolardot et al., 2007). These differences can be attributed to the variation in quantity and quality of rhizodeposits and crop residues (Bowen and Rovira, 1999; Nicoladart et al., 2007). Crop residues from cereal crops generally have wide C:N ratio and more recalcitrant compounds compared to the residues from pasture based plant species. In addition to plant type, cultivation and management practices such as chemical inputs can also have impact on activity and C substrate use by microbial communities (Gupta et al. 1998; Kutuzov et al., 2006; Cookson et al. 2008).

Repeated cultivation is an important practice for weed control under organic farming systems whereas herbicide based weed control is common in no-till systems. The reduction in average C substrate use under organic system in the Mallee soil suggests lower availability of readily usable carbon and this observation is supported by the lower soil organic C level in these soils.

All the above observations on the differences in CLPP of microbial communities suggest that C-substrate utilization profiling can provide a useful functional based assessment of the soil microbial communities. Since carbon availability is one of the key regulators of microbial activity in Australian agricultural soils, such characterization of community capability has the potential to help unravel the complex relationship between catabolic diversity, above-ground plant productivity and functional capabilities (e.g. N mineralization) in these soils.

Disease suppression potential

Disease suppressiveness is the ability of a soil to reduce disease severity even in the presence of a pathogen, host plant and favourable climatic conditions for the disease. Higher levels of disease suppression that can result in minimal or no disease constraints to plant growth and productivity have been reported from a variety of cropping systems worldwide (Baker and Cook, 1974; Simon and Sivasithamparam, 1988; Roget, 1995; Gupta and Roget, 2007). Soils with high levels of disease suppression have also been identified in commercial farms across South Australia and Victoria (Roget et al., 1999). The level of disease suppressive activity against fungal diseases in soils is a function of the population level, activity and composition of the total microbial community (Gupta and Roget, 2007).

Management practices that supply higher levels of biologically available carbon inputs over long periods (e.g. >5-7 years) could result in changes to the composition and activity of the soil microbial community and consequently support higher levels of suppression (Roget and Gupta, 2006). A general trend of higher plant diversity and crop residue inputs under organic farming systems has the potential to influence the disease suppressive potential of soil biota in these systems compared to the conventional cropping systems. Results presented before indicate a general trend to lower levels of soilborne pathogens such as *Rhizoctonia solani* and *Gaeumannomyces graminis* var. *tritici* in soils under organic farming systems compared to conventional cropping systems especially the conventional cultivated systems. But soils under organic farming systems also contained lower amounts of MB.

Results on the disease suppression potential (DSP) against Rhizoctonia bare patch disease, measured using a bioassay test (Roget et al., 1999), indicated minor differences between the organic farming system, no-till and conventional cultivation system. Data on *Rhizoctonia solani* AG8 levels showed higher levels of *R. solani* inoculum under a conventional cultivated system but the differences in inoculum levels did not match the DSP results measured using the bioassay. Results for DSP for other soil types were variable probably due to unsuitability of the bioassay test.

Disease incidence observations for the control soils in the bioassay generally reflected the pathogen inoculum levels from the DNA test. Disease incidence is a product of a number of factors including the level of pathogen inoculum, plant health and the composition of soil microbial community. Therefore lack of direct link between inoculum levels and DSP result is not surprising. We were unable to link the pathogen inoculum measurements to field disease incidence due to the poor crop growth because of the drought experienced last year. A number of organic farm soils exhibited higher levels of MB and activity and a general trend of higher diversity of bacteria which can be linked to higher DSP (Rovira and Ridge, 1983, Alabouvette et al., 1996).

But we observed no general trend to high DSP under organic farm systems and observations specific to some farms suggested that organic farm soils may not be supporting highly disease suppressive communities. However, these preliminary general observations have to be properly evaluated prior to any general conclusions.

The DSP bioassay test as it stands is better suited for sandy soils and not well suited for red-brown earths. This method is currently under review, as part of a GRDC project, for its suitability to wide variety of soils.

Soil fungus *Trichoderma* spp. is known for its role in biocontrol activity against soilborne fungal diseases and it is suggested that this fungus may play a significant role in the overall disease suppresiveness of soils (Vinale et al., 2008). Populations of *Trichoderma* spp. can be influenced by a number of management practices e.g. plant diversity (based on crop rotation),

quality and quantity and crop residues and tillage. Results on the *Trichoderma* DNA levels (group B) showed that, in general, soils under organic farming system have less of this fungus compared to conventional cropping soils.

The differences in *Trichoderma* populations could potentially reflect the DSP of soils under different cropping systems especially when combined with the observations on the catabolic potential of microbial community systems. For example, detailed analysis of long-term farming system trials at Avon and Waikerie in SA indicated that soils that exhibited higher DSP also contained higher of *Trichoderma* populations and a microbial community with resilient catabolic potential (Gupta and Roget, 2007). However the results for organic farm soils from this project are preliminary, i.e. they are the first observations to compare cropping systems, hence they require further detailed study comparing a wider range of soils types for any definite conclusions.

Microbial biomass and activity parameters

Biological processes such as decomposition, nutrient mineralization and disease suppression are a product of the composition and activities of a variety of functional groups of soil biota. Most soil microbes require carbon as a source of energy therefore biological processes such as decomposition and nutrient mineralization are influenced by a large group of the soil microbial community.

Therefore, to effectively link the total microbial community to these processes, the total microbial community is considered as a single entity termed as 'Microbial biomass' (MB). Microbial biomass C levels in surface soil samples ranged from 150 to 1507 µg / g soil and 119 to 1283 µg/g soil in the pre-sowing and 'in crop' samples, respectively. MB-N levels ranged from 17 to 217 mg N / kg soil. MB levels were generally higher in the 'in-crop' samples, except in the Mallee organic soil. For comparison of MB levels in different soils/systems, MB is expressed as percentages of soil organic C i.e. Microbial quotient (MQ) values (Table 6). MB-C levels accounted for 3-5% of soil organic C in the pre-sowing samples and 3-7% in the 'in crop' samples. An exception to this is the MB-C level in the Pinnaroo pre-sowing samples, probably due to the decomposition of pasture residues following cultivation prior to sowing. The observed values for both MB-C and MB-N are in the general range that is reported for Australian soils i.e. 2-5 of organic C in soil is in the soil microbial biomass (Dalal and Chan, 2001).

Overall, organic soils contained higher levels of MB however the effect of the farming system on MB level varied with soil type (Tables 3-6). For example, in the Mallee soils, there was no difference in MB levels in the organic and no-till soils but both were lower than in conventional cultivated soils. Organic farm soils showed the lowest level of MB at the 'in crop' sampling. In contrast, MB levels in organic farm soils were either similar to or greater than conventional farm soils at all other sites both in the pre-sowing and 'in crop' samples. Soil type had a greater influence on the level of MB in soil, e.g. Mallee soils had lowest amount of MB, followed by the Pinnaroo loams. The highest was in the red-brown earth soils. This soil type based trend is not clear with MQ values suggesting the influence of soil physical properties on MB level in soil.

There was a significant correlation between the levels of MB and soil organic C ($R=0.86$, $P<0.01$) supporting the importance of C availability to the development of microbial communities and high levels of MB. The general trend in the farming system effects on soil organic C generally reflects that of soil MB.

Habitat characteristics of light textured (sandy and sandy loam) soils result in less protection of organic matter from microbial breakdown and lower soil organic matter build-up.

Similarly microorganisms have fewer protected places where they can survive during periods of harsh conditions (e.g. dehydration) and escape from predation by soil fauna. Since clay based protection is less in the sandy soils (e.g. Mallee soils near Loxton used in this study) organic matter is more readily available for decomposition and accumulation of soil organic carbon is more difficult than that in the clay soils.

Our results for soil type based differences in MB levels, i.e. higher MB in red-brown earths compared to Mallee sands, concur with previous reports from Australia and worldwide. MB levels in the 'in crop' samples were generally higher than those in pre-sowing samples except for the Mallee organic farm soils. Increased levels of available C due to the rhizodeposition from growing plants are the main reason for higher levels of MB in crop. The low level of MB in 'in crop' organic samples suggest a reduction in available C levels even with the presence of a crop. Nitrogen and phosphorus in MB are considered to be short-term sources of nutrients for plants, therefore, the amount of nutrients in MB is used as an indicator of nutrient supply capacity of soil.

All the organic farming systems we sampled followed a pasture-crop rotation and our sampling was done after the fallow phase prior to a cereal crop. The pastures in organic farms were legume-grass mixtures where as the conventional farms were intensive cropping systems with cereal stubble dominating the crop residues. Cereal crop residues are generally low in N (i.e. wide C:N ratio; 100:1) compared to the N-rich legume residues (narrow C:N ratio; 25:1). Therefore, decomposing pasture legume residues can provide higher levels of N for microorganisms thus higher levels of MB-N in organic farming systems.

We measured the level of microbial activity in the soil using 3 different methods, i.e. short-term (5h) and long-term (21d) incubation assays and substrate induced respiration (SIR) assays. The long-term incubation assay was also combined with the measurement of potential N mineralization assay. The long-term incubation assay is referred as 'mineralization potential' whereas the short-term assay as 'respiration assay'. The trend with both the short-term and long-term microbial activity levels for different soil types followed that of the MB levels i.e. lowest activity in the Mallee soils compared to that in red-brown earths (Table 2).

Also microbial activity or C mineralization potential was generally higher in the organic farm soils compared to conventional soils. Similar to the MB levels, no-till and conventional cultivation soils in the Mallee exhibited higher levels of microbial activity than the organic farm soil. Microbial activity measurements are converted into 'respiratory quotient' values, i.e. microbial activity per unit MB, in order to compare the relative level of microbial activity across farming systems and soil types. Average RQ values for different soil types were not significantly different (Table 6), however, RQ values were higher for conventional farm soils than for organic farm soil at all sites and both pre-sowing and 'in crop' soil samples. Differences in RQ or relative levels of microbial activity are generally attributed to differences in the (i) composition of microbial community, or (ii) metabolic status of microorganisms due to constraints associated with nutrition, presence of agrochemicals etc. Tillage induced disturbance can also affect RQ values in soils, e.g. RQ values under conventional cultivation systems are higher than no-till systems.

In the systems we sampled, organic systems were subjected to more tillage than the no-till systems. In addition organic systems don't use chemicals where as the conventional systems use herbicides and fungicides as part of their management practice. Therefore, lower RQ in organic farm soils may be attributed to differences in microbial composition (diversity) and nutrition (N, P etc) constraints. Data from the genetic diversity of bacteria and fungi (presented previously) showed some differences between soils under organic and conventional farming systems. The significance of lower RQ but higher MB values in terms of ecosystem functions required further investigation.

Populations of select members of functional groups of soil microorganisms

We determined the populations of microorganisms involved in C and N turnover, e.g. cellulolytic bacteria and fungi and nitrifying microorganisms in all soil samples using culture based (most probable number) methods. In addition, populations of ammonia oxidizing bacteria (one of the important members of nitrifying microbial community) were quantified using a DNA based technique.

Populations of nitrifying microorganisms (AO) ranged between $1.9x10^3$ to $1.5x10^5$ in pre-sowing samples and $2.6x10^3$ to $1.5x10^4$ in 'in crop' samples (Figure 15 and 16). Overall, populations were slightly higher in no-till, pre-sowing samples than in organic samples but there was no difference between systems in the 'in crop' samples.

However, the trend between the systems varied between soil types and sampling time. Populations were generally lower in the Mallee soils compared to other soils (Figure 14 and 15). Results from quantification of '*amoA*' gene showed similar trends e.g. a significant positive correlation (R^2=0.68, P<0.05) between the AO population data and *amoA* quantification (Figure 17). In the Mallee soils, populations were higher in soils from conventional cultivated systems than in to no-till or organic soils, probably due to the higher amounts of organic N substrate available from the decomposing legume residue. This could also be the reason for the general trend of a higher AO populations in organic farm samples at pre-sowing and the lack of significant differences in the 'in crop' samples may be due to the similarity in crop type, except for soils from organic farm at Ardrossan in SA.

Populations of cellulolytic bacteria and fungi observed in these soils are in the general range reported for agricultural soils in southern Australia (Gupta and Roper, 1994). The overall magnitude of the effect of farming system type on cellulolytic bacterial populations in the pre-sowing samples was small (non-significant) and varied with soil type (site) (Figure 16). However, in the 'in crop' samples populations of cellulolytic bacteria were significantly higher in the organic farm soils than conventional farm samples.

The effect of farming system type on cellulolytic fungi also varied with soil type. Both CB and CF populations were lower in the organic farm soils from Loxton where as general trend was reversed in soils from Jamestown. There was no difference in CF populations between organic and conventional systems from Ardrossan, SA and Cootamundra, NSW. At both sampling times both CB and CF populations were generally lower in the Mallee (Loxton) soils. Reduced till systems generally support higher populations of soil fungal populations compared to cultivated systems (Roper and Gupta, 1995) and continuous crop systems such as those present in the conventional systems in this study provide lower quality crop residues (wide C:N ratios of cereal stubble) which generally support decomposing fungal populations, e.g. supporting the observation of higher populations of CF in the no-till Mallee soils.

Organic farm soils generally received more cultivations than conventional systems and also had a higher diversity of plant residues. However CB and CF populations did not reflect these higher levels of C inputs. The higher level of disturbance in organic farming systems would result in higher levels of C lost through microbial decomposition, in particular in the light textured soil types, because these are not able to support higher microbial population base. Reports from overseas on soil types with higher levels of organic matter (i.e. soil organic C levels >2%) show higher populations of microorganisms under organic systems.

Rates of biological processes involved in nutrient cycling

Nitrification, the conversion of ammonia N to nitrate N is one of the key biological processes involved in the mineralization of nitrogen in soils. This is considered the rate limiting process and is sensitive to management and substrate availability. Results on rate of nitrification, measured using a laboratory incubation assay, are shown in Figure 19. In general, wide ranging rates of nitrification were observed, i.e. 10-fold difference between lowest and highest values. The highest rate of nitrification was measured in soils from Ardrossan pastures, e.g. organic pasture soils exhibited higher rate than the fertilized pasture soils. Rate of nitrification (RON) was significantly influenced by farming system and soil type. For example, soils under organic farms showed higher rates of nitrification than no-till / conventional farm soils.

However, in the Mallee soils, soils under conventional cultivation exhibited higher rate than no-till or organic farm soils. The very high rates of nitrification observed in the Ardrossan pastures could be attributed to high levels of substrate from the legume pasture residues and the presence of grazing animals (pigs). This was supported by the high levels of ammonia N measured in these samples. Flowers and O'Callaghan (1983) found higher rates of nitrification after the application of pig slurry and higher levels of RON after pastures is widely reported especially after legume pastures. Rates of nitrification were generally lower in the 'in crop' samples than in the pre-sowing samples, however the effect of sampling time was small. This trend reflected what was observed with the AO populations.

A significant positive relationship was observed between the measures of AO populations and rates of nitrification ($R=0.59$, $P<0.05$, pre-sowing samples). The strength of relationship was stronger in the Mallee samples e.g. $R^2 = 0.71$ ($P<0.05$). Overall, the observations in this study suggest that the effects of farming system and soil type on the populations and activity of nitrifying microorganisms were similar.

With soil microorganisms, presence of the organisms does not automatically result in or reflect their activity / performance. Data on the populations provide indications of potential activity. In addition, for biological processes mediated by a group of organisms (a community), activity by the entire community is influenced by both the number of organisms and the composition of the community. Reflecting the effects of environment, the same group of microbial community may perform at different levels of activity depending upon their metabolic status. In this project, we measured both the population size and activity specific functional groups of microorganisms, e.g. nitrifying microbial communities and the rates of nitrification. Results presented above indicated that both farming system and soil type influenced the populations and the rate of process.

A comparison of the relationship between the population size for nitrifying microorganisms in the Mallee soils and the rates of nitrification showed a significant positive linear relationship in soils from both sampling times. The rate of nitrification per unit AO population was higher for the 'in-crop' samples compared to that in the pre-sowing samples (Figure 20). Wheatley et al. (1997) observed temporal variation in rates of nitrification and barley plants had a significantly positive effect on RON especially early in the growing season. This clear difference in RON per unit population could be attributed to (i) differences in the diversity of AO populations seasonally or (ii) metabolic status of the specific functional group. Populations in the pre-sowing samples access the ammonia N substrate from the products of SOM decomposition where as the 'in-crop' communities can get the N substrate from SOM and rhizodeposition.

Nitrification has traditionally been attributed to a small group of microbial species and the diversity of AO populations is considered narrow and may not change seasonally. The nature

of culture based methods did not allow detailed studies on the diversity of nitrifying microorganisms whereas the recent developments in DNA methods will facilitate a detailed analysis of this functional group in the future. The implication of this result in terms of biological process in field situations requires further investigation. These results clearly emphasize the need to properly understand the temporal variations in the community structure and activity, e.g. such as those induced by rhizodeposition or cultivation, in order to properly utilize the data on microbial parameters for field-based prediction and management.

The nature of relationship between AO populations and RON was similar with population data obtained with both the culture based (MPN) and DNA based methods suggesting the suitability of both methods. However the culture based method is time consuming (2-3 weeks) and may be prone to methodological variability although it reflects the actual population values. The method can also be labour intensive if large numbers of samples have to be analysed. While the DNA method is quicker and can deliver high throughput, the method is yet to be evaluated for diverse soil types and communities.

Mineralization of nitrogen

Data on N mineralization potential measured using laboratory incubation assay showed significant differences between organic and conventional farm soils and soil types (Tables 3-5). N mineralization potential (Pot-N) values ranged from 0.4 to 2.1 mg N/kg/day and 0.36 to 2.54 mg N/kg/day in the pre-sowing and 'in crop' samples, respectively. Pot-N values were generally higher in the organic farm soils and pasture soils (Ardrossan) than in the conventional farming soils. In the Mallee soils, differences between systems were smaller and the highest values were observed in the conventional cultivated system soils. Pot-N values were also higher in the 'in crop' soils than in pre-sowing soils, except that in the Mallee organic farm soil.

Disturbance of soil samples prior to laboratory analysis has the potential to modify or mask the treatment effects on biological processes such as mineralization of nutrients. Our results for N mineralization potential using 'intact cores' for the Mallee soils showed a trend similar to that measured using disturbed soil samples, except that the absolute values were lower. N mineralization capacity of a soil can be influenced by the quantity and quality of organic matter, size of MB, populations and rate of activity of nitrifying microorganisms.

There was a strong and significant positive relationship between Pot-N values and MB-C, respiration, C mineralization potential, organic C, total N and AO populations (Tables 8-9). The positive relationship between MB-C and Pot-N values was the strongest and most consistent (R^2=0.79; Figure 25). MB is the engine room of SOM turnover and C and nutrient mineralization processes therefore a strong and positive relationship between MB and Pot-N is not surprising. Mineralization is a product of activity of number groups of microbial communities. Our results showed a low and variable relationship between pot-N measures and specific functional groups of microorganisms.

Over all, our observations suggest that soils under organic farms with adequate pasture organic matter inputs, have the potential to supply similar or higher levels of nitrogen through biological mineralization to the conventional farming systems. Most organic systems follow pasture-crop rotations and pastures with legumes as components can increase organic N inputs, hence N mineralization in our pre-sowing samples is higher in organic soils. If the soil organic matter build up in the pasture phase is adequate to meet the demand of microbial community then the N mineralization can also be maintained for longer periods.

However, if the pastures were grazed heavily and the amounts of C inputs were low, similar to that observed in the Mallee organic farms, it would lead to a decline in the N

mineralization potential. Since organic farms do not allow external fertilizer inputs and N requirements of crops have to be met from the biological sources it is necessary that the pasture phase is maintained well to meet the energy of microbial community and allow sufficient levels of N mineralization to occur. In addition, a healthy legume component is critical to harness the full potential of N fixation through the legume-*Rhizobium* symbiosis. In this study although a general trend of higher N mineralization potentials were observed in organic farm soils they did not seem sufficient to meet N demand by a crop with full potential of water-limited yield.

Mineral N in soil profile prior to sowing

Results on the levels of mineral N (NH_4 and NO_3-N) in the soil profile on farms near Loxton in SA are shown in Figure 21. Mineral N levels in the soil profile prior to sowing are sometimes used as an indicator (a coarse measure) of off-season N mineralization capacity of farming systems. Total mineral N levels in the profile were lowest in the organic farm soil compared to the no-till intensive cropping soil profile with greater difference in the surface 30cm soil. The large amount of mineral N in the soil profile under the conventional pasture-crop rotation can be attributed to the N mineralized from the decomposition of pasture legume from the year before.

Although our sampling on the organic farm was after a grass-legume pasture, and had received cultivations, profile mineral N levels were low suggesting little if any contribution from legume residues from the previous year. Heavy grazing of pastures during the drought, may have limited the N contribution from pasture residues. In addition, the low levels of MB and microbial activity in the organic farm soils would also have contributed to the lower mineral N in the soil profile.

Nitrogen fixation

Legumes are an important source of N input in cropping systems. In particular, in organic farming systems N fixation by pasture legumes is a key source of N to crops in rotation. Soil diazotrophs, (free-living N fixing microorganisms) can be an important and useful source of biological N input in the broadacre cropping system, especially in cereal grain cropping systems (Roper and Ladha, 1995; Kennedy and Islam, 2005, Poly et al. 2001). Nitrogen fixation can occur in a wide range of bacterial phyla, e.g. *Archaebacteria* to *Eubacteria* and all N fixers carry a *nif*H gene that encodes the Fe-protein of the nitrogenase enzyme.

Methods for field based measurement of N fixation by free-living N fixers are laborious and not reliable at present, in particular during dry periods (e.g. similar to the drought conditions experienced last year). Traditionally estimation of populations of FLN microorganisms is done using an MPN method. We used a DNA based technique to quantify the populations of *nif*H containing populations. Results for Mallee soils from pre-sowing sampling showed no difference in *nif*H copies between the no-till and organic farm soils and both were lower than those in conventional cultivated soils (Figure 18). Levels of *nif*H were higher in the organic farm soils from Jamestown compared to the no-till soils but no such differences were observed in the pre-sowing Ardrossan soils. Similarly, there were no significant difference in *nif*H copies the ‘in crop’ samples from Pinaroo (978 to 1017 copies per ng DNA) and Cootamundra (290 to 640 copies per ng DNA).

The data on the population size of the FLN microorganisms provide a measure of the potential for N fixation but the actual inputs from these organisms are influenced by a number of soil physical, chemical and environmental factors such as soil moisture and temperature, biologically available C, mineral N level etc (Gupta et al. 2006).

It has been suggested that cereal crop residues provide optimal conditions for higher FLN fixation in cropping soils because of the wide C:N ratio and lower 'after crop' soil mineral levels (Roper and Ladha, 1995). Measurement of the population size of these organisms using the DNA technique (as it is available at present) may not provide a true / complete picture of the contribution from these communities. In addition, we measured these populations in the bulk soil and not near the specific crop residues therefore may have underestimated the FLN potential of these systems.

Phosphatase activity

Data for the activities of soil phosphatases, enzymes involved in the mineralization of soil P into plant available forms, is shown in Figure 22. In general, the trend in phosphatase activities between the organic and conventional farms is varied. For example, on Mallee soils, no-till soils exhibited higher levels of activity compared to organic farm soil. However, soils from James Town showed an opposite trend i.e. activities of phosphatases (acid and alkaline) were higher in soils from the organic farm compared to a nearby conventional farming soil, probably due to the ~400kg rock phosphate applied on the organic farm. Application of P containing compounds such as rock phosphate etc is a common practice for organic farmers. Soils under cropping systems with higher levels of microbial activity e.g. pasture based rotation and stubble retention systems, generally exhibit higher levels of phosphatase enzymes demonstrating the potential for transformation of unavailable P into plant available forms.

However, adequate substrate availability is needed for this biological potential to meet the P demand by a crop. It is assumed that the P reserves from the long-term history of fertilizer P application in Australia can serve as the source of P demand by crop under organic farming. The lower level of phosphatases in the organic farm near Loxton suggests that the effect of lack of adequate C inputs on general activity is also reflected in phosphatase activities.

A general trend of higher levels of mycorrhizal colonization of plants has been shown under organic farming systems (Ryan et al. 2004) and application of soluble P fertilizers is suggested to reduce the colonization by arbuscular mycorrhizal fungi. Arbuscular mycorrhizal fungi, through their symbiotic relationship with plant roots have been linked to enhanced plant uptake of P, Zn, Cu, Mn etc (Marschner and Dell, 1994).

Differences in soil properties at the farming system level

Results from the multivariate analysis of data for chemical, biological and biochemical properties of soils from all treatments are shown in Figures 23-24. Canonical variate analysis results for pre-sowing samples showed a clear clustering of farming system types, i.e. organic, no-till and conventional cultivated systems, irrespective of soil type (Figure 23). When the results for the Ardrossan pasture samples were included in the analysis, then differences between the two pasture soils dominated the variate factor i.e. separation between the farming system groups under cropping was smaller than their separation from pasture systems suggesting the greater influence of pastures on biological properties. Ardrossan pastures were used for grazing by pigs which differed from the sheep based grazing or hay harvesting practices followed at other places.

Thus the difference between Ardrossan systems and other sites may not be entirely due to crop management practices but also the influence of livestock. Overall, this analysis clearly demonstrated the system level differences in terms of biological properties between organic and conventional agricultural systems.

5. Discussion of results and conclusions

In recent years, the increasing popularity of organic farming systems has spread from the intensively managed vegetable production systems to broad acre rain fed cropping systems. The main differences between organic and conventional farms are the lack of use of inorganic nutrient fertilizers and the substitution of cultivation for agrochemicals in weed control. Crop N requirements are expected to be met by N inputs through biological processes and P and other nutrients from soil reserves from long earlier periods of fertilizer inputs.

The living part of soil organic matter, excluding large fauna and living plant roots, is known as microbial biomass. MB is the engine for a multitude of biological processes important for nutrient cycling and availability and in promoting soil aggregation. The size, composition and dynamics of MB is regulated by a variety of soil physical and chemical and environmental factors including pH, organic matter level, texture and structure, moisture content and redox potential.

Since the majority of the soil microbial community is heterotrophic i.e. depended upon organic materials for energy purposes, management practices that influence the quality and quantity of organic inputs can modify the composition and size of soil microbial component. For example, crop rotation, stubble retention and grazing related practices have been known to influence the size of microbial biomass and the composition of different functional groups of soil microbial communities (Gupta and Roper, 1993; Roper and Gupta, 1995; Shannon et al., 2002; Nelson and Mele, 2006; Wu et al. 2007). Tillage is known to influence the amount of MB, composition of microbial community and in general increase the rates of biological processes.

The duration of tillage induced increase in the rate of biological process depends upon the intensity of the practice and the original SOM status. The effects of inorganic fertilizers on microbial populations and biological processes are variable because the observed effects are the net effects of direct impacts of fertilizer compounds and the indirect effects through changes to plant growth. Although there are some reports of undesirable changes in biological properties due to long-term application of high levels of inorganic fertilizers, many such observations can be linked to changes in soil properties which indirectly affect some specific biological properties. A number of cases have been reported where fertilizer application increased the size and dynamics of MB due to the increased C inputs from robust plant growth. Sarathchandra et al. (2001) found a greater functional diversity of soil microflora that received inorganic N fertilizer but there were no apparent effects on total numbers of soil bacteria and microbial activity. In the lower fertility Australian soils, application of inorganic N fertilizer generally leads to increased C inputs thereby increasing the populations of a variety of microbial groups and general measures of biological processes (Pankhurst et al, 1995; Bunemann et al., 2006; Gupta and Roget, 2007).

Application of inorganic fertilizers at very high rates can have a negative impact on populations of some microbial groups however such effects may be temporary until after the applied chemical is utilized or transformed into other compounds. For example, application of anhydrous ammonia (Coldflo®) at rates higher than 100kg N / ha could result in a decline in the size of MB and activity levels (Gupta VVSR and John Angus, unpublished) but this reduction is temporary and recovery in total MB can be seen within a crop season. More importantly such effects are generally seen in the zone of fertilizer application and the effects may not be seen in soils away from this zone. Generally littlke or no effects on microbial

populations are observed as a result of P fertilizer application at rates recommended for Australian crops.

The effects of pesticides (herbicides, fungicides) on soil microflora are well studied and contrary to the general belief large and persistent effects of pesticide application on soil microbial properties are rarely seen, especially when applied at recommended rates. Research investigating the effects of herbicides applied at recommended rates on general soil biological properties in broad acre agriculture indicated that most of the observed effects were transitory and recovery was seen within 3-6 months after application (Gupta et al., 2004; Gupta, VVSR 2007, GRDC report). However the magnitude and duration of the effect varied with chemical type and soil system they were used in. Not all the herbicides have negative effects on all microbial properties. Drew et al. (2007) reported that 'in-crop' use of herbicides could cause a reduction in N fixation by legume crops however the reduction is not universal and depends upon the soil fertility and plant health.

Since organic farming does not involve application of agrochemicals it is perceived that the negative effects from chemicals can be avoided and therefore cause an increase in biological properties. However reports showing direct evidence for such effects are rarely seen.

One of the major reasons for the recent popularity of organic farming systems is that they are considered ecologically more sustainable than the input driven conventional farming practices, in particular for improving soil microbial diversity and functions (Mader et al., 2002). Although a number of studies, mainly from overseas, have produced evidence showing beneficial effects of organic farming practices on soil biota and activities, there are as many reports showing either very little or no effects (Raupp, 1995).

Some reports even show negative effects of organic farming on selected soil biological properties (Yeates et al., 1997). The limited number of reports from Australia show variable results particularly for P availability and the role of arbuscular mycorrhizal fungi (AMF). Colonization of plants by AMF has been shown to be significantly increased under organic farming systems and this is attributed to reduced applications of soluble P fertilizers (Ryan et al., 2004).

The majority of studies evaluating the impact of management on soil biology use measurements on individual properties or specific microorganisms in isolation, thereby limiting the relevance of results to the overall soil biological capability. The enhanced soil microbial community under organic systems may be better interrogated with a polyphasic approach that includes measurement of the dynamics of populations of functional groups of microorganisms and key biological functions (Widmer et al., 2006; Gupta, 2007). With the recent availability of DNA based techniques, it is now possible to determine the genetic diversity and functional capability of soil microbial communities (Gupta et al., 2008).

The underlying aim of this scoping project was to evaluate a research approach that can be used to determine the soil quality/biological health under organic farming systems, in particular to determine the dynamics of entire microbial communities for their diversity and functional capability. For this we used a polyphasic approach to determine the properties and dynamics of soil microbial communities under the organic farming systems, e.g. biological properties related to the diversity of microbial communities along with the size and composition of MB and key biological activities. Such an approach will allow for a better characterization of the entire microbial community and differentiate the effect of farming system as a whole.

Results presented in this report clearly show the benefits of using the polyphasic approach to compare the impacts of organic farming systems in terms of both the diversity and

functionality of the system. For example, data on MB and biological processes such as nitrification give a picture on the dynamics of N mineralization and supply potential of soils. The data on soilborne pathogen inoculum levels can indicate the potential for soilborne disease risk where as the catabolic and genetic diversity measurements provide the status of soil microbial communities.

The measurement of the biological properties of sils at times relevant to plant growth and environmentally significant periods allowed us to make interpretation of results in relation to plant performance related functions. For example, data on N mineralization capacity and nitrification from pre-sowing samples are indicators of soil N supply potential in the particular farming system whereas the N mineralization capacity in the 'in-crop' soil represents the N availability to the crop at the time of grain filling. Although pathogen inoculum level is one of the factors contributing to the disease incidence, the practice of using the data on the levels of soilborne pathogens such as Ggt, measured using soil samples prior to sowing, has been in use in southern Australian rainfed cropping systems i.e. generally used as indicators of Take-all disease potential as part of the decision making process about rotations.

Finally, we compared the soil biological status in organic farm soils with that on a neighbouring farm under a conventional agricultural system. Since the differences between two farms are multi-factor oriented the comparison is mainly at a system level and may not be used as definitive features of the two systems.

Nitrification is one of the key components of N mineralization process in soils and the rate of nitrification is a product of the population level of nitrifying microorganisms and the metabolic status of the community.

The plethora of changes to management practices followed by the organic farming systems, e.g. no application of soluble fertilizers, increased cultivation to facilitate weed control, can influence nitrification directly through their effect on the population or activity or indirectly through modifications to the soil habitat. Results in this study indicated higher populations of AO populations in soils after pastures including in organic farming systems than in no-till conventional systems. These differences were higher in the pre-sowing samples supporting the hypothesis that the availability of organic or ammonia N substrate influences these microbial populations.

The lack of differences between organic and conventional systems in the 'in-crop' samples suggest that the effects of pastures under organic systems may not be sufficient to maintain higher levels of these populations or these functions. The significant differences between organic and conventional no-till systems could also be the consequence of cultivations done prior to sowing which would have caused a short burst of substrate availability. The presence of differences in pre-sowing and in-crop samples supports the need to make multiple measurements in a season which was the approach we used. Laanbroek and Gerards (1991) reported that increasing rates of nitrification may not be matched by an equal increase in AO populations.

Our results from the Mallee soils show a significant positive relationship between the populations and rates of nitrification, however the nature of the relationship was different between the pre-sowing and in-crop samples. This suggest that nitrification rates in agricultural soils including organic farm soils are not solely regulated by a single factor such as availability of ammonia N and other edaphic (physical and biological) and plant factors may play a significant role in this key biological process. Wheatley et al. (1997) reported that manures stimulated nitrification and the presence of barley plants significantly affected its

temporal patterns. They concluded that the nitrification rate in mineral soils is regulated by water or spatial restrictions and interactions between heterotrophic and autotrophic activity.

The changing relationship between AO populations and RON seasonally could also be linked to the changes in the functional diversity and/or the metabolic status of the members of the nitrifying community. In this one year study, we did not measure the diversity of nitrifying populations and this could be part of any future research to identify the factors that regulate this key biological process in organic soils.

The diversity of microbial communities is known to be influenced by a variety of soil, environmental and plant related factors. Organic farming systems differ from the conventional input based farming systems in terms of inputs application, tillage and rotation practices and could therefore differ in the diversity and activity soil microbial communities. Widmer et al. (2006) reported that T-RFLP (a measurement of genetic diversity) and community level substrate utilization profiling showed consistent differentiation of soil bacterial community structure in relation to the influence of farming systems and crops, e.g. farm yard based farming systems and crop types (wheat and grass-clover mixture). Our results on genetic diversity of soil bacteria and fungal communities indicate that the diversity of these soil microbial communities is influenced by soil type and farming systems. For example, the genetic richness based on the number of DNA fragments in DGGE analysis showed higher numbers for soils from Jamestown farms compared to Loxton or Ardrossan soils. This suggests a significant soil type influence on the genetic richness of soil microflora.

A general trend to higher genetic richness in the bacterial community in organic systems can be attributed to the diversity of plant types in the pasture-crop rotations compared to the intensive conventional cropping systems. In the lower fertility Mallee sands at Loxton, the genetic richness of soil fungi was higher in the no-till systems compared to the cultivation dependant organic farming systems. The variation of farming system type effect on soil fungi suggests the complex nature of factors that can influence the fungi e.g. tillage, residue quality and quantity.

Grazing is one of the important management practices in organic farming system and intensive grazing can remove the crop residues that are essential for the development of a diverse soil fungal community. The various farms we sampled varied in the level of grazing they practiced during the last couple of years, due to drought, hence no clear and consistent trend can be seen. Soil fungi are an important group in the soil microbial community and our results suggest that management practices followed as part of organic farming systems can influence the diversity of these communities. Wu et al. (2007) reported that soil fungal communities are strongly influenced by land management practices and fungal communities within organically management systems can be more resistant to anthropogenic and meteorological disturbances.

The observation of differences in soil fungal communities between organic and conventional systems is further strengthened by the differences seen in the amount of DNA of selected fungal species including both plant pathogenic (*R. solani,Ggt, Pythium* spp. etc.) and beneficial fungi (*Trichoderma* spp.). A trend to lower levels of *Trichoderma* spp., a beneficial fungus, needs further detailed investigations. *Trichoderma* species that are part of the *Trichoderma* group B are generally dependant upon the presence of crop residues and like many other soil fungi repeated cultivation of soils can impact *Trichoderma* populations.

As indicated before intensive grazing or hay baling (i.e. removal of crop residues for hay) can result in removal of crop residues essential for the build up of soil fungal communities. This is supported by the high levels of *Trichoderma* group B populations in the Mallee soils from the no-till farm (>5 years of no-till + stubble retained continuous cereal system).

The observation of higher levels of some of the soilborne fungal pathogen inocula in soils under organic farming systems raises a caution and suggests that organic farmers should monitor these populations more closely to assist them in selecting crop rotations. Although pathogen inoculum level can provide an indication of disease potential other factors such as general soil microbial health and plant health and management practices such as targeted tillage can modify the level of disease incidence seen in the field (Neate, 1994; Gupta and Roget, 2007). It is considered that a higher level of aboveground plant diversity and below ground microbial diversity that can be seen in organic farming systems could potentially increase disease suppressive nature of the soils resulting in reduced disease incidence.

A number of reports from overseas support this hypothesis but these systems evaluated organic systems that apply large volumes of manures or composts (Hoitink and Fahy, 1986; Workneh and van Bruggen, 1994). It is suggested that the high levels of organic matter in organic farming systems could encourage the build up of microorganisms antagonistic to plant pathogens. None of the organic farms we investigated showed any indication of applying large amounts of organic manures.

In general, the large farm size of the broad acre organic farms in Australia make such applications impractical. In addition, dry matter production on a number of broad acre organic farms in Australia is generally considered to be less compared to input-based conventional systems. Our analysis of disease suppressive potential of Mallee soils showed no evidence of build up of high levels of disease suppressive communities under organic farming system. The management factors consistently related to soils with improved disease suppression included intensive cropping, stubble retention, limited grazing, limited or no cultivation and above average yields (high water use efficiency). These management practices increase biologically available carbon inputs and result in changes to the composition and activity of the soil microbial community over time (Gupta and Neate, 1999, Gupta and Roget, 2007).

While the genetic diversity of microbial communities provides a background picture of the potential for various soil biological processes, it may not reflect the actual catabolic activity of the communities and the resultant level of biological activities. Since the majority of soil microbial communities are heterotrophic, i.e. use C from organic materials for energy source, the ability of microbial communities to utilize a diverse array of carbon substrates has been effectively used to determine a catabolic profile of community composition (Garland and Mills, 1991; Campbell et al., 2003; Gupta et al., 2008).

Such community level substrate utilization patterns can provide information on the catabolic potential of microbial communities and have been used to determine the effects of plant type, application of herbicides or manures and other management practices. Results obtained in this study indicated clear and significant differences in the catabolic diversity of microbial communities between soil types and farming systems.

Catabolic potential was generally higher in soil types that provide protection to microorganisms and organic substrates compared to the Mallee sands. Microbial community profiling in soils under organic farming systems was significantly different to that under conventional farming systems. These results confirm the hypothesis that the differences in plant community and quality of crop residues in the two types of farming systems support different functional capability of microbial communities.

When combined with the genetic diversity differences these results clearly indicate that organic farming systems support a different microbial diversity to conventional input-driven farming systems. However, data on genetic or catabolic richness is varied and there is no consistent trend of higher diversity for all microbial communities under organic farming

systems. Overall, these results strongly support such analysis across a broader farmer data base in order to properly evaluate the extent of influence of organic farming systems on soil microbial diversity and catabolic capability.

Data on the dynamics of soil microbial biomass, the living part of soil organic matter, and microbial activity measurements have been used as indicators of overall capacity of soil microbes to maintain key ecosystem functions and nutrient supply potential (Doran, 1996). In addition, microbial indices such as 'microbial quotient' (MQ) and 'respiratory quotient' (RQ) provide an indication of the nature of biological and chemical changes that occur under different farming systems (Waldle and Ghani, 1995).

A higher level of fresh crop residues under organic farming systems and increased disturbance resulted in higher levels of MB and MQ and this supports the belief that the increased supply of available C under organic systems can increase the turnover of C. The higher amount of MB also suggests a larger microbial reservoir of nutrients (e.g. N and P) and nutrients immobilized in MB are less prone to leaching. However increased cultivations under organic farming also accelerate the rate of decomposition and turnover of microbial component thereby releasing the nutrients into the available pool.

The specific microbial activity or RQ is a measure of physiological status of the microbial community and is influenced by the composition of community and a variety of abiotic factors such as soil temperature, moisture level, presence of chemicals etc. Data on RQ show lower values for soils from organic farming systems. It has been suggested that soil MB with a lower RQ are utilizing the available C more efficiently (Fliebach and Mader, 2000). In the presence of available C, a higher RQ value combined with decreasing MB levels indicates a microbial community under stress (Gupta and Roberts, 2004). Unlike the heavier textured soils, MB in the Mallee organic farm showed signs of decreasing levels of available C as the season progressed. Mallee sands are generally low in soil organic matter levels and provide little or no protection for organic matter.

Therefore, the combined effect of reduced C inputs from crop residues and accelerated decomposition due to repeated cultivations has resulted in a microbial community that may not be resilient and is not performing to its full potential. The significant positive correlation between MB and organic C levels confirms the importance of C availability to the development of microbial communities in Australian soils. Since the SOM is the key source of nutrients for production in the organic farming systems it is critical that available C levels are kept at levels required to maintain MB and its activity.

Organic manures along with the N inputs through the biological processes such as nitrogen fixation are the major sources of N in the organic farming systems. Legume based pastures are a major part of organic farms we sampled indicating that N fixation through legume-*Rhizobium* symbiosis can contribute a major component of N taken up by the cereals in rotation. High levels of mineral N in the soil profile, higher levels of MB-N and potential mineralizable N after pastures (in the pre-sowing samples) suggest that N fixation by legumes may be contributing significantly to the N cycle under organic farming systems. Roper and Ladha (1995) suggested that nitrogen fixation by free-living N fixing microorganisms can make a significant contribution to the soil N cycle either as part of microbial communities in the rhizosphere or near cereal stubble. The potential for N fixation by FLN microbial communities can be estimated by measuring either their populations or activity.

Our results on the amount of DNA of FLN microorganisms (based on the amount of *nif*H gene copies) showed differences between soil types but no consistent effect of organic farming compared to conventional farming systems. In the Mallee soils, *nif*H amount was lower in the organic farm soils and no-till soils compared to the cultivated system. Gupta et

al. (2006) reported that the potential for FLN fixation activity, measured using acetylene reduction activity was higher in systems retaining cereal stubble than in no stubble treatment.

The presence of high mineral N levels in soil in the organic systems could inhibit FLN fixation activity (Roper and Ladha, 1995). The increasing trend to growing cereal crops as part of broad acre organic farming system suggests a greater potential for increased N inputs from this process. Available information on the dynamics of FLN fixation in organic farming systems is very limited and our results are some of the first available information about *nif*H DNA levels in organic farming soils in Australian soils.

Evidence for improved P uptake through increased AMF colonization under organic farming systems has been established widely (Ryan et al., 2004) whereas the effect of increased microbial activity on P mineralization in agricultural soils is not known. There are a number of phosphatase enzymes, both plant and microbial in origin, that facilitate the mineralization of organic and inorganic P from plant unavailable pools to available pools.

Soils that support higher levels of microbial biomass and activity tend to exhibit higher levels of phosphatase enzymes but application of some agrochemicals can cause a temporary reduction in their activity. We found only a small difference in the activity of monoester phosphatases in soils under organic farming system compared to the conventional farming soils. Our observation of higher levels of phosphatases in organic farm soils from Jamestown in SA that received ~400kg of rock phosphate suggests that higher microbial activities in organic farm soils seem to support higher P mineralization capacity.

Overall, data on phosphatase activities are only indicators of the potential for P mineralization and the actual level of P availability can depend upon soil and environmental factors. There has been a long history of higher than required levels of P fertilizer application in Australian agricultural soils resulting in large reserves of P being present in soil. Our results showing similar potential for biological P mineralization in the organic farm soils compared to conventional farm soils suggest that P availability may not be a limiting factor. However, a lack of increase in phosphatase activity in spite of higher amounts of MB suggests some type of limitation.

The significant positive response in the levels of phosphatases to RP addition in Jamestown organic farm soils suggests that lack of substrate may be one of the reasons for not finding higher levels of phosphatases at other sites. Gosling and Shepherd (2005) reported that, in Europe, organic mixed arable systems are mining reserves of phosphorus and recommends increased inputs of P and K, if long-term declines in soil fertility, and thus yields are to be avoided. Ryan et al. (2004) found no evidence of increasing grain mineral concentrations due to the replacing of soluble P fertilizers with insoluble P fertilizers under organic farming systems. They attributed the higher P grain concentrations in the conventional produce to the application of soluble P fertilizers.

Management of nutrient flows and plant health in organic farming systems is followed differently to the input-driven conventional farming systems. Therefore it is believed that underlying processes of nutrient cycling and plant health may be different, i.e. greater diversity and higher inputs from natural processes. However, the evidence to support this has been varied and sometimes conflicting, mainly because of the diversity of management practices that are categorized under the generic term ‘organic farming system’ combined with regional and soil type differences which make it difficult to generalize the conclusions.

Finally, there are a number of key soil biological processes that are important for sustainable management of any farming system and a polyphasic approach may be needed to assess and describe the overall soil health relevant at farming system scale. Widmer et al. (2006)

suggested that a polyphasic approach is needed to properly describe the soil microbiological characteristics for successful soil quality management.

Comparison of system level differences of soil health are generally done using multivariate analysis of data for soil physical, chemical and biological properties. Multivariate analysis is also used to assess differences in biodiversity data related to genetic or catabolic diversity. We compared the organic and conventional farming systems based on data on the biophysical data of soils. Results showed a clear separation of organic and conventional farming systems suggesting that the biophysical processes that dominate in these systems may be different.

Finally, results from this one year scoping study show that important differences in specific soil biological properties do exist between organic and conventional farming systems but due to the regional soil type and environmental variation it may be difficult to arrive at a generalized overarching conclusion. Results also show that individual measurements of soil properties at gross levels may not clearly reflect the differences between systems. Results also strongly support a comprehensive (polyphasic) assessment of soil biological health of organic farming systems, in particular broad acre agriculture. In addition, the belief in an enhanced soil microbial community, relative to conventional farming system, may not be a definitive feature of organic farming systems on all soil types and in all regions of Australia.

Appendix 1. Tables and figures

Table 1. Details of management practices under different farming systems on Mallee soils near Loxton, SA.

Name	Site	Farming System	Property	2007	2006	2005	2004	2003
DN	Loxton	No-Till	Crop	Wheat	Wheat	Triticale	Wheat	Wheat
		Intensive cropping	Grain yield (t/ha)	0.5	0.5	1.5	0.6	1.4
			Fertilizer (kg/ha)	18N:8P	13N:9P	5N:6P	10N:12P	16N:10P
			Cult	No-till	No-till	No-till	No-till	No-till
			Grazing	n/a	n/a	n/a	n/a	n/a
			Chem	Pre and post emergence herbicides @ 3 sprays/y				
JS	Loxton	Organic Farming	Crop	Wheat	Pasture*	Pasture	Rye	Pasture
			Grain yield (t/ha)	0.3	-	-	0.15	-
			Fertilizer (kg/ha)	Basalt-80	-	Basalt-80	-	-
			Cultivtaions	4	-	St retained	3	-
			Grazing	-	Yes	Yes	-	Yes
			Chem	n/a	n/a	n/a	n/a	n/a
		* grass-medic pasture with less than 1/5/ha drymatter						
CAH	Loxton	Conventional	Crop	Wheat	Pasture**	Wheat	Pasture	Wheat
			Grain yield (t/ha)	1.4	-	1.6	-	1.6
			Fertilizer (kg/ha)	5N:10P	-	5N:10P	-	MAP+Zn
			Cultivtaions	1	-	2	-	2
			Grazing	Yes	Yes	Yes	Yes	Yes
			Chem	Pre&Post	Pre	Pre&Post	Pre	Pre

** grass-medic pasture with >2.5 t/ha drymatter

Table 2. Details of management practices under different farming systems in southern Australian rainfed cropping region.

Site	Farming System	Property	2007	2006	2005	2004	2003
Pinaroo	Organic farming	Crop	Wheat	Clover+grass pasture			Oats
SA/Vic		Grain yield (t/ha)	0.5	-	-	-	0.6
		Fertilizer (kg/ha)	n/a	n/a	n/a	n/a	n/a
		Cultivtaions	3	-	-	-	3
		Grazing	Yes	Yes	Yes	Yes	Yes
		Chem	n/a	n/a	n/a	n/a	n/a
Pinaroo	No-Till	Crop	Wheat	Barley	Barley	Wheat	Oats/Vetch
SA/Vic	Intensive cropping	Grain yield (t/ha)	1.33	0.96	2.57	1.88	DM-3t
		Fertilizer (kg/ha)	6N:7P	24N:11P	9N:10P	12N:13P+Zn	-
		Cultivtaions	no-till	no-till	no-till	no-till	no-till
		Grazing	Yes	Yes	Yes	Yes	Yes
		Chem	Pre and post emergence herbicides@3 sprays/y				-

Jamestown	Organic farming	Crop	Barley	Ryegrass+subclover		Wheat	Pasture
SA		Grain yield (t/ha)	0.7	-	-	0.5	-
		Fertilizer (kg/ha)	Lime+Zn	-	-	Humate, Zn,Mn	
		Cultivtaions	3	-	-	3	-
		Grazing	-	Yes	Yes+hay	-	Yes+hay
		Chem	n/a	n/a	n/a	n/a	n/a

2-3 foliar sprays of carbohydrates, fish products during cropping year. Also biodynamic soil preparation 500 applied in most years

Jamestown	No-Till	Crop	Wheat	Barley	Oats	Canola	Wheat
SA	Intensive cropping	Grain yield (t/ha)	1.5	0.8	3.5	0.7	2.5
		Fertilizer (kg/ha)	20N:6P	9N:6P+Zn	9N:6P	50N:10P	18N:20P
		Cultivtaions	no-till	no-till	no-till	no-till	no-till
		Grazing	Yes	Yes	Yes	Yes	Yes
		Chem	Pre and post emergence herbicides @ 3 sprays/y				

Ardrossan	Fertilized pasture-	Crop	Grass+Medic	Oats	Barley	Pasture	Wheat
SA	crop	Grain yield (t/ha)	-	-	1.25	-	1.5
		Fertilizer (kg/ha)	-	AS+SSP#	Lime	-	Lime
		Cultivtaions	-	Direct drill	4	-	5
		Grazing	Yes	Yes	-	Yes	-
		Chem	n/a	n/a	n/a	n/a	n/a

120 kg Ammonium sulfate and 90kg Single superphosphate per ha was incorporated

Ardrossan	Organic pasture	Crop	Grass+Medic pasture (3-4 t DM/ha)				
SA		Grain yield (t/ha)	-	-	-	-	-
		Fertilizer (kg/ha)	-	AS+SSP	Lime	-	Lime
		Cultivtaions	-	Direct drill	4	-	5
		Grazing	Yes (also used for grazing by pigs)				
		Chem	n/a	n/a	n/a	n/a	n/a

Figure 1. Diversity of bacterial populations in pre-sowing soil samples under different farming systems near Loxton, SA. Dendograms based on Ward's analysis of 16S rDNA DGGE profiles using universal bacterial primers (Muyzer *et al.* 1993; Lane 1991).

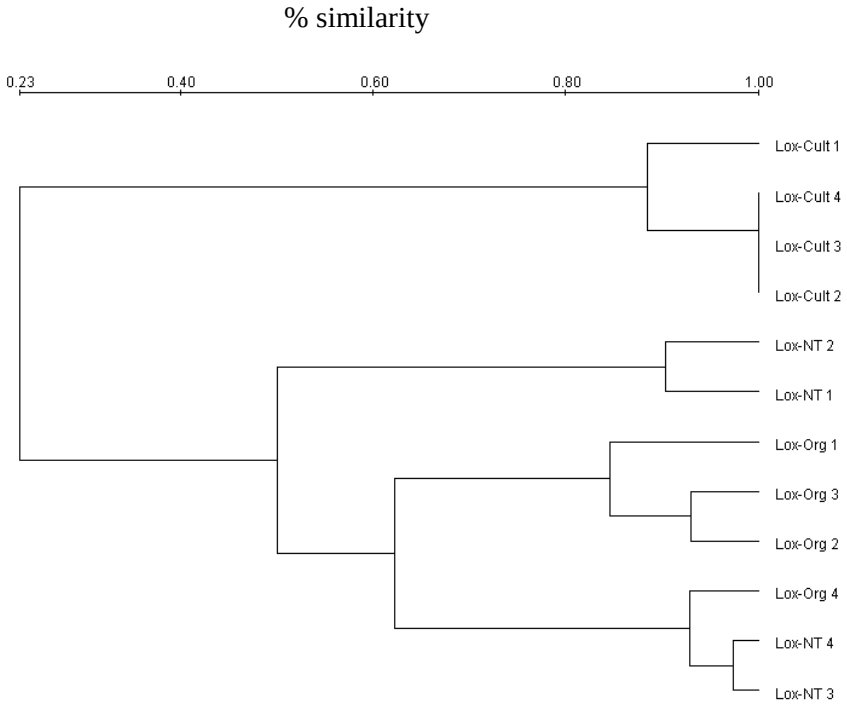


Figure 2. Diversity of soil fungal communities in pre-sowing soil samples from different farming systems near Loxton, SA. Dendograms based on Ward's analysis of ITS rDNA DGGE profiles using fungal-specific primers.

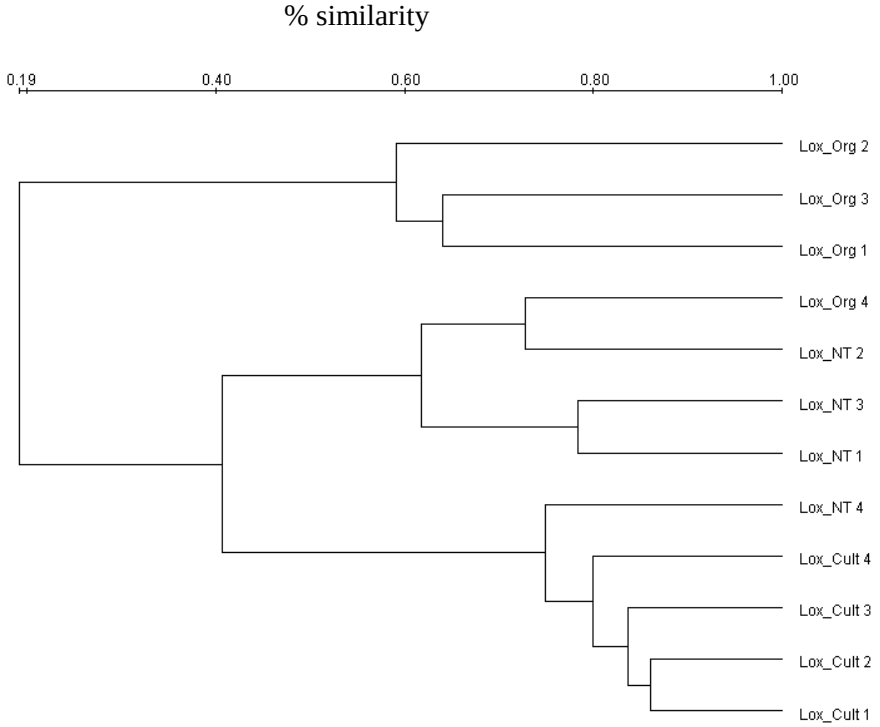


Figure 3. Diversity of bacterial communities in pre-sown samples collected from all farms. Dendograms based on Ward's analysis of 16S rDNA DGGE profiles using universal bacterial primers (Muyzer *et al.* 1993; Lane 1991).

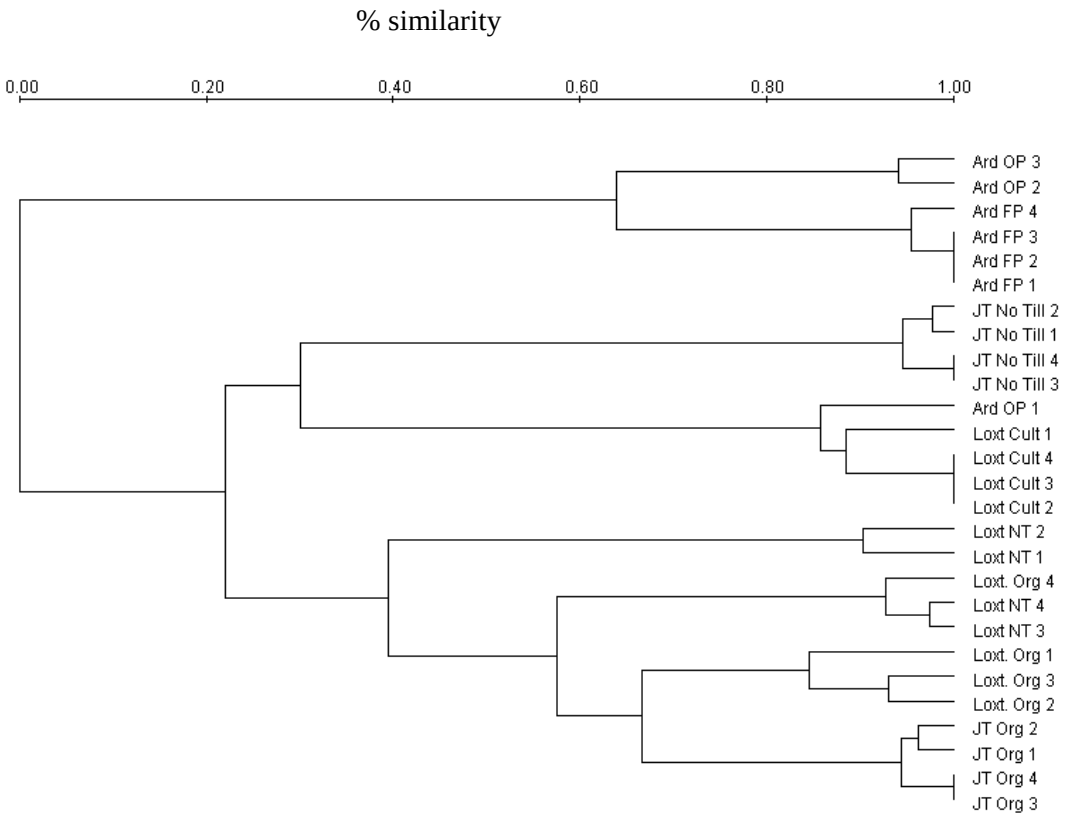


Figure 4. Diversity of soil fungal communities in pre-sowing soil samples from all farms. Dendograms based on Ward's analysis of ITS rDNA profiles using fungal-specific primers.

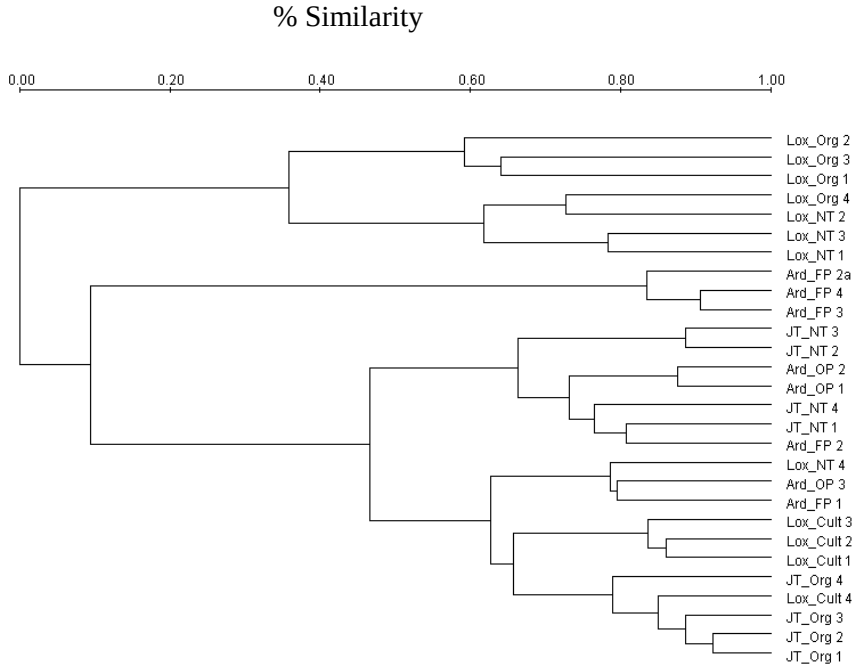
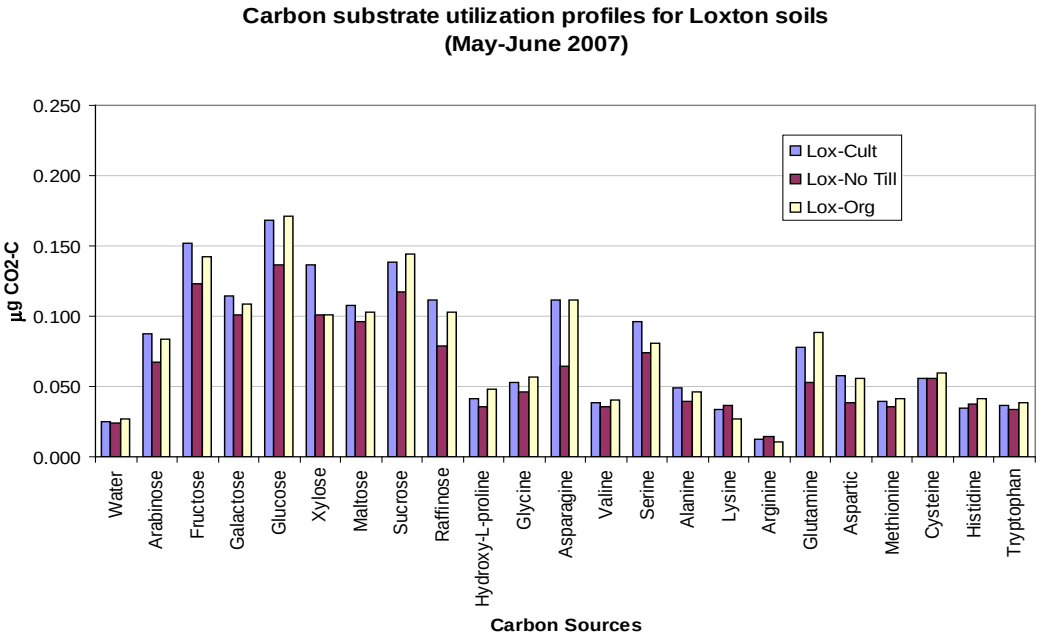


Figure 5. Carbon substrate utilization patterns for microbial communities in pre-sowing soils under different farming systems in South Australia.



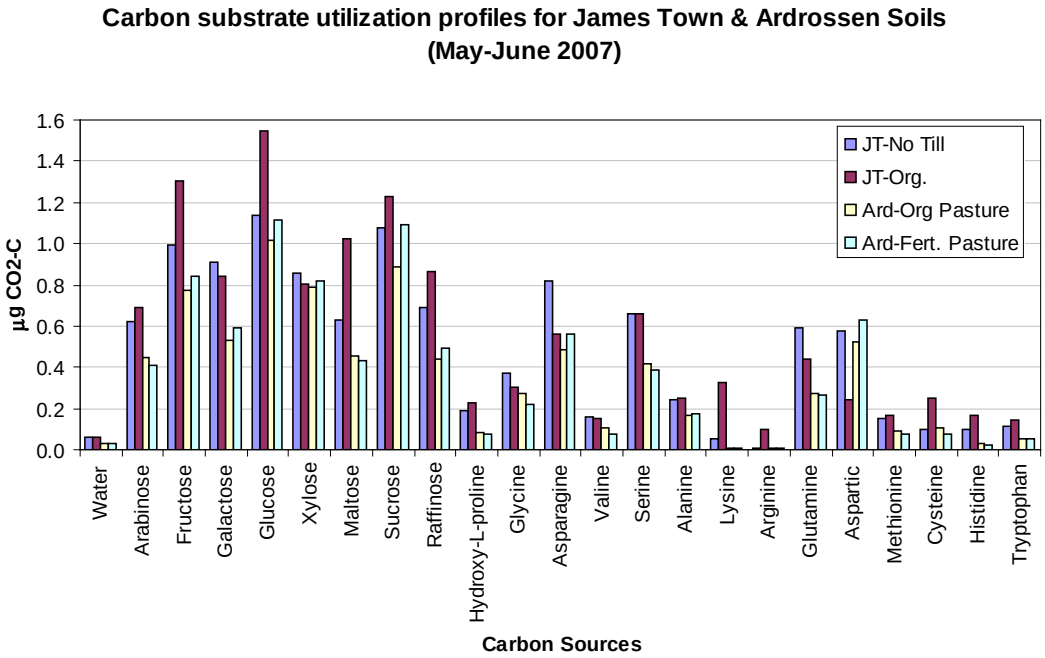


Figure 6. Carbon substrate utilization patterns for microbial communities in soils collected 'in-crop' from red-brown earth soils from SA (Jamestown) and NSW (Cootamundra).

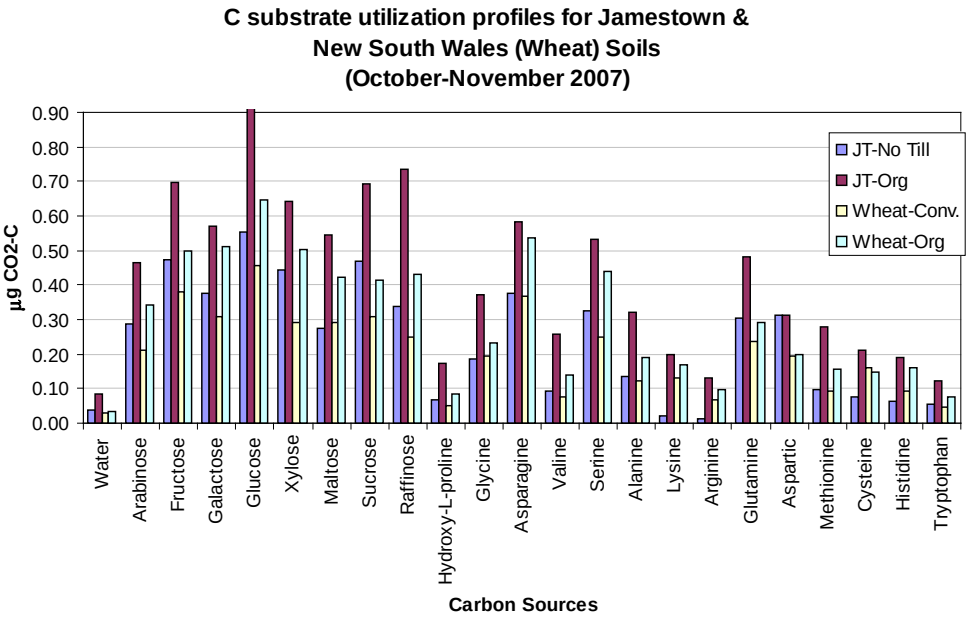


Figure 7. Canonical variate plot based on data on carbon susbstrate utilization by microbial communities in soils collected pre-sowing from different farming systems in SA. (CVA1 – 64%; CVA2 – 24%)

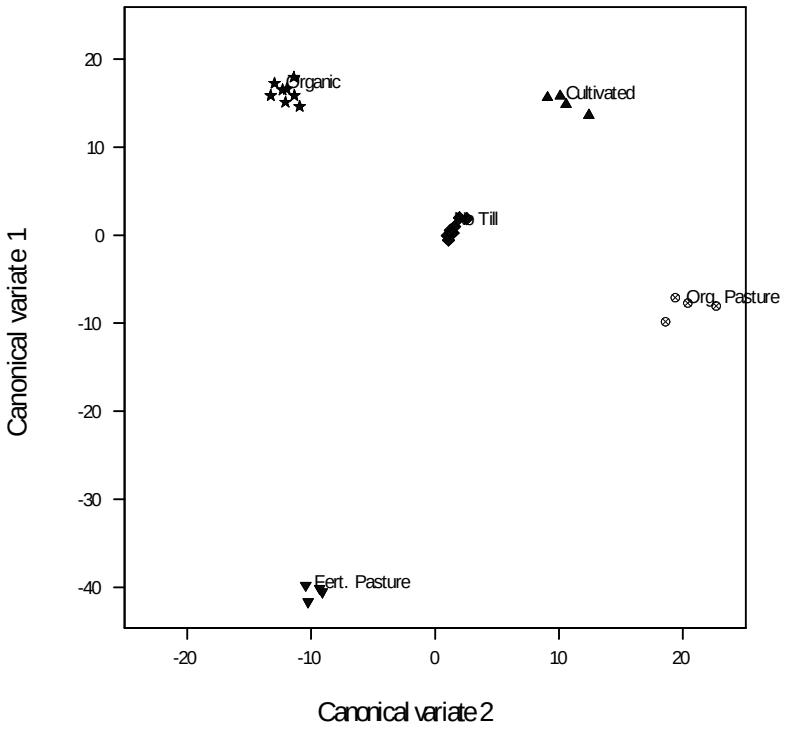


Figure 8. Canonical variate plot based on C substrate utilization profile data for 'in-crop' soil samples from different farming systems on Mallee soils in SA (CVA1 – 89%, CVA2 – 7%).Main vectors include glycine, serine and alanine.

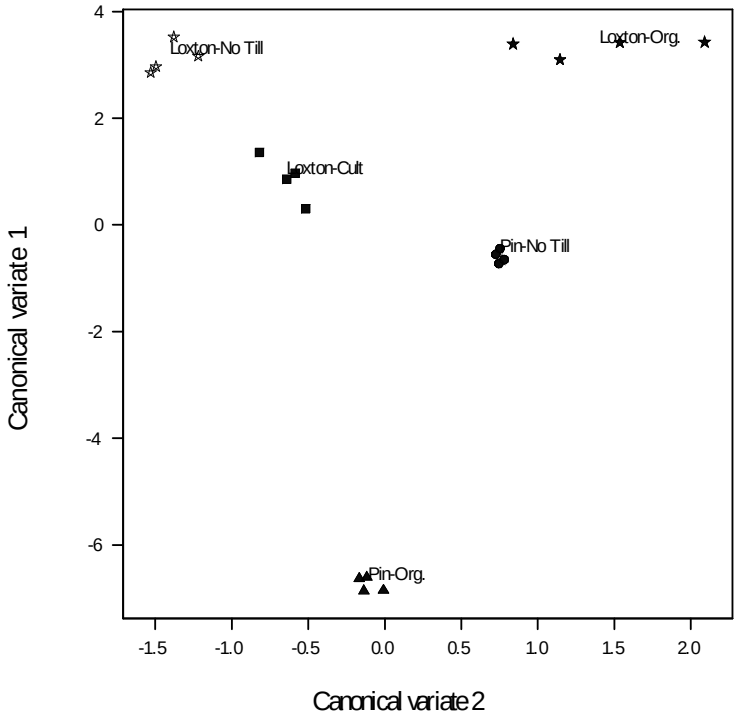


Figure 9. Canonical variate plot based on C substrate utilization profile data for 'in-crop' soil samples from organic and no-till systems at Jamestown, SA and Cootamundra, NSW (CVA1 – 53%, CVA2 – 44%). Main vectors include glucose, fructose, methionine and hydroxyproline.

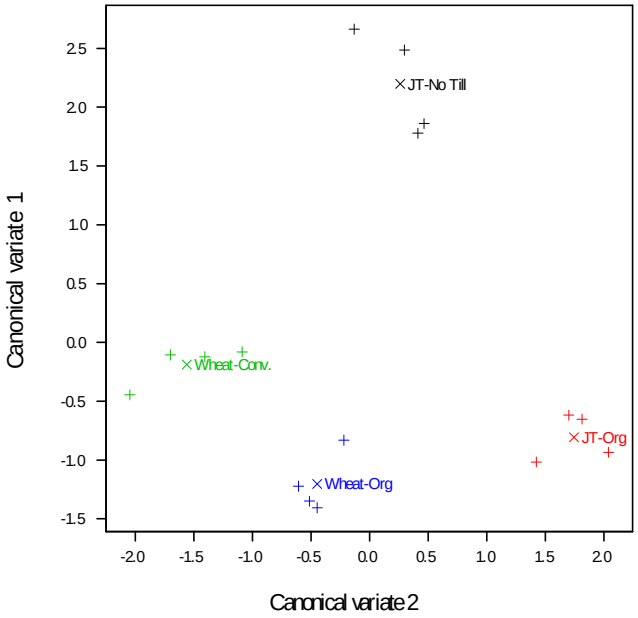


Figure 10. Canonical variate plot based on C substrate utilization profile data for 'in-crop' soil samples under no-till vs. organic farming systems in SA and NSW (CVA1 – 39%, CVA2 – 36%). Major vectors include arginine, hydrozyproline, alanine and glycine.

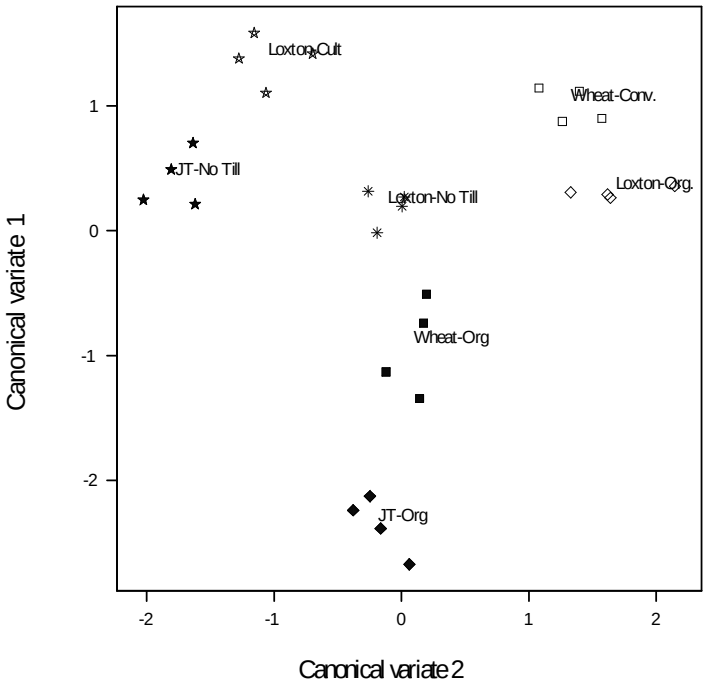


Figure 11. Canonical variate plot based on C substrate utilization profile data showing a difference between 'pre-sow and 'in-crop' soil samples from organic farming systems but no such difference for no-till samples (from Jamestown, SA; CVA1 – 66%, CVA2 – 24%).

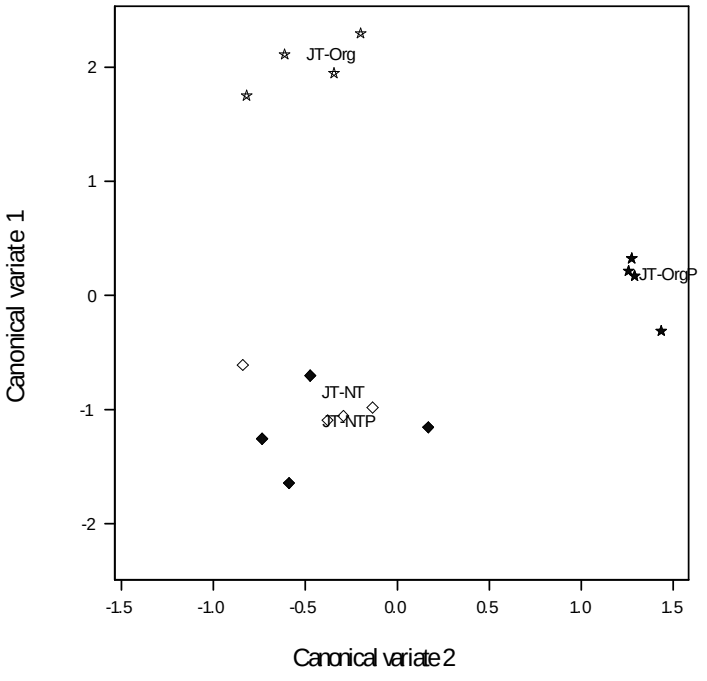


Figure 12. Canonical variate plot for catabolic profiles of soil microbial communities (pre-sowing samples) from organic farms in SA and Victoria.

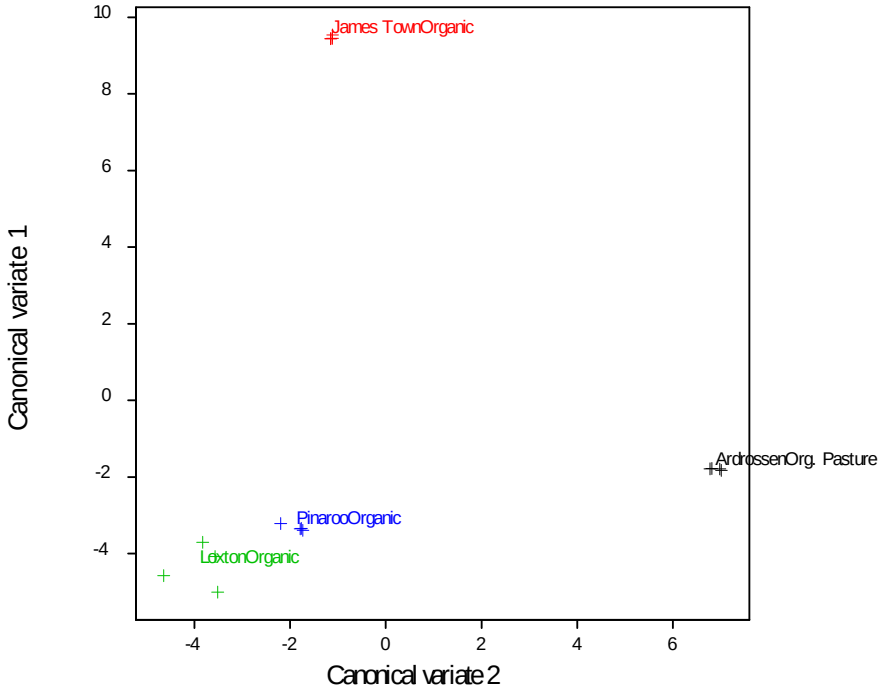


Figure 13. Canonical variate plot of catabolic profiles of microbial communities, in pre-sowing soils, from the three farming systems on Mallee soils.

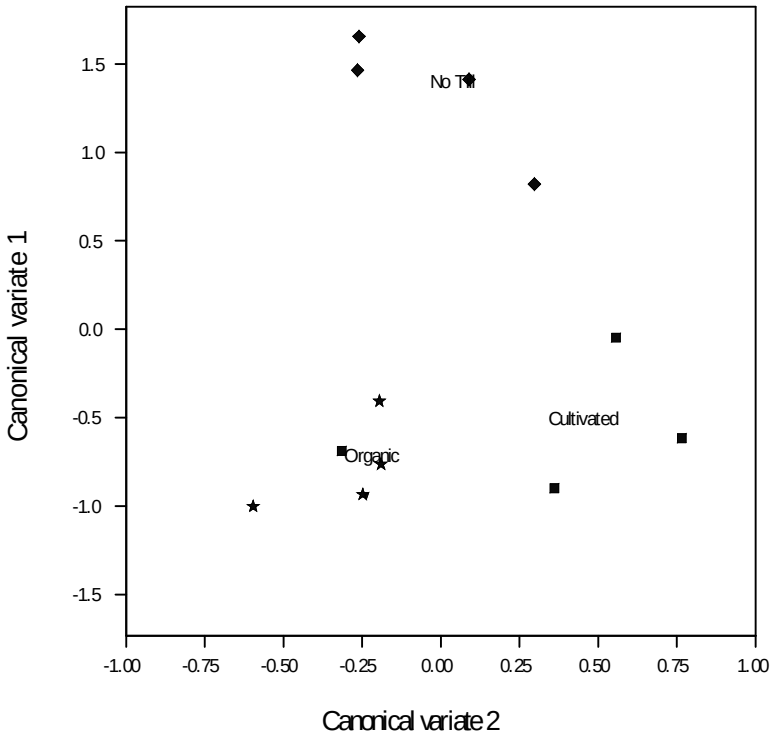


Table 2. Data on various soil biological parameters for soils under different farming systems on farms near Loxton, SA.

		Conventional cultivated system (LH)				No-Till system (DN)				Organic farming system (JS)			
		Pre-Sow	Std Dev.	In Crop	Std Dev.	Pre-Sow	Std Dev.	In Crop	Std Dev.	Pre-Sow	Std Dev.	In Crop	Std Dev.
Parameter	Units	Value	(+/-)	Value	(+/-)	Value	(+/-)	Value	(+/-)	Value	(+/-)	Value	(+/-)
Microbial Biomass-N	mgN/kg	32.23	4.78	53.81	4.41	21.70	4.54	25.89	5.27	25.03	4.44	17.13	2.89
Microbial Biomass-C	mg C/kg	223.50	33.12	373.11	30.58	150.42	31.51	179.53	36.56	173.56	30.76	118.75	20.01
Potential C Mineralisation	mg CO2/kg/day	4.93	0.41	9.94	2.74	3.99	0.25	4.09	0.95	3.11	0.33	1.97	0.30
Potential N Mineralisation (Net)	mgN/kg (21 days)	10.24	0.44	13.21	1.04	8.22	0.92	11.24	1.37	8.37	0.72	7.64	1.49
Mineral N Surface Soil (at collection)	mgN/kg	19.35		9.79		13.01		5.96		6.11		3.14	
Potential C Mineralisation (Intact Cores)	mg CO2/kg/day	13.51	2.12			8.96	0.97			8.50	1.45		
Potential N Mineralisation (Intact Cores)	kg/Ha (21 days)	11.10				9.96				8.07			
Catabolic Response	mg CO2-C/kg/hour	1.17	0.21	1.11	0.14	1.35	0.10	1.18	0.04	1.25	0.27	1.03	0.08
Rate of Nitrification (Amended)	mg N/kg/day	0.019		0.017		0.007		0.003		0.011		0.011	
Rate of Nitrification (Unamended)	mg N/kg/day	0.003		0.008		0.003		0.003		0.002		0.003	
Phosphatase Enzyme Activity	µg pNP/g	294.36				247.85				193.95		0.07	
Catabolic Diversity	# of Sources (out of 22)	15		13		21		19		20		13	
Ammonia Oxidizers		11857	1008	3818	1345	909	438	1898	874	4686	1494	2656	450
Cellulolytic Bacteria		262819	26419	141571	20826	502411	73821	69209	9911	131719	17726	72174	7998
Cellulolytic Fungi		30594	5355	90430	12807	144382	43911	143735	41962	52386	7494	41115	5533
Take All (Standardised Risk Rating)		23 (Low Risk)				<20 (BDL)				<20 (BDL)			
Rhizoctonia (AG8)	pg DNA/g Soil	110 (Medium Risk)				60 (Medium Risk)				46 (Low Risk)			
Pratylenchus neglectus	number/g Soil	4 (Low Risk)				2 (Low Risk)				<1 (BDL)			
Pratylenchus thornei	number/g Soil	<1 (BDL)				<1 (BDL)				<1 (BDL)			
Pseudogrami nearum	pg DNA/g Soil	19 (Low Risk)				0 (Detection Limit)				0 (Detection Limit)			
Common Root Rot (Bipolaris)	pg DNA/g Soil	232 (Medium Risk)				57 (Low Risk)				77 (Low Risk)			
Pythium Clade F	pg DNA/g Soil	2 (Detection Limit)				6 (Low Risk)				6 (Low Risk)			
Disease suppression	Soils from all sites showed limited disease suppression potential in a bioassay; there was a trend for higher DS potential in soils from NT systems												

Table 3. Microbial biomass and soil organic matter related parameters for pre-sowing samples.

Soil Type	Treatment	MB-N	MB-C	Mineralization potential		SIR	Respiration	Org-C	Total N
		mg / kg soil		mgN/kg/21d	mg C/kg/d	ugC/g/hr		%	%
Loxton	Cultivated	32	223	10.24	4.30	1.169	0.614	0.574	0.047
Loxton	No Till	22	150	8.22	3.85	1.346	0.576	0.474	0.037
Loxton	Organic	25	174	8.37	3.11	1.246	0.426	0.363	0.026
Pinnaroo	Organic	88	611	10.43	3.95	1.602	0.446	0.867	0.073
James Town	No Till	74	512	16.39	11.97	1.856	1.136	1.236	0.123
James Town	Organic	93	644	35.29	10.65	3.111	1.560	1.913	0.191
Ardrossan	Org. Pasture	217	1507	43.69	18.70	2.484	0.615	3.712	0.235
Ardrossan	Fert. Pasture	141	709	35.98	16.77	2.661	0.515	3.286	0.197
	LSD (P<0.05)	*44*	*148*	*12.8*	*3.5*	*0.590*	*0.250*	*0.67*	*0.025*

Table 4. Microbial biomass and soil organic matter related parameters for in-crop samples.

Soil type	Treatment	MB-N	MB-C	Mineralization potential		SIR	Respiration	Org-C	Total N
		mg / kg soil		mgN/kg/21d	mg C/kg/d	ugC/g/hr		%	%
Loxton	Cultivated	54	373	13.21	6.39	1.105	1.939	0.574	0.047
	No Till	26	180	11.24	4.09	1.181	1.775	0.474	0.037
	Organic	17	119	7.64	1.97	1.034	1.589	0.363	0.026
Pinnaroo	No Till	49	342	14.28	5.45	1.012	1.522	0.820	0.060
	Organic	79	550	14.91	6.58	1.399	1.563	0.867	0.073
James Town	No Till	102	705	23.34	12.31	2.928	2.235	1.236	0.123
	Organic	185	1283	53.34	22.53	5.846	4.930	1.913	0.191
NSW	Conventional	74	511	27.35	14.11	2.506	2.226	1.781	0.153
	Organic	123	851	43.92	15.51	3.391	2.257	1.781	0.153
	LSD (P<0.05)	33	229	22.1	6.5	0.95	0.42	0.19	0.018

Table 5. Microbial biomass and soil organic matter related parameters for 'in-crop' samples.

Factor		MB-N	MB-C	Mineralization potential		SIR	Respiration	Org-C	Total N
		mg / kg soil		mgN/kg/21d	mg C/kg/d	ugC/g/hr		%	%
Treatment	conventional	62.7	434.6	19.05	8.99	1.907	1.939	1.078	0.093
	organic	101.1	700.8	29.95	11.65	2.917	2.585	1.231	0.111
	LSD (P<0.05)	*17.0*	*115.0*	*11.70*	*2.70*	*0.468*	*0.197*	*0.100*	*0.010*
Soil type	Loxton	21.5	149.1	9.44	3.03	1.107	1.682	0.418	0.032
	Pinnaroo	64.3	445.9	14.59	6.01	1.205	1.543	0.843	0.066
	Jamestown	143.4	994.0	38.34	17.42	4.387	3.582	1.574	0.157
	NSW	98.3	681.7	35.64	14.81	2.948	2.241	1.781	0.153
	LSD (P<0.05)	*23*	*162*	*16.6*	*3.9*	*0.661*	*0.279*	*0.15*	*0.0135*
Soil type X Treat	*LSD (P<0.05)*	*33*	*230*	*ns*	*5.5*	*0.935*	*0.395*	*0.21*	*0.0195*

Table 6. Microbial biomass (MQ) and respiration quotient (RQ) values for microbial populations in pre-sowing and in-crop soil samples.

Soil Type	Treatment	MQ	RQ	MQ	RQ
		Pre-sowing		In-crop	
Loxton	Cultivated	0.041	0.020	0.065	0.027
	No Till	0.033	0.029	0.038	0.027
	Organic	0.049	0.019	0.034	0.017
Pinnaroo	No Till	-	-	0.042	0.021
	Organic	0.071	0.007	0.064	0.016
James Town	No Till	0.041	0.025	0.057	0.018
	Organic	0.035	0.017	0.068	0.018
Ardrossan	Org. Pasture	0.043	0.013	-	-
	Fert. Pasture	0.029	0.019	-	-
NSW	conventional	-	-	0.029	0.029
	Organic	-	-	0.048	0.018
	LSD (P<0.05)	*0.019*	*0.001*	*0.0162*	*ns*
Treatment	Conventional	0.036	0.027	0.0414	0.0238
	Organic	0.048	0.014	0.0535	0.0175
	LSD (P<0.05)	*0.010*	*0.007*	*0.0115*	*ns*
Soil type	Loxton	0.041	0.023	0.036	0.022
	Pinaroo	0.071	0.007	0.053	0.019
	Jamestown	0.038	0.021	0.063	0.018
	NSW	-	-	0.038	0.024
	Ardrossan	0.036	0.016	-	-
	LSD (P<0.05)	*ns*	*ns*	*0.0162*	*ns*
Soil X Treatment	*LSD (P<0.05)*	*0.0179*	*ns*	*ns*	*ns*

Figure 14. Comparison of soil biological properties under organic and conventional farming systems on Mallee soils.

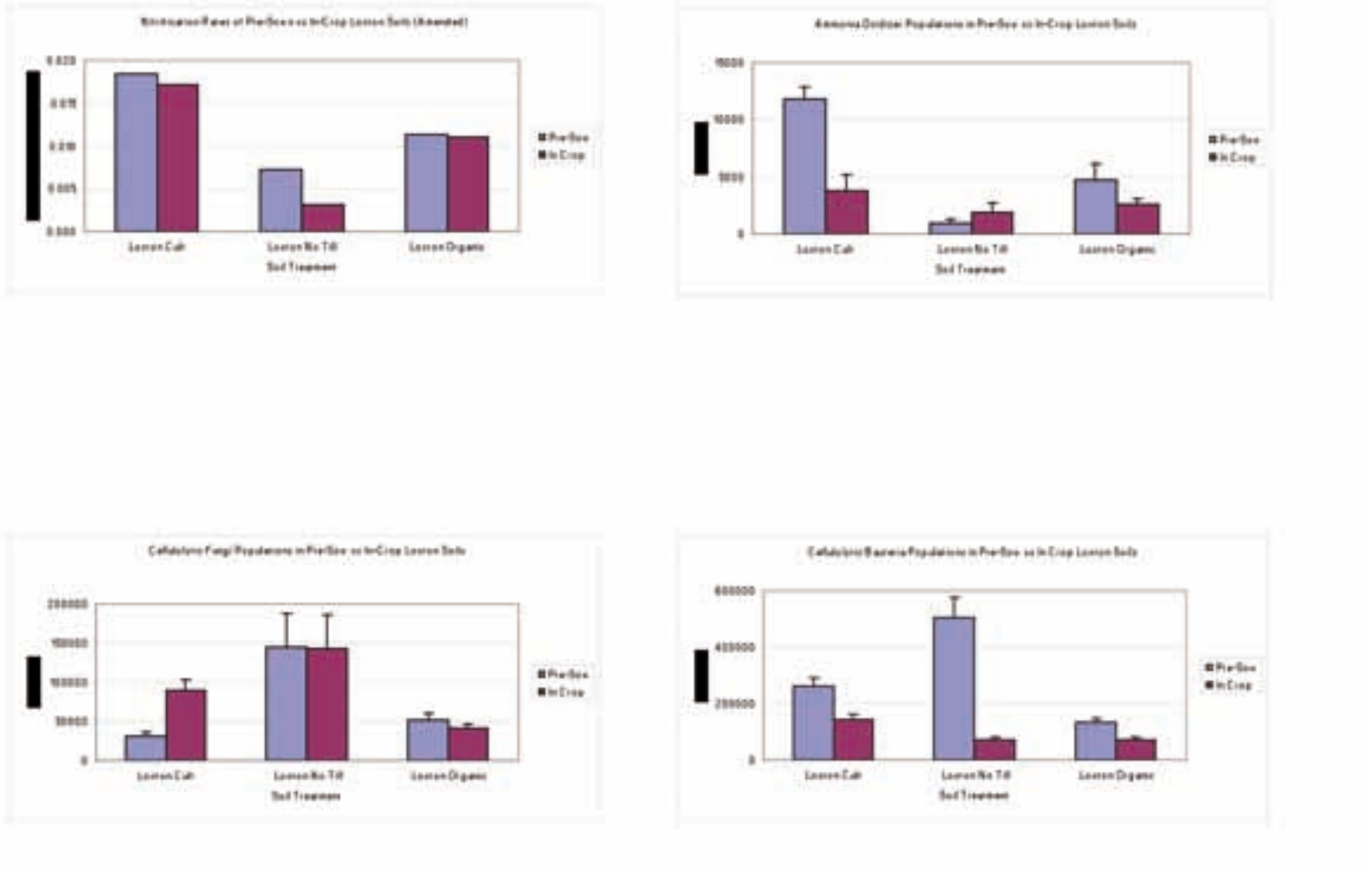
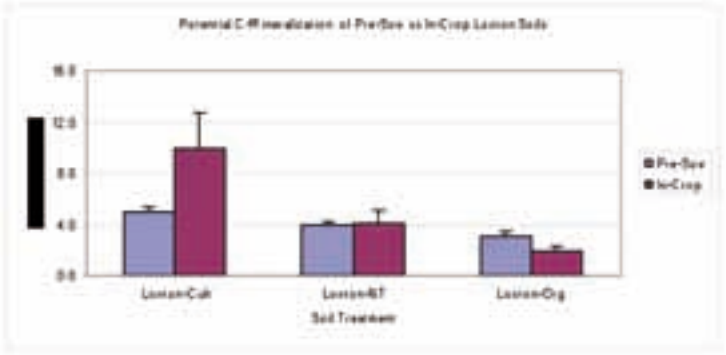
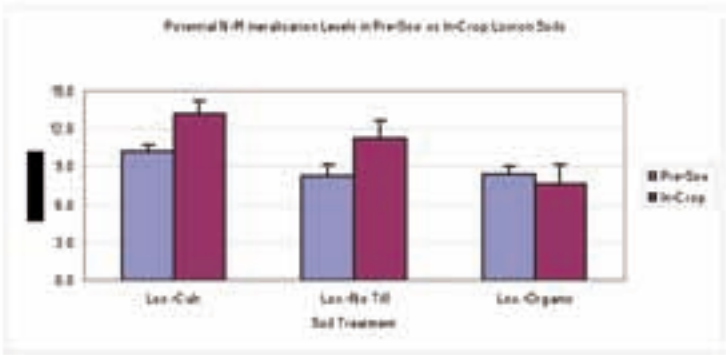
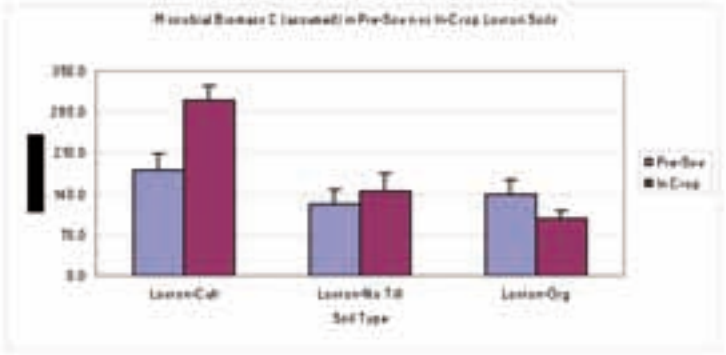


Figure 14. continued….







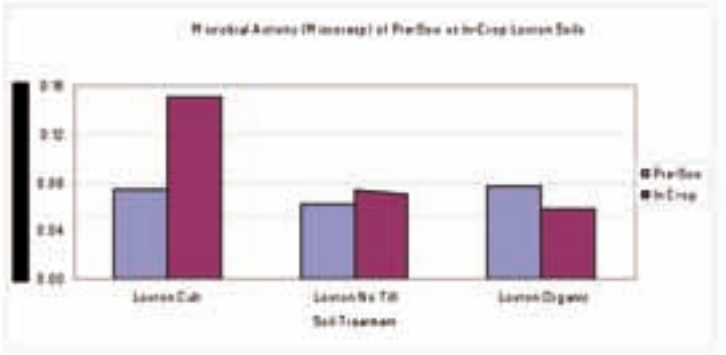


Figure 15. Populations of nitrifying microorganisms in soils from different farming systems.

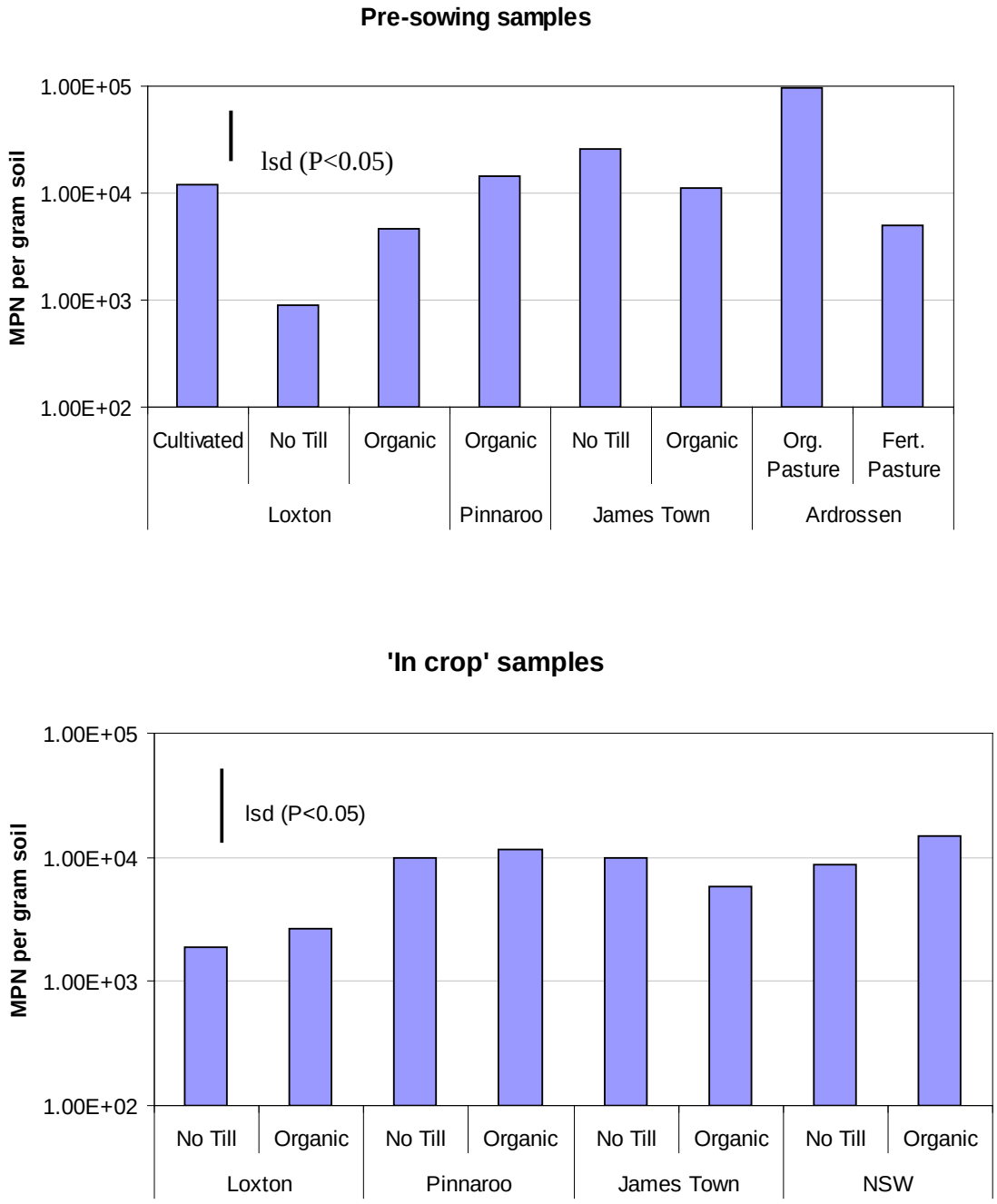
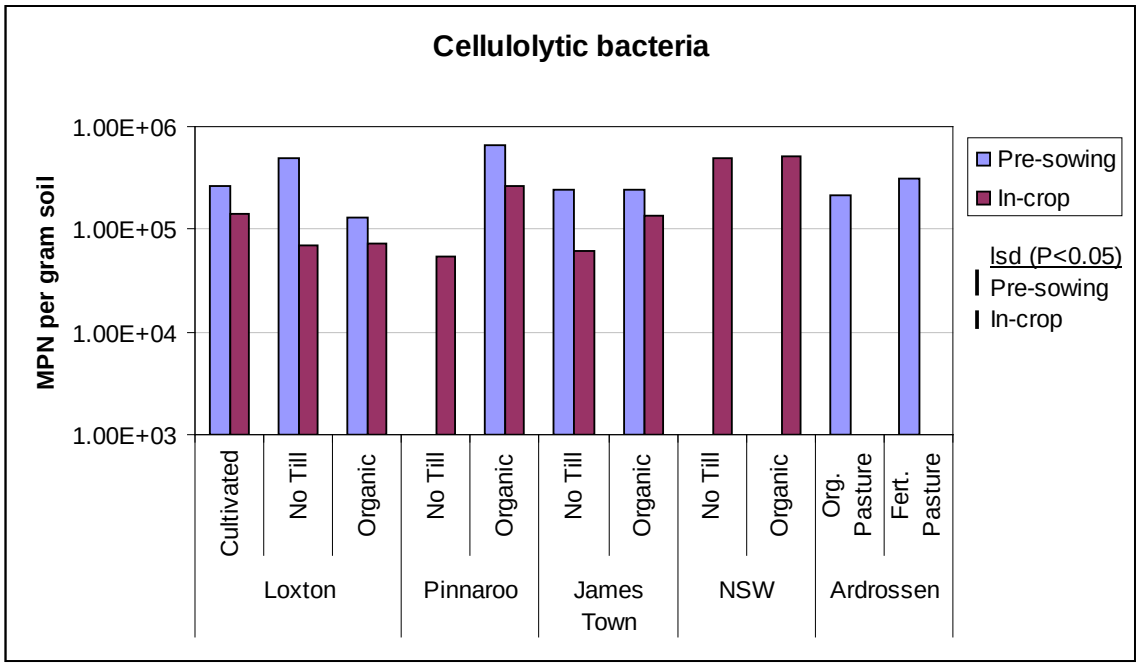


Figure 16. Populations of cellulolytic microorganisms in soils from different farming systems



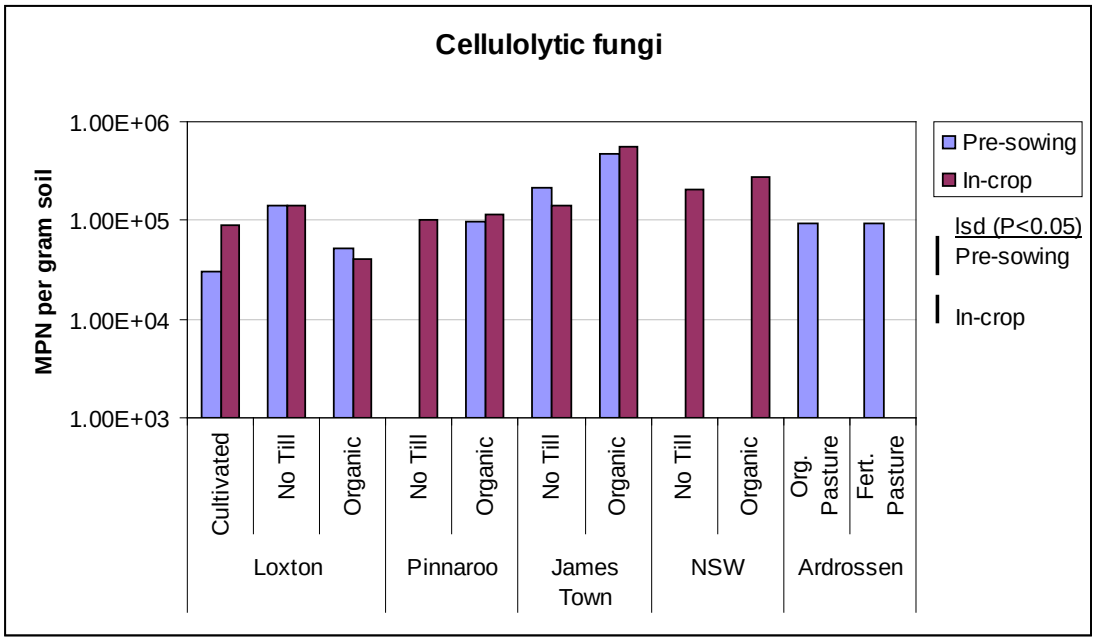


Figure 17. Relationship between the population sizes of nitrifying microorganisms measured using the culture based MPN method and DNA based technique.

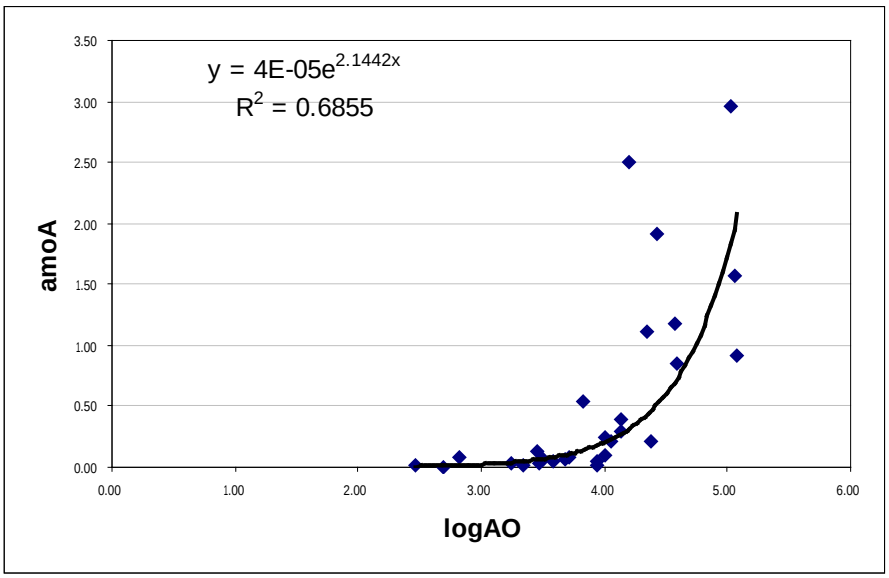


Figure 18. Relative amounts of DNA for microbial communities involved nitrification (*amoA*) and nitrogen fixation (*nifH*) in soils from different farming systems near Loxton, SA.

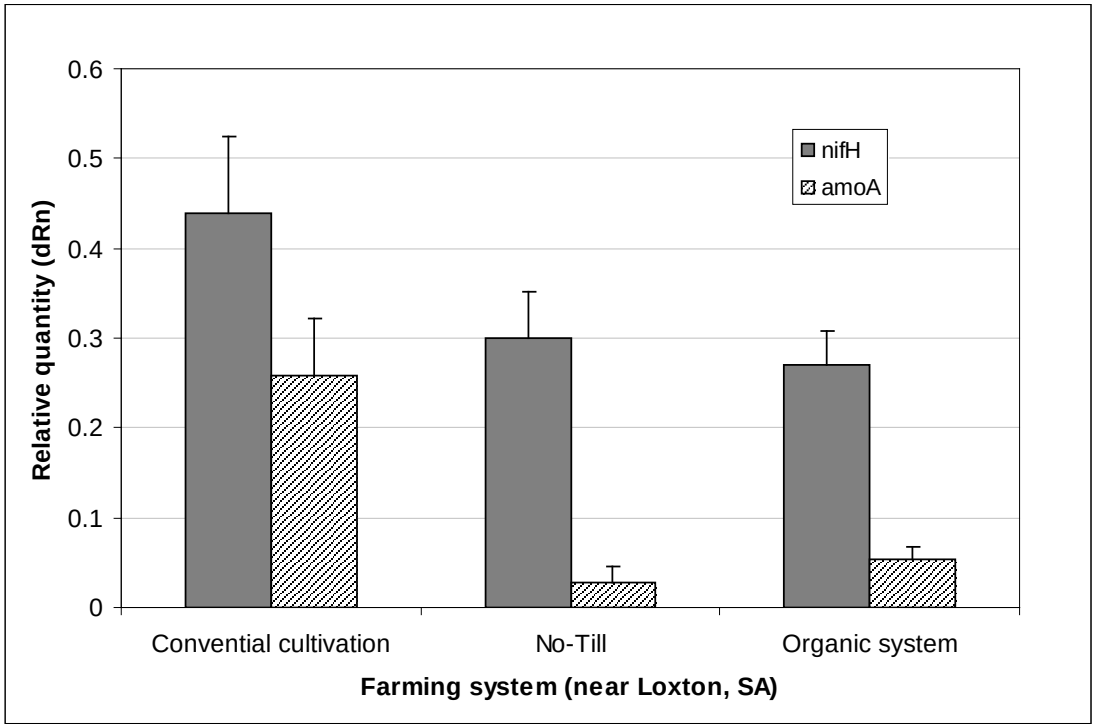


Figure 19. Data on rate of nitrification in soils from different farming systems.

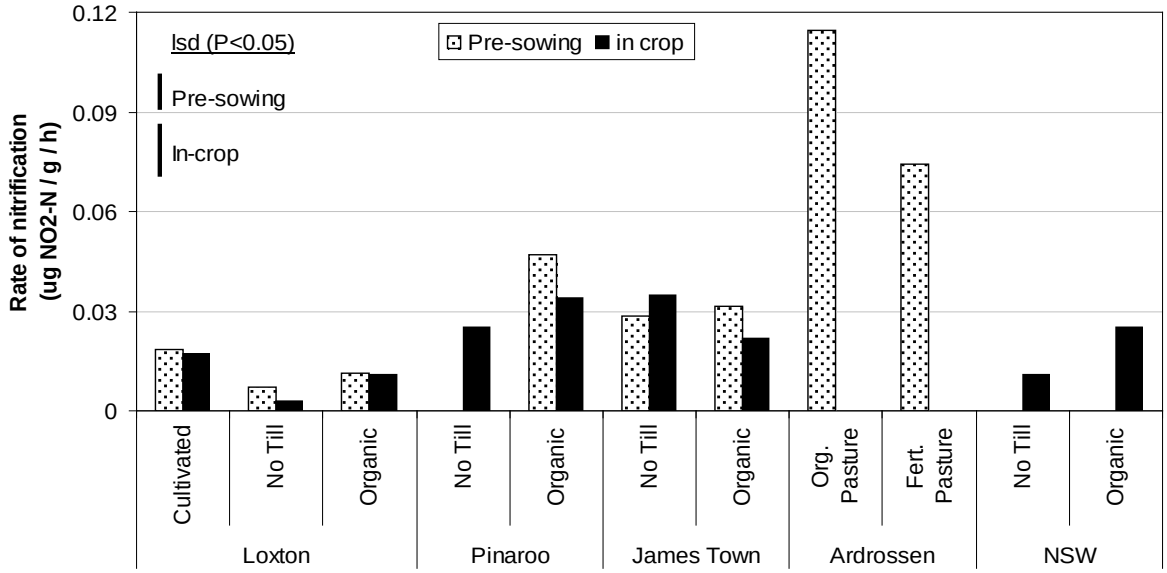


Figure 20. The influence of sampling time on the relationship between populations of nitrifying microorganisms and rates of nitrification in Mallee soils.

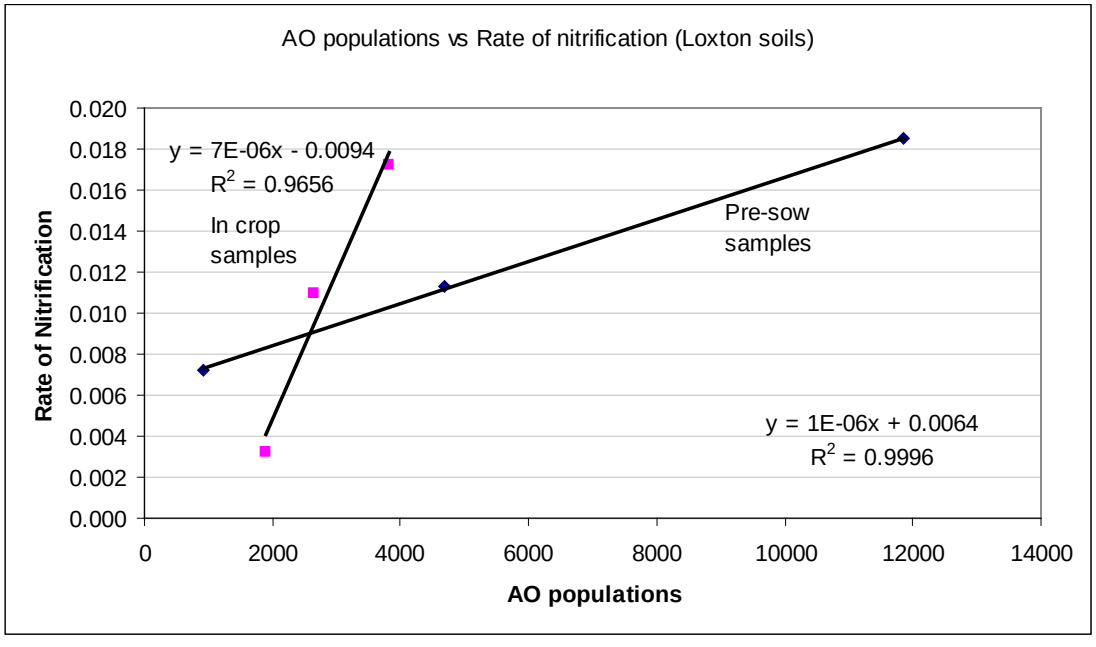


Figure 21. Mineral N levels prior to sowing in soil profiles under different farming systems on farms near Loxton, South Australia.

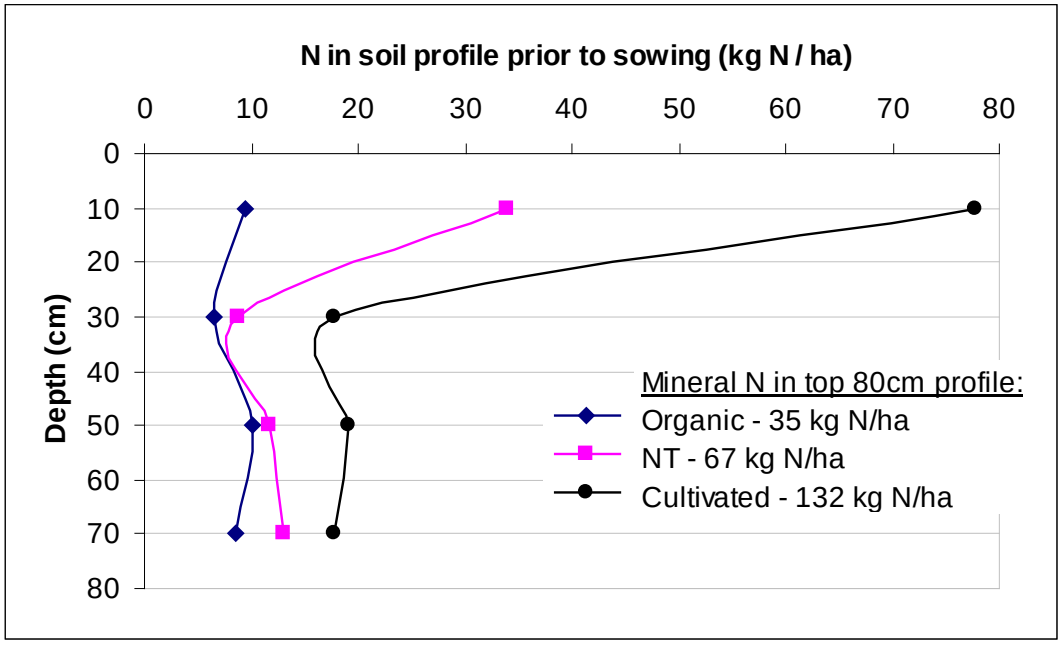


Figure 22. The activity of acid and alkaline phosphatase enzymes in organic and conventional farm soils in SA collected prior to sowing during 2007).

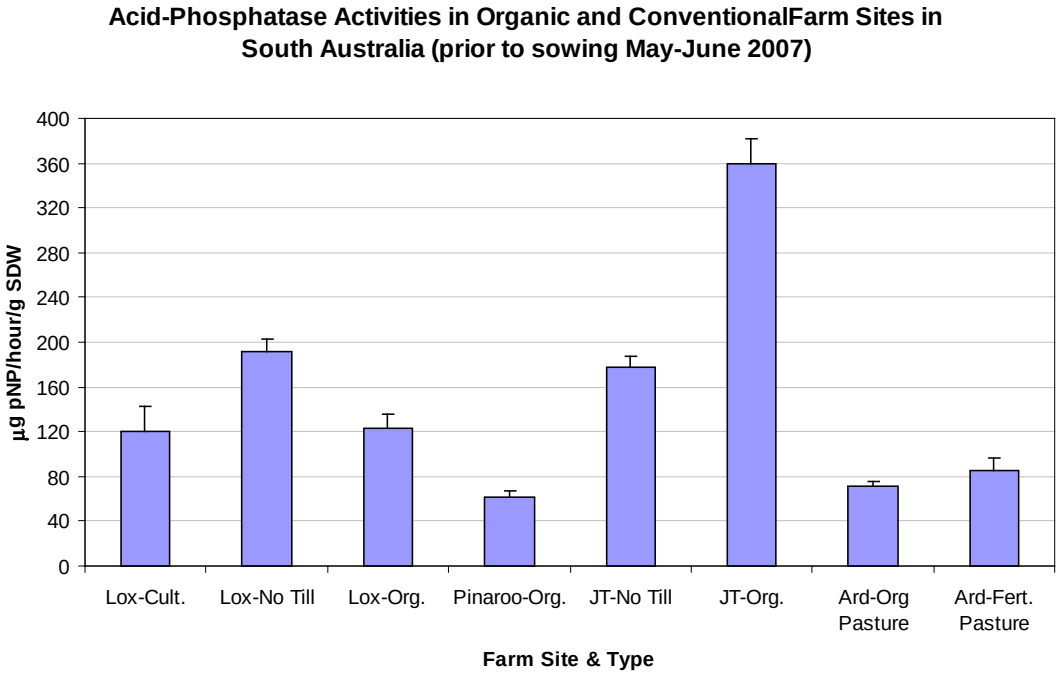


Table 7. Soil DNA levels for *Trichoderma* spp in soils from different farming systems in southern Australia.

	Trichoderma-A		Trichoderma-B	
Farming system	**(pg DNA/g Soil)**	**std err.**	**(pg DNA/g Soil)**	**std err.**
Loxton-Cult	1.62	1.26	48.4	14.1
Loxton-NT	0.36	0.36	658.2	409.3
Loxton-Org	0.62	0.62	20.8	5.9
Pin-Conventional	94.67	93.42	36.2	22.1
Pin-Organic	0.78	0.46	6.5	4.4
Jamestown-NT	0.00	0.00	15.0	8.8
Jamestown-Org	0.00	0.00	182.7	79.7
Ardrossen-OP	1.88	1.19	5.7	5.0
Ardrossen-FP	0.00	0.00	3.7	1.3
Con-Wheat (NSW)	2.08	0.93	181.3	91.6
Org-Wheat (NSW)	0.84	0.84	59.6	10.6
Con-Oats (NSW)	5.73	5.02	233.4	21.9
Org-Oats (NSW)	3.59	2.37	181.3	83.2

Table 8. Correlation matrix (R values) for biological and chemical properties of pre-sowing soil samples from organic and conventional cropping farms in SA and Victoria.

	AO_s	Bact_Diversity	Basal_C_DW	CB_s	CF_s	MB_C	MB_N	Min_C_7	Min_C_21	Min_N	Org_C_%	RofN_N	RofN_noN	SIR_Glu_DW	Total_N_%	amoA	logAO	logCB	logCF	nifH
AO_s	1																			
Bact_Diversity	0.3929	1																		
Basal_C_DW	0.4148	0.7923	1																	
CB_s	-0.1613	-0.4711	-0.0404	1																
CF_s	0.1966	0.5685	0.7299	0.2281	1															
MB_C	0.4937	0.8149	0.9142	-0.1571	0.7579	1														
MB_N	0.4937	0.8149	0.9142	-0.1571	0.7579	1.0000	1													
Min_C_7	0.6897	0.5877	0.7238	-0.0886	0.6137	0.8563	0.8563	1												
Min_C_21	0.691	0.6554	0.8311	-0.0762	0.5971	0.8209	0.8209	0.8426	1											
Min_N	0.1083	0.7331	0.7258	-0.1042	0.7829	0.7383	0.7383	0.5735	0.6573	1										
Org_C_%	0.4332	0.7964	0.8729	-0.0443	0.8611	**0.8671**	0.8671	0.7634	0.7955	0.8551	1									
RofN_N	0.6003	0.7952	0.7967	-0.2828	0.5438	0.8366	0.8366	0.8034	0.792	0.6774	0.8313	1								
RofN_noN	0.2022	0.7239	0.7756	-0.1149	0.7379	0.7734	0.7734	0.6222	0.7203	0.8805	0.8763	0.679	1							
SIR_Glu_DW	0.2525	0.805	0.8722	-0.0249	0.814	0.8629	0.8629	0.6166	0.6532	0.7986	0.8748	0.7316	0.8266	1						
Total_N_%	0.4471	0.8068	0.8838	-0.0662	0.85	0.8798	0.8798	0.7789	0.8156	0.8562	0.9988	0.8416	0.8811	0.8771	1					
amoA	0.6417	0.2846	0.3692	-0.1507	0.1788	0.5246	0.5246	0.7478	0.5629	0.0868	0.3342	0.4962	0.1599	0.161	0.3577	1				
logAO	0.8418	0.5309	0.4092	-0.3495	0.2251	0.5433	0.5433	0.6061	0.546	0.2148	0.4563	**0.7207**	0.1598	0.3103	0.4638	0.5509	1			
logCB	-0.0307	-0.3692	0.0802	0.9356	0.2958	-0.0387	-0.0387	0.0485	0.039	-0.0147	0.0784	-0.154	-0.0198	0.0613	0.0542	-0.0867	-0.2437	1		
logCF	0.247	0.5089	**0.7689**	0.2419	0.9159	0.7921	0.7921	0.63	0.6632	0.6416	0.7699	0.5097	0.6731	**0.8056**	0.771	0.2891	0.1878	0.2967	1	
nifH	0.2847	0.7779	0.8707	-0.1713	0.7005	0.85	0.85	0.7054	0.6256	0.6543	0.8378	0.7302	0.7039	0.7765	0.8432	0.4001	0.3754	-0.0448	0.6601	1

Table 9. Correlation matrix (R values) for biological and chemical properties of pre-sowing soil samples from organic and conventional farms (cropping and pasture) in SA and Victoria.

	AO_s	Bact_Diversity	Basal_C_DW	CB_s	CF_s	MB_C	MB_N	Min_C_7	Min_C_21	Min_N	Org_C_%	RofN_N	RofN_noN	SIR_Glu_DW	Total_N_%	amoA	logAO	logCB	logCF	nifH
AO_s	1																			
Bact_Diversity	-0.123	1																		
Basal_C_DW	-0.014	0.7833	1																	
CB_s	-0.152	-0.3333	-0.0498	1																
CF_s	-0.067	0.5849	0.7312	0.2388	1															
MB_C	0.6664	-0.1787	0.077	-0.1897	0.0591	1														
MB_N	0.6664	-0.1787	0.077	-0.1897	0.0591	1	1													
Min_C_7	0.5352	-0.2099	0.0981	-0.0801	0.1085	0.9085	0.9085	1												
Min_C_21	0.5455	-0.1602	0.1892	-0.1084	0.1131	0.8997	0.8997	0.9351	1											
Min_N	0.47	0.0466	0.2229	-0.095	0.3351	0.8384	0.8384	0.8119	0.7986	1										
Org_C_%	0.6236	-0.2074	0.0286	-0.0058	0.1307	0.8847	0.8847	0.8985	0.8607	0.8825	1									
RofN_N	0.7191	**-0.3515**	-0.1173	-0.1016	-0.0952	0.9161	0.9161	0.8729	0.8614	0.772	0.917	1								
RofN_noN	0.4027	0.0797	0.3104	-0.1745	0.3516	0.6994	0.6994	0.6781	0.7408	0.7977	0.7119	0.6605	1							
SIR_Glu_DW	0.2764	0.3031	0.5059	-0.0265	0.5372	0.6481	0.6481	0.6657	0.6403	0.8159	0.7279	0.5172	0.7463	1						
Total_N_%	0.5659	0.0522	0.3236	-0.0867	0.3814	0.8473	0.8473	0.8734	0.8653	0.9078	0.9209	0.8115	0.8603	0.8462	1					
amoA	0.648	0.1048	0.2638	-0.2256	0.0598	0.4422	0.4422	0.4707	0.441	0.224	0.283	0.374	0.2616	0.1754	0.3813	1				
logAO	0.7746	0.1702	0.2035	-0.3568	0.0751	0.5831	0.5831	0.5373	0.5394	0.4119	0.5056	0.5895	0.3962	0.3438	0.5742	**0.6641**	1			
logCB	-0.083	-0.275	0.0333	0.9436	0.2889	-0.1108	-0.1108	0.0207	-0.0166	-0.0043	0.0933	-0.0269	-0.0891	0.0641	0.0237	-0.1864	-0.2588	1		
logCF	0.0279	0.4556	**0.7111**	0.2751	0.902	0.1983	0.1983	0.2546	0.2699	0.3774	0.2652	0.0526	0.4042	0.6282	0.4611	0.1367	0.1024	0.3271	1	
nifH	0.5088	-0.125	0.1862	-0.1421	0.1641	0.7815	0.7815	0.8233	0.7836	0.7264	0.8585	0.7706	0.7145	0.7091	0.8775	0.3458	0.4673	-0.0415	0.274	1

Note: P<0.05 – light blue, P<0.01 – yellow; P<0.001 – dark blue (for both Table 8 and 9).

Table 10. Amounts of DNA for various fungal and nematode pathogens in soils from organic and conventional cropping systems.

			pseudogrami				Pythium					
	AG8		nearum		Bipolaris		Clade F		Blackspot		Take-All	
Farmer	(pg DNA /g soil)	std err.	(pg DNA/g soil)	std err.	(pg DNA/g Soil)	std err.	(pg DNA/g Soil)	std err.	(pg DNA/g Soil)	std err.	(pg DNA/g Soil)	std err.
Loxton-Cult	93.50	27.34	10.50	8.21	101.00	31.46	4.75	1.03	0.00	0.00	4.50	0.87
Loxton-NT	75.75	43.29	0.00	0.00	41.75	14.52	16.50	4.94	0.00	0.00	0.00	0.00
Loxton-Org	25.50	9.19	0.00	0.00	21.25	12.04	35.25	15.80	0.00	0.00	0.00	0.00
Pin-Conventional	384.00	115.78	0.00	0.00	5.25	1.25	21.00	10.32	0.50	0.29	0.00	0.00
Pin-Organic	47.25	17.13	0.00	0.00	7.75	2.50	17.00	2.35	0.00	0.00	0.00	0.00
Jamestown-NT	12.50	12.50	3.75	1.89	5.25	1.80	105.50	13.03	2.25	0.75	2.00	0.82
Jamestown-Org	0.25	0.25	108.25	107.92	20.00	13.27	392.50	70.31	90.25	28.14	43.75	38.50
Ardrossen-OP	0.00	0.00	1.67	1.67	475.67	85.25	36.33	18.77	3.00	3.00	54.67	27.34
Ardrossen-FP	0.00	0.00	1.25	0.95	29.25	5.94	17.50	5.04	11.00	2.61	3.00	1.00
Con-Wheat (NSW)	0.25	0.25	0.00	0.00	2.00	1.35	199.00	55.48	12.50	4.41	2.50	1.89
Org-Wheat (NSW)	0.00	0.00	0.00	0.00	1.00	0.41	201.25	26.75	9.75	2.59	3.00	1.78
Con-Oats (NSW)	0.25	0.25	0.25	0.25	0.50	0.29	216.25	19.19	28.50	6.06	0.00	0.00
Org-Oats (NSW)	0.00	0.00	0.00	0.00	0.25	0.25	140.75	14.73	22.75	11.51	4.50	3.84

									Fusarium	
Farmer	CCN	std err.	P. neglectus	std err.	P. thorneii	std err.	Stem Nematode	std err.	(pg DNA/g Soil)	std err.
Loxton-Cult	<1	n/a	2	0	<1	n/a	0	0	0.00	0.00
Loxton-NT	<1	n/a	1	n/a	<1	n/a	0	0	0.00	0.00
Loxton-Org	<1	n/a	1	n/a	<1	n/a	0	0	0.00	0.00
Pin-Conventional	<1	n/a	1	0	1	n/a	0	0	0.00	0.00
Pin-Organic	<1	n/a	<1	n/a	<1	n/a	0	0	0.00	0.00
Jamestown-NT	<1	n/a	<1	n/a	<1	n/a	0	0	0.00	0.00
Jamestown-Org	<1	n/a	<1	n/a	2	1	0	0	0.00	0.00
Ardrossen-OP	<1	n/a	6	9	<1	n/a	0	0	0.00	0.00
Ardrossen-FP	8	3	10	0	<1	n/a	0	0	0.00	0.00
Con-Wheat (NSW)	<1	n/a	33	10	<1	n/a	0	0	0.00	0.00
Org-Wheat (NSW)	<1	n/a	<1	n/a	<1	n/a	0	0	2.00	0.91
Con-Oats (NSW)	<1	n/a	<1	n/a	<1	n/a	0	0	0.00	0.00
Org-Oats (NSW)	<1	n/a	<1	n/a	<1	n/a	0	0	0.00	0.00

Table 11. Root disease risk ratings based on the DNA levels for fungal pathogens and plant parasitic nematodes in soils from organic and conventional cropping systems

No.	Farmer	Ggt_a Risk	Take All (SRR)	CCN Risk	CRcg Risk	Bip Risk	PythF Risk	Pn Risk	Pt Risk	SN Risk	BSr Risk
1	Loxton-Cult	Low	23	BDL	BDL	Low-Medium	BDL-NR	BDL-Low	BDL	BDL	BDL
2	Loxton-NT	BDL	<20	BDL	BDL	Low	BDL	BDL-Low	BDL	BDL	BDL
3	Loxton-Org	BDL	<20	BDL	BDL	Low	BDL	BDL-Low	BDL	BDL	BDL
4	Pin-Conventional	BDL	<20	BDL-Low	BDL	BDL-Low	NR	BDL-Low	BDL	BDL	BDL
5	Pin-Organic	BDL	<20	BDL	BDL	BDL-Low	NR	BDL	BDL	BDL	BDL
6	Jamestown-NT	BDL-Low	21	BDL	BDL	BDL-Low	BDL	BDL	BDL	BDL	BDL
7	Jamestown-Org	BDL-Medium	23	BDL	BDL	BDL-Low	NR	BDL	Low	BDL	Low
8	Ardrossen-OP	Low-Medium	37	BDL	BDL	Medium-High	BDL	Low	BDL	BDL	BDL
9	Ardrossen-FP	BDL-Low	21	Low-High	BDL	Low	BDL	Low-Medium	BDL	BDL	BDL
10	Con-Wheat (NSW)	BDL-Low	21	BDL	BDL	BDL	NR	BDL	BDL	BDL	Low
11	Org-Wheat (NSW)	BDL-Low	22	BDL	BDL-Low	BDL	NR	BDL	BDL	BDL	Low
12	Con-Oats (NSW)	BDL	<20	BDL	BDL	BDL	NR	BDL	BDL	BDL	Low-Medium
13	Org-Oats (NSW)	BDL-Low	23	BDL	BDL	BDL	NR	BDL	BDL	BDL	Low-Medium

Note: Risk categories for various diseases are based on the DNA levels of specific pathogen and the information on the soil and environmental factors that result in disease occurrence. Currently there is insufficient information on the different factors that can influence the disease occurrence therefore RDTS does not give risk categories for all the DNA data.

Table 12. Biological and chemical properties for soils under conventional and organic farming systems near James Town (SA).

		No Till				Organic			
		Pre-Sow	Std Dev.	In Crop	Std Dev.	Pre-Sow	Std Dev.	In Crop	Std Dev.
Parameter	Units	Value	(+/-)	Value	(+/-)	Value	(+/-)	Value	(+/-)
Microbial Biomass-N	µgN/g	73.79	9.22	101.65	13.51	92.87	5.18	185.09	19.04
Potential N Mineralisation (Net)	µgN/g	16.39	1.31	23.34	9.50	35.29	8.12	53.34	18.85
Mineral N Surface Soil (at collection)	µgN/g	24.97	1.91	31.36	2.26	44.92	4.64	41.22	1.32
Rate of Nitrification (Amended)	mg N/kg/hour	0.027		0.067		0.030			
Rate of Nitrification (Unamended)	mg N/kg/hour	0.006				0.010			
Microbial Biomass-C	µg C/g Soil	511.64	63.95	704.76	93.65	643.93	35.90	1283.31	132.01
Microbial Activity (DW)	µg CO2-C/hour	1.14		2.23		1.56		4.93	
Substrate Induced Respiration (Glu-DW)	µg CO2-C/hour	1.86	0.04	2.93	0.21	3.11	0.04	5.85	0.74
Catabolic Potential	µg CO2-C	0.50		0.24		0.54		0.43	
Potential C Mineralisation	µg CO2/g SDW	15.03	1.71	12.31	0.90	12.15	0.50	22.53	2.83
Catabolic Diversity	# of Sources (out of 22)	17		14		20		22	
Ammonia Oxidizers		25504	4586	9896	2982	11158	4537	5795	1927
Cellulolytic Bacteria		238114	37963	61726	6936	247886	26158	135414	21302
Cellulolytic Fungi		214538	78984	142930	20073	465196	58505	568217	42257
MB-C/Org C Quotient		0.041	0.005	0.057	0.008	0.035	0.004	0.068	0.008
CO2/MB-C Quotient		0.035	0.004	0.018	0.002	0.017	0.001	0.018	0.003
MB-N/Total N Quotient		0.060	0.008	0.083	0.011	0.050	0.006	0.098	0.012
Phosphatase Enzyme Activity	µg pNP/g Soil	329.35	20.86			436.05	15.86		
Take All (Standardised Risk Rating)		21 (Low)	0			38	14		
Rhizoctonia (AG8)	pg DNA/g Soil	<20	12.5			<20	0.25		
Pratylenchus neglectus	#/g Soil	<1 (BDL)	0			<1 (BDL)	0		
Pratylenchus thornei	#/g Soil	<1 (BDL)	0			2 (Low Risk)	1		
pseudograml nearum	pg DNA/g Soil	4 (Low Risk)	2			0 (Detection Limit)	1		
Common Root Rot (Bipolaris)	pg DNA/g Soil	5	2			20	13		
Organic C Content	%	1.236	0.344			1.913	0.178		
Total N Content	%	0.123	0.003			0.191	0.017		
Pythium Clade F	pg DNA/g Soil	106	13			392	70		

Table 13. Biological and chemical properties for soils under conventional and organic farming systems at Cootamundra in NSW.

		Conventional					Organic			
		In-Crop	Std Dev.				In-Crop	Std Dev.		
Parameter	Units	Value	(+/-)				Value	(+/-)		
Microbial Biomass-N	µgN/g	58.85	16.77				122.81	9.91		
Potential N Mineralisation (Net)	µgN/g	27.35	2.40				43.92	1.36		
Mineral N Surface Soil (at collection)	µgN/g	18.11	0.61				33.69	2.32		
Rate of Nitrification (Amended)	µg N/g/hour	0.022								
Rate of Nitrification (Unamended)	µg N/g/hour									
Microbial Biomass-C	µg C/g Soil	407.99	116.25				851.48	68.69		
Microbial Activity (DW)	µg CO2-C/hour	2.11					2.26			
Substrate Induced Respiration (Glu-DW)	µg CO2-C/hour	2.29	0.25				3.39	0.24		
Catabolic Potential	µg CO2-C	0.21					0.30			
Potential C Mineralisation	µg CO2/g SDW	14.11	2.37				15.51	1.39		
Catabolic Diversity	# of Sources (out of 22)	14					16			
Ammonia Oxidizers		8661	3129				14746	2671		
Cellulolytic Bacteria		501778	31505				508101	82648		
Cellulolytic Fungi		202914	55195				276859	33456		
MBC/Org C Quotient		0.023	0.007				0.048	0.004		
CO2/MB-C Quotient		0.074	0.049				0.018	0.002		
MB-N/Total N Quotient		0.038	0.011				0.080	0.006		
Phosphatase Enzyme Activity	µg pNP/g Soil				Conv. Oats	Std Dev.			Organic Oats	Std Dev.
Take All (Standardised Risk Rating)		21			<20		22		23	
Rhizoctonia (AG8)	pg DNA/g Soil	<1			0		0		0	
Pratylenchus neglectus	#/g Soil	<1			<1		<1		<1	
Pratylenchus thornei	#/g Soil	33	10		<1		<1		<1	
pseudogrami nearum	pg DNA/g Soil	0			<1		0		0	
Common Root Rot (Bipolaris)	pg DNA/g Soil	<1			<1		1		<1	
Organic C Content	%	1.781	0		1.571		1.791	0	1.641	
Total N Content	%	0.1531	0		0.1384		0.154	0	0.1494	
Pythium Clade F	pg DNA/g Soil	199	55.48		216	19.19	201	26.75	140	14.73

Table 14. Biological and chemical properties for soils under conventional and organic farming systems near Pinnaroo (SA and Vic border).

		Organic				Conventional	
		Pre-Sow	Std Dev.	In Crop	Std Dev.	In Crop	Std Dev.
Parameter	Units	Value	(+/-)	Value	(+/-)	Value	(+/-)
Microbial Biomass-N	µgN/g	88.18	8.65	79.29	14.28	49.34	12.64
Potential N Mineralisation (Net)	µgN/g	10.43	1.34	14.91	7.34	14.28	3.49
Mineral N Surface Soil (at collection)	µgN/g	15.90	1.63	12.68	0.26	5.56	0.17
Rate of Nitrification (Amended)	µg N/g/hour	0.047		0.033		0.024	
Rate of Nitrification (Unamended)	µg N/g/hour	0.006		0.014		0.012	
Microbial Biomass-C	µg C/g Soil	611.36	60.00	549.78	99.04	342.08	87.63
Microbial Activity (DW)	µg CO2-C/hour	0.45		1.56		1.52	
Substrate Induced Respiration (Glu-DW)	µg CO2-C/hour	1.60	0.07	1.40	0.00	1.01	0.04
Catabolic Potential	µg CO2-C	0.15		0.16		0.11	
Potential C Mineralisation	µg CO2/g SDW	5.41	0.36	6.58	1.20	5.45	0.59
Catabolic Diversity	# of Sources (out of 22)	18		15		15	
Ammonia Oxidizers		14220	1968	11531	2463	9765	3251
Cellulolytic Bacteria		654591	80879	262857	16429	54703	7542
Cellulolytic Fungi		99193	15990	116594	13779	100088	28703
MBC/Org C Quotient		0.069	0.008	0.063	0.012	0.032	0.008
CO2/MB-C Quotient		0.009	0.001	0.016	0.009	0.021	0.006
MB-N/Total N Quotient		0.119	0.014	0.108	0.020	0.077	0.020
Phosphatase Enzyme Activity	µg pNP/g Soil	303.76	5.90				
Take All (Standardised Risk Rating)				<20 (BDL)	n/a	<20 (BDL)	n/a
Rhizoctonia (AG8)	pg DNA/g Soil			47	17	384	116
Pratylenchus neglectus	#/g Soil			<1	n/a	1	n/a
Pratylenchus thornei	#/g Soil			<1	n/a	1	n/a
pseudogrami nearum	pg DNA/g Soil			0	n/a	0	n/a
Common Root Rot (Bipolaris)	pg DNA/g Soil			8	2.5	5	1.25
Organic C Content	%	0.873	0.300			1.068	0.000
Total N Content	%	0.074	0.003			0.064	0.000
Pythium Clade F	pg DNA/g Soil			17	2.3	21	10.3

Table 15. Biological and chemical properties for soils under conventional and organic farming systems near Ardrossan (SA).

		Fertilized Pasture		Organic Pasture	
		Pre-Sow	Std Dev.	Pre-Sow	Std Dev.
Parameter	Units	Value	(+/-)	Value	(+/-)
Microbial Biomass-N	µgN/g	140.57	38.32	217.28	11.19
Potential N Mineralisation (Net)	µgN/g	35.98	4.44	43.69	7.13
Mineral N Surface Soil (at collection)	µgN/g	16.56	3.78	51.27	9.74
Rate of Nitrification (Amended)	µg N/g/hour	0.146		0.224	
Rate of Nitrification (Unamended)	µg N/g/hour	0.008		0.011	
Microbial Biomass-C	µg C/g Soil	974.59	265.69	1506.50	77.57
Microbial Activity (DW)	µg CO2-C/hour	0.51		0.62	
Substrate Induced Respiration (Glu-DW)	µg CO2-C/hour	2.66	0.06	2.48	0.38
Catabolic Potential	µg CO2-C	0.41		0.37	
Potential C Mineralisation	µg CO2/g SDW	18.64	1.91	20.17	1.18
Catabolic Diversity	# of Sources (out of 22)	14		14	
Ammonia Oxidizers		5071	1297	95537	18944
Cellulolytic Bacteria		310729	56076	216016	34251
Cellulolytic Fungi		93098	11096	94496	19594
MBC/Org C Quotient		0.0292	0.0064	0.0431	0.0060
CO2/MB-C Quotient		0.0187	0.0028	0.0028	0.0008
MB-N/Total N Quotient		0.071	0.018	0.093	0.004
Phosphatase Enzyme Activity	µg pNP/g Soil	441.21	11.438	326.15	44.11
Take All (Standardised Risk Rating)		21	0	37	7
Rhizoctonia (AG8)	pg DNA/g Soil	0	0	0	0
Pratylenchus neglectus	#/g Soil	10	2	6	4
Pratylenchus thornei	#/g Soil	<1	n/a	<1	n/a
pseudogrami nearum	pg DNA/g Soil	1	1	2	1.5
Common Root Rot (Bipolaris)	pg DNA/g Soil	29	6	476	74
Organic C Content	%	2.200	0.240	2.500	0.200
Total N Content	%	0.197	0.005	0.241	0.022
Pythium Clade F	pg DNA/g Soil	18	5	36	16

Figure 23. Canonical variate plot showing a clear difference between soil samples, collected prior to sowing, from organic, no-till and conventional cultivated systems based on soil biological and chemical properties (three sites in SA; CVA1 – 81%, CVA2 – 19%)

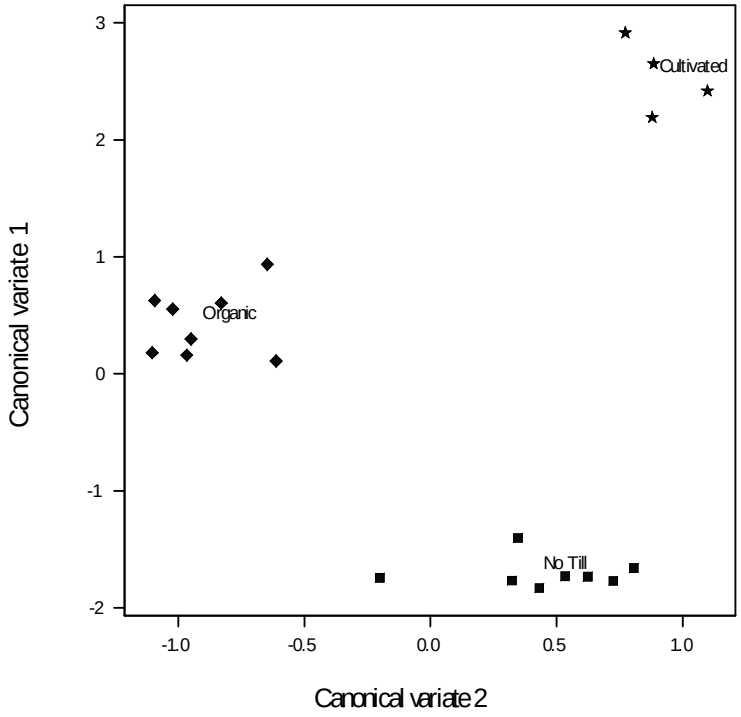


Figure 24. Canonical variate plot showing differences between cropped and pasture soils, collected prior to sowing, from organic, no-till and conventional cultivated systems based on soil biological and chemical properties (four sites in SA; CVA1 – 68%, CVA2 – 20%)

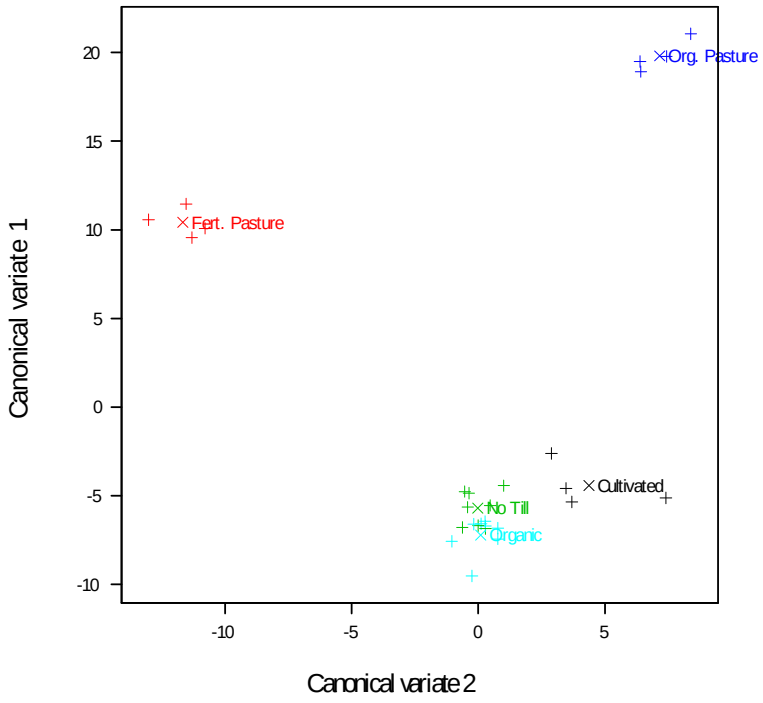
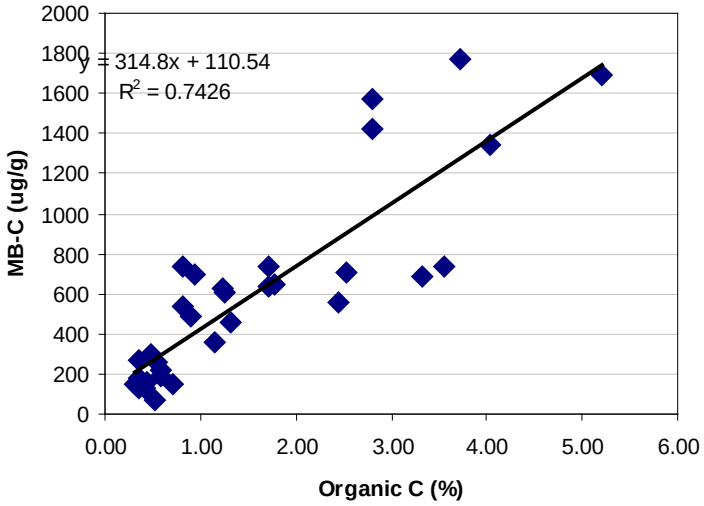
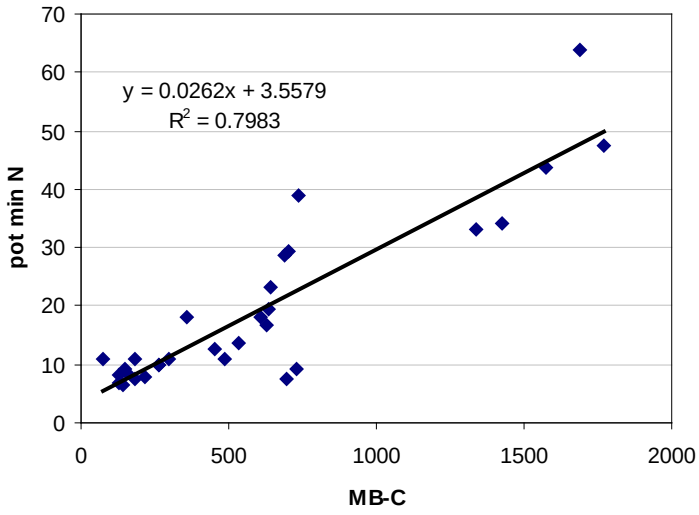


Figure 25. Relationship between soil organic C, microbial biomass C and N mineralization potential values for 'pre-sowing' samples from organic and conventional farming systems.





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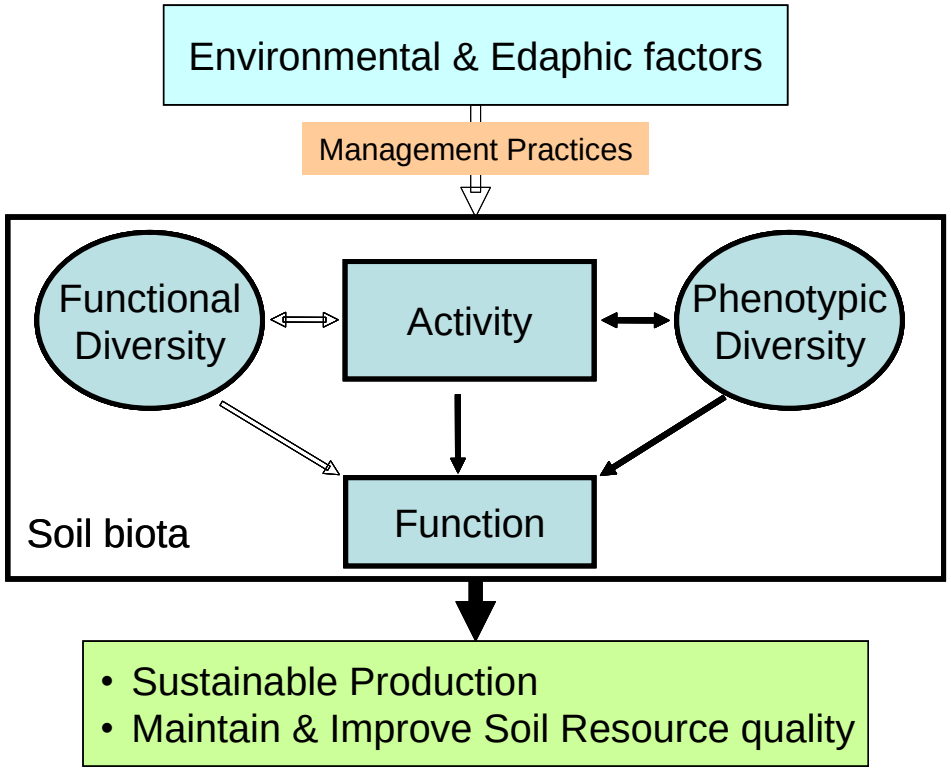
Appendix 3. Unravelling the soil biology black box

Unravelling the soil biology black box to assess the soil biological status under organic farming systems – an integrated polyphasic approach



Phenotypic diversity:
Soil bacteria
Soil Fungi

Functional diversity:
Catabolic diversity
Soilborne pathogens
Nitrifying microorganisms
Cellulolytic microorganisms
Free-living N fixing bacteria

Activity:
Microbial biomass
Microbial activity
Nitrification
Phosphatase activity

Function:
N Mineralization
Disease suppression potential

Sustaining Soil Biological Functions in Organic Systems

by Vadakattu V.S.R. Gupta

Publication No. 08/203

This report provides information from one of the few comprehensive assessments of the diversity and functional capability of soil microbial communities under broad acre organic farming systems in the southern Australian agricultural region.

Results reported clearly show the importance of using a polyphasic approach to the proper assessment of soil biological health relevant to nutrient cycling, plant health and overall catabolic potential under organic farming systems and allows comparison with neighbouring conventional farms.

Cover photo: Wheat grown organically (left) and under a conventional system (right) and soil microbes (below)

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