Natural Resources
Eyre Peninsula

RURAL
SOLUTIONS SA
PIRSA

UNDERSTANDING SOIL BIOLOGY: WHAT LIES BENEATH THE SURFACE?

AN INVESTIGATION INTO THE DIVERSITY AND ABUNDANCE OF SOIL BIOLOGY IN SOME TYPICAL SOILS ON EYRE PENINSULA (2016-2018).

Final Project Report

Report prepared by;

Brett Masters

Soil and Land Management Consultant

PIRSA Rural Solutions SA, Port Lincoln

Government of South Australia
Department of Environment and Natural Resources

Australian Government

National Landcare Programme

This project was supported by Natural Resources Eyre Peninsula Project with funding from the Australian Government and the Department of Environment, Water and Natural Resources "Healthy Soils for Premium Food" Project.

SOUTH AUSTRALIA

Government of South Australia
Primary Industries and Regions SA

UNDERSTANDING SOIL BIOLOGY: WHAT LIES BENEATH THE SURFACE?

AN INVESTIGATION INTO THE DIVERSITY AND ABUNDANCE OF SOIL BIOLOGY IN SOME TYPICAL SOILS ON EYRE PENINSULA (2016-2018).

Information current as of 30th June 2018

Disclaimer

All enquiries

Brett Masters
Primary Industries and Regions SA (PIRSA)
PO BOX 1783, Port Lincoln SA 5606
T 08 8688 3460 F 08 8688 3407 M 0428 105 184
E brett.masters@sa.gov.au

TABLE OF CONTENTS

1 INTRODUCTION AND PROJECT BACKGROUND 3
2 PROJECT OUTLINE 3
2.1 Phase I. Soil Sampling 3
2.2 Phase II. Extension of results 3
2.3 Phase III. Reporting on project activities and key learnings from soil sampling result 3
3 Phase 1. Soil SAMPLING 4
3.1 SITE SELECTION 4
3.2 PROJECT SITES 4
3.3 SOIL SAMPLING METHODOLOGY 6
4 SAMPLING RESULTS 8
4.1 SITE #1. WH 9
4.2 SITE # 2: NL 11
4.3 SITE # 3: MH 13
4.4 SITE #4: TY 15
4.5 SITE #5: JH 17
4.6 SITE #6. SM (SATELLITE) 19
4.7 SITE #7. JP (SATELLITE) 19
5 Discussion OF RESULTS 20
5.1 Site 1. WH 20
5.2 Site 2. NL 20
5.3 Site 3. MH 20
5.4 Site 4. TY 21
5.5 Site 5. JH 21
5.6 Satellite sites 6 (SM) and 7 (JP) 21
6 PHASE II. UNDERSTANDING SOIL BIOLOGY WORKSHOPS 22
6.1 Brett Masters (Soils Consultant, PIRSA, Port Lincoln) 23
6.2 Dr Helen Hayden (Soil Microbiologist, Agriculture Victoria) 23
6.3 Dr Michael Rose (Soils project officer, DPI NSW) 23
6.4 Farmer Speakers 23
7 SUMMARY AND CONCLUSIONS 24
8 ACKNOWLEDGEMNTS 24
9 ABBREVIATIONS USED IN THIS DOCUMENT 25
10 REFERENCES, TOOLS AND FURTHER READING 25

EXECUTIVE SUMMARY

An increasing number of farmers recognise that an abundance and diversity of soil biology is important in many of the processes which drive the productivity and sustainability of agricultural soils. However, there is limited understanding of the critical concentrations and variety of beneficial soil biota in the soils of Eyre Peninsula (EP). This project aimed to:

- Improve understanding of soil biology in EP farming systems by sampling a number of regional soil types;
- Use biological assays to identify biology present in EP soils;
- Examine the impact of soil treatments on microbial biomass.

The project comprised of three distinct phases; soil sampling, extension of results and drafting a final report summarising the project activities and key learnings from soil sampling. Soil samples from 5 sites across Eyre Peninsula were collected in September 2017 to a depth of 30 cm for analysis of soil physical, chemical and biological parameters.

There is little information on critical values for biological assays in cropping soils in South Australia. To provide comparative values, samples were collected within a paddock from two areas of the same soil type but with different management history or distinctly different crop production (i.e. 'control vs treated' or 'good vs poor growth'). Bulked composite samples from each 10 cm depth increment were sent for laboratory analysis.

Results of soil analyses showed clear trends between microbial abundance as Microbial Biomass Carbon (MBC) and microbial activity (soil basal respiration) and chemical parameters (pH and organic matter). Applied treatments that either changed pH to a level considered optimal for plant growth (5.5 to 6.5 $CaCl_2$) or increased organic matter, increased both microbial abundance and potential microbial activity.

Although assays for total bacteria, fungi and nematodes indicated increased abundance and activity of soil microbes in response to soil modification treatments on some sites, there is currently little data directly linking an increase in these parameters to increased crop and pasture yield response.

Three workshops held in March 2018 at Streaky Bay, Rudall and Ungarra aimed to provide landholders with an introductory understanding of soil biological functions, abundance and activity. Speakers included Brett Masters (PIRSA Soils Consultant, Port Lincoln), Dr Helen Hayden (Soil Microbiologist, Agriculture Victoria), Dr Mick Rose (Soils project officer, NSW DPI) and a number of local and interstate farmer speakers.

The workshops were well attended with around 75 participants in total at the three events. Key messages from the workshops and results of soil sampling include;

- Results of soil biology analysis should not be interpreted in isolation from soil chemical and physical characteristics.
- Soil biology analysis can be expensive, thus it is important to work out which tests will provide meaningful information for changing management practices.
- For useful results advice should be sought from the laboratory on protocols for sampling, processing and delivery of samples to the laboratory.
- Pore size is critical for determining the types of organisms that can live in a soil. Compacted soils with pore size <3 um will dominated by fungi.
- Herbicide impacts on bulk soil biota and functions are minimal at label rates. However soil biota are likely to be impacted by fungicides and insecticides.
- Cover cropping can be incorporated profitably in systems which contain livestock. When trialling new systems it is important to leave control strips to enable comparison and provide information on whether the treatment imposed is providing a benefit or a cost.

1 INTRODUCTION AND PROJECT BACKGROUND

An increasing number of farmers recognise that an abundance and diversity of soil biology is important in many of the processes which drive the productivity and sustainability of agricultural soils. However, there is limited understanding of the critical concentrations and variety of beneficial soil biota in the soils of Eyre Peninsula (EP). At Eyre Peninsula Agricultural Research Foundation (EPARF) Farmer Updates in early 2017 landholders were asked whether they would be interested in attending a workshop on soil biology. There was a positive response from landholders in a number of districts including Warramboo (Central Eyre Ag Bureau), Minnipa, Rudall (Tuckey Ag and Verran-Roberts Ag Bureaux) and Franklin Harbour.

This project aimed to increase the understanding of soil biology in EP farming systems by:

- Sampling a number of regional soil types.
- Using biological assays to identify biology present in EP soils;
- Identifying and examining the impact of soil treatments on microbial biomass.

2 PROJECT OUTLINE

The project consisted of three distinct phases with specific milestones.

2.1 Phase I. Soil Sampling

Soil samples were collected in September 2017 from 5 representative soil types. Two project case study sites were sampled in Western/Central Eyre (WEP), one in Eastern Eyre (EEP) and two on Lower Eyre (LEP). In addition two satellite sites were sampled for less detailed analysis at Mt Hill and Ungarra. As there is little information on critical values for biological assays in cropping soils in South Australia, samples were taken from two areas within a paddock of the same soil type but with different management history or distinctly different crop production (i.e. 'control vs treated' or 'good vs poor growth') to provide a comparison. Bulked composite samples from each 10 cm depth increment were sent for laboratory analysis

Samples were collected and packaged according to laboratory protocols and sent to two laboratories, Microbiology Laboratories Australia (MBA) and University of South Australia (UniSA) for assays of soil microbiology (and for chemical analysis where required). Data on soil chemical and physical parameters were gathered for each project site to provide an understanding of the relationships between the various components contributing to soil health.

2.2 Phase II. Extension of results

Three 1/2 day workshops were held in March 2018 at Streaky Bay (WEP), Rudall (EEP) and Ungarra (LEP). The aim of these workshops was to provide landholders with an introductory understanding of microbial abundance and activity and soil biological functions by engagement with knowledgeable and credible scientific speakers. There was also the opportunity for participants to engage in discussion with local landholders who have adopted soil management options for improved soil biological health to on their properties.

2.3 Phase III. Reporting on project activities and key learnings from soil sampling result

This report (Phase III) aims to summarise the project activities and key learnings from soil sampling results.

3 PHASE 1. SOIL SAMPLING

3.1 SITE SELECTION

In consultation with Mary Crawford, Natural Resources Eyre Peninsula (NREP) Sustainable Agriculture program manager and David Davenport, Primary Industries and Regions SA (PIRSA) Senior Soils Consultant it was determined the key production constraints to be targeted by the sampling program were;

- Acid soils (pH <5.5 $CaCl_2$)
- Alkaline and highly calcareous soils.
- Soils with poorly structured dispersive subsoil layers (Red brown earths)
- Sands with low inherent fertility (sandy duplex soils)

It was intended that the results from analysis of soil samples would be used to;

- Identify and describe targeted microbial biology present in different soil horizons, and
- Examine the effect of various soil modifications/treatments to enhance or deter microbial activity.

3.2 PROJECT SITES

Five core sites were selected for sampling. These were; Lock (Wayne Hodge), Port Kenny (Nathan Little), Cleve (Mark Hannemann), Ungarra (Terry Young) and Cockaleechie (Jim Holman) (Figure 1). A further 2 sites were sampled at Mt Hill (Malcolm) and Ungarra (Phillis) as opportunistic satellite sites.

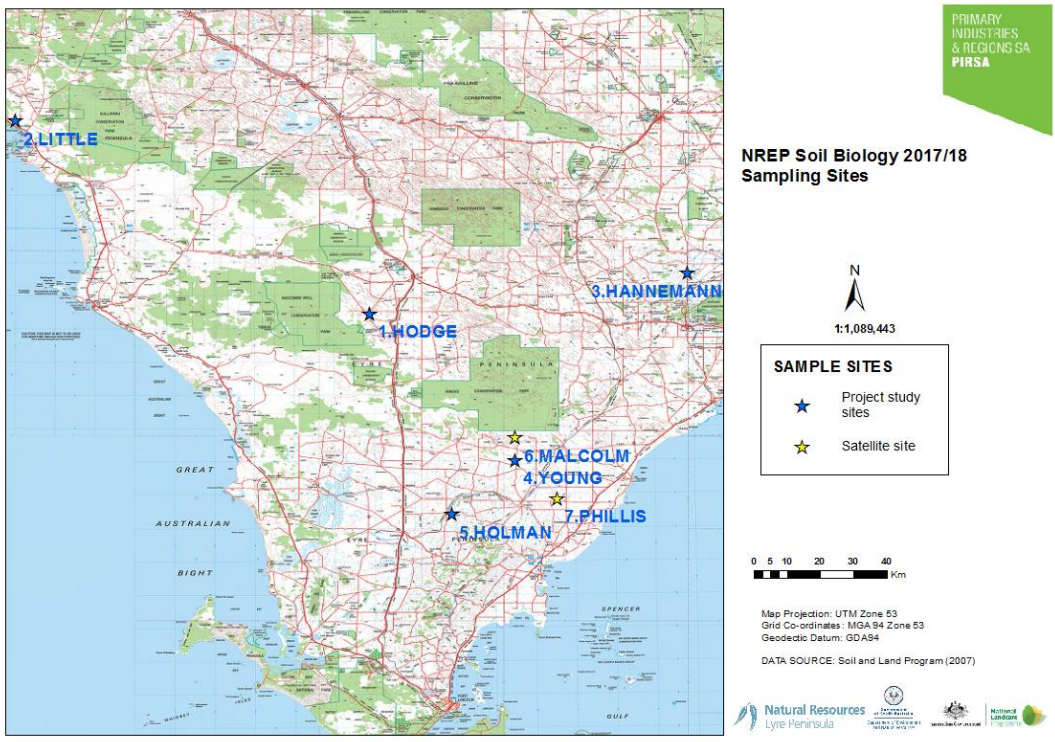

Figure 1. **Location of sampling points.**

Of the 5 core sampling sites 3 (Hannemann, Young and Holman) were trial sites developed under the 'Overcoming subsoil constraints for increased carbon sequestration in Eyre Peninsula soils' project. Established in 2014 these sites were funded by the NREP Carbon Farming Initiative Action on the Ground (CFI AOG) project. Each of these sites (and the Phillis satellite site) had a soil modification treatment applied in 2014 to overcome a specific subsoil constraint. A description of soil type, major

soil constraints and modification/treatment applied are detailed in Table 1. Soil samples were taken from untreated and treated areas and analysed separately to enable comparison (Figure 2).

As there was no treatment applied on the grey calcareous site at Pt Kenny (Site 2. NL) samples were taken from distinct areas of poor and good growth within the same paddock. At the sandy soil (Site 1. WH) at Lock the landholder had used a modified disc plough to mix the O and A1 soil layers into the infertile bleached A2 horizon (Figure 3).

Table 1. Project site descriptions.

SITE #	LANDHOLDER AND LOCATION	SOIL DESCRIPTION	KEY PRODUCTION CONSTRAINT	SOIL MODIFICATION/ TREATMENT	CROP AND STAGE
1	WH, LOCK	DEEP YELLOW SAND	LOW INHERENT FERTILITY	DEEP MIXING USING MODIFIED ONE WAY PLOUGH	BARLEY – EARLY TILLERING
2	NL, PT KENNY	CALCAREOUS LOAMY SAND	POOR NUTRIENT AVAILABILTY DUE TO VERY HIGH CARBONATE	POOR GROWTH VS GOOD GROWTH	WHEAT - LATE TILLERING
3	MH, CLEVE	RED BROWN EARTH	HARDSETTING (SODIC) SUBSOIL LAYERS	RIP + GYPSUM + ORGANIC MATTER	OAT AND VETCH FOR HAY – FLOWERING
4	TY, UNGARRA	DUPLEX SANDY SOIL	LOW INHERENT FERTILITY IN SUBSURFACE LAYERS	DEEP INCORPORATED CLAY AND ORGANIC MATTER	CANOLA AND VETCH – FLOWERING
5	JH, COCKALEECHIE	ACIDIC IRONSTONE	LOW SOIL pH AND HIGH AVAILABLE ALUMINIUM	INCORPORATED LIME - 3 t/ha	CANOLA – FLOWERING

Figure 2. **Site 4. TY, Ungarra. Control on left compared to spaded clay and organic matter treatment on right**

Figure 3. **Modified one way disc plough mixing A horizon on sandy soil at Lock site 1. WH (May 2017)**

In addition to sampling the 5 key project sites, samples were also collected from nearby modified sites at Mt Hill (Site 6. SM) (Figure 4) and Ungarra (Site 7. JP). Descriptions of soil type production constraints and treatments are detailed in Table 2.

Table 2. Satellite site descriptions (analysed for PQR's by Uni SA only)

SITE #	LANDHOLDER AND LOCATION	SOIL DESCRIPTION	KEY PRODUCTION CONSTRAINT	SOIL MODFICATION/ TREATMENT	CROP STAGE AND TYPE
6	SM, MT HILL	DUPLEX SAND	LOW INHERENT FERTILITY IN SUBSURFACE LAYERS	SURFACE APPLIED ORGANIC MATTER	BARLEY, EARLY TILLERING
7	JP, UNGARRA	RED BROWN EARTH	HARDSETTING (SODIC) SUBSOIL LAYERS	GYPSUM, RIPPING, ORGANIC MATTER	LENTILS – EARLY CANOPY CLOSURE

Figure 4. **Site 6. SM (Mt Hill). Surface spread medic hay on left compared to untreated control on right**

3.3 SOIL SAMPLING METHODOLOGY

Soil sampling was initially scheduled for April/May of 2017. However, very dry conditions in summer/autumn 2017 resulted in extremely dry soil profiles (gravimetric soil moisture data from a sandy soil at Lock in early May 2017 indicated topsoil moisture of <2%)*. With many districts not receiving opening rains until the first week July it was decided to postpone sampling until September 2017 when soils still contained good levels of soil moisture and soil temperatures had begun to increase.

Samples were collected using a 50 mm soil sampling tube hammered to 30 cm depth at 10 locations within each sampling area (individual plots on CFI trial sites, otherwise a 25 x 25 m area) (Figure 5).

Figure 5. **Soil core to 30 cm taken from JP site at Ungarra.**

Advice from UniSA (Dr Barbara Drigo, personal communication via email 26/05/2017) stated that the ideal moisture for bacteria and fungi is around 20% and that at 2% moisture bacteria and fungi were likely in a dormant state, with only a few phyla adapted to extreme conditions active under those conditions. She suggested that because bacteria and fungi in a dormancy state would resuscitate in 24 hours or less after the first rain it would be wise to delay sampling until soil moisture and temperatures were such that the soil microbial community was functioning at its maximum capacity.

Cores were separated and bulked by 10 cm depth increments (0-10, 10-20, 20-30 cm). These were thoroughly mixed to form a composite sample for each depth and treatments from which a subsample was sent for analysis. As subsoil constraints which severely restrict microbial activity are often present at depths greater 30 cm in Eyre Peninsula soils, analysis of samples for soil biology below 30 cm was not considered necessary. Three photographs were taken at each site and included; the view to the north, the view to the east, the view diagonally to the north-east

There is little information on critical values for assays of soil biota in dryland cropping soils in South Australia. In order to usefully interpret the data, comparative samples from areas within the same paddock and soil type which had been treated differently or had distinctly different crop growth would be taken (i.e. 'control vs treated' or 'good vs poor growth'). Soil chemical and physical (bulk density) data were obtained to identify any correlations with soil biology. Samples for chemical analysis were sent to CSBP for comprehensive nutrition analysis including boron and chloride. Phosphorus Buffering Index (PBI) analysis was undertaken on soils with carbonate present.

Protocols for correct treatment of samples in the field and packaging and sending samples were obtained with both MBA and UniSA recommending 100-200 g of soil per sample in sterile containers, kept as cold as possible after sampling (stored in an insulated container with ice packs in the field, then frozen as soon as possible for delivery to the laboratory). Microbiology Labs Australia has a detailed guide for sampling which can be downloaded from their website (http://www.ciaaf.com.au/wp-content/uploads/2016/12/Microbe-Labs-Sampling-Instructions-10-2016.pdf)

Samples (approximately 200 g subsamples of a well-mixed bulked composite of 10 cores separated into 3 x 10 cm depth increments) were taken between Monday 18th and Wednesday 20th of September 2018. Samples bags were placed in an esky containing icepacks in the field and transferred into a +4°C refrigerator on return to the office each evening. Once sampling had been completed (Thursday 21st September) all samples were placed in the freezer (-18°C) over the weekend before release to freight company (in a cooler bag with icepacks) on the Monday morning for overnight freight and delivery to the laboratory. The aim of freezing the samples and placing in a cool insulated bag was to protect the soil biota DNA from degrading before arrival at the laboratory.

Samples from the 0-10 cm layer (control and modified) were sent to Microbiology Laboratories Australia (MBA). There is no specific information on the methodology used by MBA. Samples were analysed for;

- Microbe Wise - an analysis of species abundance and diversity,
- Microbiological Activity Wise- analysis of the potential activity of microbial groups in soil functions, and
- Nitrogen Wise – a measure of the potential N mineralisation based on the abundance and activity of microbial groups.

Consultation with Professor Enzo Lombi at UniSA resulted in analyses including DNA and qPCR (Polymerase Chain Reaction) assays to determine abundance of Bacteria (16S) and fungi (ITS) being undertaken. He also suggested we assess abundance of a number of genes involved in the C and N cycles including; ammonia oxidation (amo), nitrous oxide reductase (nosZ) and nitrite reductase (nir). Samples from all sites and depths were sent to UniSA for these assays.

4 SAMPLING RESULTS

4.1 REPORTING OF RESULTS- MBA

Analytical results from MBA were returned within a fortnight from sample submission. Results were reported using a standard MBA template, which reports the value (using mg/kg or kg/ha as appropriate). Although there are not currently well calibrated critical values for many of the microbiological analyses in dryland cropping soils in South Australia, the MBA reports compare the reported value from the sample to a 'guide figure' using a 'traffic light' gradational colour bar where red is 'poor', yellow is 'fair' and green is considered to be a 'good' level. Orange cells represent values between poor and fair (red and yellow) and lime green cells represent values between fair and good (yellow and green). To facilitate comparison and interpretation, the values from the MBA reports and colours were transposed to an excel worksheet. This also allowed data to be presented in a suitable manner at workshops and in the tables below.

4.2 REPORTING OF RESULTS – UNI SA

Due to high laboratory workloads there was some delay with receiving the results from UniSA. As a result, only the absolute abundance data for bacteria, fungi and nematodes were available for presentation at March 2018 workshops. Bacteria, fungi and nematode abundance was assessed using quick Polymerase Chain Reaction (PCR) assays (Bacterial 16S rDNA, fungal 18S rDNA and real time nematode PCR).

Relative quantification was used to assess the nitrogen and carbon cycle genes (nifH, narG, nasA, AmoA and pmoA). Dr Helen Hayden (DEDJTR) (in a personal communication via email 27/06/2018) provided some further information on these soil cycling genes which is summarised below.

- nifH gene - fixation of N based on free living N fixers in soil (as opposed to those in nodules in legumes). These organisms required carbon for fixation to occur.
- narG and nas genes - measure nitrate reductase (the conversion of nitrate (NO_3^-) back to nitrite (NO_2^-) and is generally related to the soil NO_3^- content reported in soil tests.
- amoA gene - the conversion of ammonia (NH_3) to NO_2^- by ammonia oxidizing bacteria (AOB) and ammonia oxidising archaea (AOA) and its subsequent conversion to NO_3^-.
- pmoA - particulate methane monooxygenase gene. A carbon cycling gene. These genes occur in methanotrophs which are microbes that metabolize methane as their only source of carbon and energy.

Results were reported as CQ values, which have an inverse relationship to gene abundance (i.e. the higher the value reported the lower the abundance of organisms performing those functions in the soil) relative to a control sample (DNA free water). CQ values ≥43 indicate nil DNA found in the sample. As there were no specific guide values for interpreting the UniSA results a simple colour bar was used in the tables below to highlight differences between the control and modified site. Values in the modified site which are lower than the equivalent control sample are highlighted by the use of red cells and those which are higher than the equivalent control sample highlighted using green cells. The blue cells in the modified site data are where the differences between the control and modified values are negligible.

Results of soil physical, chemical and biological analysis are summarised in Tables 3 to 26 in Sections 4.1 to 4.6 of this report. Discussion of the results can be found in sections 5.1 to 5.6.

4.3 SITE #1. WH		SOIL TREATMENT
LANDHOLDER LOCATION	WAYNE HODGE, LOCK	DEEP SAND – MODIFIED WITH ONE WAY DISC PLOUGH

Table 3. Soil Physical and Chemical Data – Site 1. WH

		Bulk Density	pH	Org. C	EC1:5	CEC	Exc.Na+K %	DTPA Cu	Col. P	Col. K	S	Boron	Chloride	PBI
		g/m3	pH	%	dS/m	sum c /mol	%	mg/Kg	mg/Kg	mg/ Kg	mg/ Kg	mg/ Kg	mg/ Kg	
CONTR	**0-10**	1.39	5.6	0.67	0.035	2	4	0.29	17	38	5.3	0.28	11.1	8
	10-20	1.72	6.2	0.26	0.024	1	9	0.24	10	28	1.1	0.15	4.4	6
	20-30	1.72	5.6	0.23	0.020	1	7	0.26	14	28	2.5	0.19	9.3	7
MOD	**0-10**	1.54	5.9	0.40	0.019	2	5	0.32	14	34	1.7	0.23	3.7	6
	10-20	1.61	6.4	0.63	0.036	3	5	0.36	15	48	3.1	0.33	5.8	5
	20-30	1.67	7.3	0.41	0.059	2	5	0.34	12	34	3.3	0.26	7.4	5

Table 4. Microbiology Laboratories Australia Soil biology data – Site 1. WH

	MICROBIAL ACTIVITY			MICROBE GROUPS		USEFUL INDICATORS		NITROGEN				
	SOIL BASAL RESPIRATION	SOIL BASAL RESPIRATION	SOIL MICROBIAL BIOMASS CARBON	TOTAL MICROORGANISMS (mg/kg)	MYCHORRIZAL FUNGI (INC VAM)	MICROBIAL DIVERSITY	FUNGI: BACTERIA	N MINERALISATION (est)	TOTAL N	C:N	N FIXATION (net)	N MINERALISATION (net)
TREATMENT	mg C/kg soil	mg CO2/kg soil		mg/kg	mg/kg	mg/kg	mg/kg	mg/kg/mth	mg/kg	Ratio	kg/ha/month	kg/ha/month
UNMODIFIED	900	3296	249	16	2	38	3	55	300	18	720	66
ONE WAY DISC PLOUGH	335	1225	95	11	2	35	4	39	130	29	51	47

Table 5. UniSA microbial abundance data – Site 1. WH

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
1	WH	CONTROL	20 500	2 520 000	622	949 000	3	325	50	218	180
1	WH	MOD	917 000	4 190	53	26 300	2 800	245	540	41	290

Table 6. UniSA Nitrogen cycle relative quantification values – Site 1. WH

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
1	WH	CONT	26.18	27.36	27.20	25.32	26.11	25.55	24.11	23.44	24.18	31.72	32.50	32.51	29.63	30.47	30.07
1	WH	MOD	25.37	24.57	25.90	24.21	23.46	24.50	21.47	21.75	23.01	29.98	30.27	30.36	27.06	27.19	28.91

Note: CQ values are inversely proportional to the 'nil DNA' control sample.

4.4 SITE # 2: NL		SOIL TREATMENT
LANDHOLDER LOCATION	NATHAN LITTLE, PT KENNY	HIGHLY CALCAREOUS GREY LOAMY SAND – POOR VS GOOD PRODUCTION

Table 7. Soil Physical and Chemical Data – Site 2. NL

		Bulk Density	pH	Org. C	EC1:5	CEC	Exc.Na+K %	Col. P	Col. K	S	Boron	Chloride	PBI
		g/ m3	$CaCl_2$	%	dS/ m	sum c/ mol	%	mg/Kg	mg/Kg	mg/Kg	mg/Kg	mg/Kg	
POOR	**0-10**	1.17	7.8	1.42	0.215	17	5	36	129	15.8	2.30	99.7	110
	10-20	1.26	7.9	1.14	0.204	18	5	14	114	12.4	2.89	63.7	133
	20-30	1.27	7.6	1.1	0.153	17	5	7	117	12.4	3.24	57.2	155
GOOD	**0-10**	0.99	7.6	2.56	0.199	27	6	57	480	12	2.59	59.3	196
	10-20	1.12	7.2	2.87	0.152	32	5	24	468	11	3.08	16.8	235
	20-30	1.11	7.1	2.57	0.153	29	3	16	290	13.6	2.76	23.8	239

Table 8. Microbiology Laboratories Australia Soil biology data – Site 2. NL

	MICROBIAL ACTIVITY			MICROBE GROUPS		USEFUL INDICATORS			NITROGEN			
	SOIL BASAL RESPIRATION	SOIL BASAL RESPIRATION	SOIL MICROBIAL BIOMASS CARBON	TOTAL MICROORGANISMS (mg/kg)	MYCHORRIZAL FUNGI (INC VAM)	MICROBIAL DIVERSITY	FUNGI: BACTERIA	N MINERALISATION (est)	TOTAL N	C:N	N FIXATION (net)	N MINERALISATION (net)
TREATMENT	mg C/kg soil	mg CO2/kg soil		mg/kg	mg/kg	mg/kg	mg/kg	mg/kg/mth	mg/kg	Ratio	kg/ha/month	kg/ha/month
POOR GROWTH	739	2704	205	22	4	42	2	113	950	43	0	136
GOOD GROWTH	1420	5197	391	74	16	49	3	231	2890	23	0	278

Table 9. UniSA microbial abundance data – Site 2. NL

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
2	NL	CONTROL	20 500	1 250	4 490 000	949 000	3 820 000	1, 690	50	63002	1150
2	NL	MOD	917 000	9 020	440 000	26 300	5	2470	540	42	408

Table 10. UniSA Nitrogen cycle relative quantification values – Site 2. NL

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
2	NL	CONT	24.01	24.65	24.16	22.43	23.73	23.30	20.00	21.41	20.63	27.87	28.52	26.60	22.80	24.83	26.97
2	NL	MOD	24.75	25.89	30.79	21.90	23.37	26.95	19.97	21.18	24.16	25.08	23.73	25.33	20.62	24.93	32.47

Note: CQ values are inversely proportional to the 'nil DNA' control sample.

4.5 SITE # 3: MH		SOIL TREATMENT
LANDHOLDER LOCATION	MARK HANNEMANN, CLEVE	HARD SETTING (SODIC) RED BROWN EARTH – DEEP RIPPING WITH GYPSUM AND INCORPORATED ORGANIC MATTER

Table 11. Soil Physical and Chemical Data – Site 3. MH

	Depth	Bulk Density	pH	Org. C	EC1:5	CEC	Exc.Na+K %	Col. P	Col. K	S	Boron	Chloride	PBI
		g/m3	CaCl2	%	dS/m	sum c/mol	%	mg/Kg	mg/Kg	mg/Kg	mg/Kg	mg/Kg	
CONTR	0-10	1.46	6.5	1.92	0.114	13	6	50	208	21.1	1.06	26.2	83
	10-20	1.53	6.1	0.76	0.060	10	9	17	170	8.7	2.04	8	88
	20-30	1.48	6.7	0.41	0.077	19	10	4	228	14.2	4.11	2	139
MOD	0-10	1.26	5.4	2.0	0.079	8	9	46	226	6.6	0.88	17.3	68
	10-20	1.54	6.0	0.70	0.06	17	8	6	272	2.6	1.80	3.3	118
	20-30	1.60	6.4	0.55	0.093	17	9	5	239	7.0	2.07	3.9	135

Table 12. Microbiology Laboratories Australia Soil biology data – Site 3. MH

	MICROBIAL ACTIVITY			MICROBE GROUPS		USEFUL INDICATORS		NITROGEN				
	SOIL BASAL RESPIRATION	SOIL BASAL RESPIRATION	SOIL MICROBIAL BIOMASS CARBON	TOTAL MICROORGANISMS (mg/kg)	MYCHORRIZAL FUNGI (INC VAM)	MICROBIAL DIVERSITY	FUNGI: BACTERIA	N MINERALISATION (est)	TOTAL N	C:N	N FIXATION (net)	N MINERALISATION (net)
TREATMENT	mg C/kg soil	mg CO2/kg soil		mg/kg	mg/kg	mg/kg	mg/kg	mg/kg/mth	mg/kg	Ratio	kg/ha/month	kg/ha/month
UNMODIFIED	531.0	1943.5	148.5	52.2	2.449	42.3	3.1	109.1	1110.0	13.2	0.0	130.9
RIP+10GYP+10OM	692.6	2535.0	192.4	58.0	4.655	46.5	3.4	114.8	1020.0	15.1	0.0	137.7

Table 13. UniSA microbial abundance data – Site 3. MH

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
3	MH	CONTROL	2 300	2 430 000	1 310	456 000	2 100	11 700	55	1120	330
3	MH	MOD	80 400	4 190	2 570	87	2 800	6 480 000	404	41	41900

Table 14. UniSA Nitrogen cycle relative quantification values – Site 3. MH

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
3	MH	CONT	24.60	25.69	28.33	21.83	24.79	26.44	19.45	21.93	24.10	28.72	30.13	34.46	23.75	28.79	34.82
3	MH	MOD	23.48	33.01	30.40	21.83	31.48	27.84	20.85	29.58	26.22	29.18	38.11	36.17	25.63	36.48	35.73

Note: CQ values are inversely proportional to the 'nil DNA' control sample.

4.6 SITE #4: TY		SOIL TREATMENT
LANDHOLDER/ LOCATION	TERRY YOUNG, UNGARRA	SAND OVER CLAY – SPADED CLAY AND ORGANIC MATTER

Table 15. Soil Physical and Chemical Data – Site 4. TY

		Bulk Density	pH	Org. C	EC1:5	CEC	Exc.Na+K %	Col. P	Col. K	S	Boron
		g/m3	CaCl2	%	dS/m	sum c/mol	%	mg/Kg	mg/Kg	mg/Kg	mg/Kg
CONT	**0-10**	1.51	5.0	0.54	0.052	2	10	16	59	3.3	0.38
	10-20	16.8	5.7	0.25	0.051	2	16	21	69	2.5	0.53
	20-30	1.80	6.3	0.16	0.081	7	24	16	185	2.8	2.61
MOD	**0-100-**	1.56	6.1	0.74	0.064	5	15	21	250	2.9	1.53
	10-20	1.66	6.4	0.36	0.051	3	15	18	100	1.8	0.89
	20-30	1.74	6.5	0.21	0.087	6	25	21	150	2.3	1.64

Table 16. Microbiology Laboratories Australia Soil biology data – Site 4. TY

	MICROBIAL ACTIVITY			MICROBE GROUPS		USEFUL INDICATORS		NITROGEN				
	SOIL BASAL RESPIRATION	SOIL BASAL RESPIRATION	SOIL MICROBIAL BIOMASS CARBON	TOTAL MICROORGANISMS (mg/kg)	MYCHORRIZAL FUNGI (INC VAM)	MICROBIAL DIVERSITY	FUNGI: BACTERIA	N MINERALISATION (est)	TOTAL N	C:N	N FIXATION (net)	N MINERALISATION (net)
TREATMENT	mg C/kg soil	mg CO2/kg soil		mg/kg	mg/kg	mg/kg	mg/kg	mg/kg/mth	mg/kg	Ratio	kg/ha/month	kg/ha/month
UNMODIFIED	520	1901	145	23	1	41	3	72	450	16	51	87
CLAY+SPADE+OM10	635	2324	177	22	2	41	3	96	540	13	154	115

Table 17. UniSA microbial abundance data – Site 4. TY

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
4	TY	CONTROL	23 200	81 700	109 000	28 000	1 070	9 570	2470	488	16
4	TY	MOD	22 200	217 000	372 000	12 800	4 120	3 209	4070	22	141

Table 18. UniSA Nitrogen cycle relative quantification values – Site 4. TY

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
4	TY	CONT	23.24	24.37	24.41	21.27	24.10	23.48	18.65	21.86	20.65	28.87	31.18	29.83	22.14	27.78	28.85
4	TY	MOD	23.20	25.08	24.99	21.57	23.60	23.99	19.43	20.83	22.18	28.23	30.96	31.24	23.45	28.11	29.23

Note: CQ values are inversely proportional to the 'nil DNA' control sample.

4.7 SITE #5: JH		SOIL TREATMENT
LANDHOLDER/ LOCATION	JIM HOLMAN, COCKALEECHIE	ACIDIC IRONSTONE SOIL – 3 t/ha INCORPORATED LIME

Table 19. Soil Physical and Chemical Data – Site 5. JH

	Depth	Bulk Density	pH	Org. C	EC1:5	CEC	Exc.Na+K %	Col. P	Col. K	S	Boron
		g/m3	CaCl2	%	dS/m	sum c/mol	%	mg/Kg	mg/Kg	mg/Kg	mg/Kg
CONT	**0-10**	0.94	4.3	1.1	0.044	5	13	54	206	7.5	0.69
	10-20	1.34	5.2	0.43	0.035	7	12	14	242	10.9	1.66
	20-30	1.41	5.7	0.34	0.048	9	11	5	276	21.3	1.86
MOD	**0-10**	1.05	5.7	1.1	0.052	8	9	47	226	10.1	1.13
	10-20	1.02	5.6	0.43	0.036	7	11	16	220	12.3	1.57
	20-30	1.20	5.9	0.33	0.041	9	11	5	271	18.3	1.93

Table 20. Microbiology Laboratories Australia Soil biology data – Site 5 JH

	MICROBIAL ACTIVITY			MICROBE GROUPS		USEFUL INDICATORS		NITROGEN				
	SOIL BASAL RESPIRATION	SOIL BASAL RESPIRATION	SOIL MICROBIAL BIOMASS CARBON	TOTAL MICROORGANISMS (mg/kg)	MYCHORRIZAL FUNGI (INC VAM)	MICROBIAL DIVERSITY	FUNGI: BACTERIA	N MINERALISATION (est)	TOTAL N	C:N	N FIXATION (net)	N MINERALISATION (net)
TREATMENT	mg C/kg soil	mg CO2/kg soil		mg/kg	mg/kg	mg/kg	mg/kg	mg/kg/mth	mg/kg	Ratio	kg/ha/month	kg/ha/month
UNMODIFIED	27	972	76	43	2	48	3	45	130	21	0	54
RIP+3LIME	600	2197	167	48	3	47	3	52	100	31	103	62

Table 21. UniSA microbial abundance data – Site 5. JH

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
5	JH	CONTROL	1 880	1 250	81 500	4 690	3 820 000	250	22	63	110
5	JH	MOD	19 200	4 490 000	132 000	839	1 690	35 500	33	1	29

Table 22. UniSA Nitrogen cycle relative quantification values – Site 5. JH

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
5	JH	CONT	24.01	24.98	28.81	22.25	23.05	26.28	21.65	21.83	24.58	29.75	30.63	32.07	24.26	26.78	30.08
5	JH	MOD	23.17	24.38	25.68	21.71	22.85	24.35	20.02	20.12	23.16	28.84	29.76	30.56	22.04	26.10	28.94

Note: CQ values are inversely proportional to the 'nil DNA' control sample.

4.8 SITE #6. SM (SATELLITE)		SOIL TREATMENT
LANDHOLDER/LOCATION	SHANE MALCOLM, MT HILL	SAND OVER CLAY- ORGANIC MATTER SPREAD ON SURFACE

Table 23. UniSA microbial abundance data – Site 6. SM

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
6	SM	CONTROL	71 400	1 870	781 000	57	4 690	1 070 000	324	22	3600000
6	SM	MOD	29 200	11 400	1 780 000	1	0	59	43	216	11

Table 24. UniSA Nitrogen cycle relative quantification values – Site 6. SM

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
6	SM	CONT	24.33	26.59	24.44	22.84	25.03	25.17	21.14	23.07	23.25	29.93	31.98	32.42	23.00	25.62	28.15
6	SM	MOD	23.77	27.62	26.23	22.21	25.07	24.37	19.70	22.34	22.08	28.80	31.35	33.51	23.07	26.08	27.31

4.9 SITE #7. JP (SATELLITE)		SOIL TREATMENT
LANDHOLDER/LOCATION	JAMIE PHILLIS, UNGARRA	HARD SETTING (SODIC) SUBSOILS – DEEP RIPPING + GYPSUM AND ORGANIC MATTER

Table 25. UniSA microbial abundance data – Site 7. JP

			Bacteria			Fungi			Nematodes		
			' thousand counts/gram soil			' thousand counts/gram soil			counts/gram soil		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
7	JP	CONTROL	917 000	83 700	7 250	26 300	1	41 200	540	40	120
7	JP	MOD	1 280 000	6 850	1 630 000	339 000	31 200	64	544	0	11

Table 26. UniSA Nitrogen cycle relative quantification values – Site 7. JP

			narG gene Cq			*nasA* gene Cq			*nifH* gene Cq			*pmoA* gene Cq			*AmoA* gene Cq		
LANDHOLDER			0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30	0-10	10-20	20-30
7	JP	CONT	24.40	24.98	25.91	22.37	22.39	24.29	20.41	21.33	21.86	30.03	30.70	30.87	25.92	27.05	29.10
7	JP	MOD	23.41	23.91	26.23	21.89	22.98	24.50	18.52	22.00	22.94	29.74	30.43	30.78	23.71	27.19	31.20

5 DISCUSSION OF RESULTS

Soil analysis results showed clear relationships between soil physical/chemical parameters and soil biology, particularly those between soil pH and organic carbon (OC) and microbial abundance and activity. Where treatments were applied that either changed pH to the optimal range for crop production (5.5 – 6.5 $CaCl_2$) and/or increased OC, the abundance and potential microbial activity increased. There also appeared to be a trend between microbial abundance and bulk density however this was less clear. On treatments that imposed gross modification of the soil (ripping, spading or discing) there was usually a corresponding reduction in bulk density to the depth of intervention. There was also often a reduction in the levels of fungi compared to bacteria at these sites. This might result from two soil processes. Firstly disturbance from the treatment may have caused disruption and consequent reduction in fungal hyphae (affecting counts of fungal rDNA). Secondly reducing soil bulk density through soil disturbance may have increased pore size and provided more favourable conditions for bacteria in the soil.

5.1 Site 1. WH.

Modification using a one-way disc plough reduced bulk density at the surface with little change in soil layers deeper than 10 cm. Mixing of the A1 horizon into the A2 reduced OC concentration in the 0-10 cm layer and increased it in the 10-20 cm layer (Table 3). There was a small increase in pH on the modified site, which is likely to be due to spatial pH variation rather than a soil treatment effect.

There was a 35% decrease in soil microbial biomass carbon and a 65% decrease in soil basal respiration (Table 4). As the mixing operation was only undertaken in June 2017, three months prior to sampling soil biota may not have time to recover from the soil disturbance.

Absolute abundance data from UniSA show an increase in bacteria in the 0-10 cm layer following modification, with a corresponding reduction in fungi levels (Table 5). This may also result from disruption of the fungal hyphae with larger pore spaces from soil disturbance providing favourable conditions for bacteria to dominate. Relative quantification (CQ) values show an increase in nearly all the major N cycling genes in the 10-20 cm layers (Table 6). This seems to correlate with the increased organic carbon in that layer following modification.

5.2 Site 2. NL

This site had no treatment applied, so samples were taken within an area of good growth and an area of poor growth for comparison. Analysis of soil physical and chemical data shows lower bulk density and soil pH on the site with better growth (Table 7). The high alkalinity in the area where the crop was growing poorly suggests the presence of sodium bicarbonate which could be impacting crop growth. OC values on the area with good growth were double those in the area with poor growth. Cation exchange capacity (CEC) were higher in this area which may be a function of the elevated OC. It is difficult to determine whether the good crop growth is due to the high OC or whether the high OC results from better production. Microbial biomass and soil basal respiration values were higher on the site with better crop growth (Table 8).

Absolute abundance figures (Table 9) show higher levels of bacteria and lower levels of fungi on the area with good growth compared to the area with poor growth. Interestingly the relative quantification values (Table 10) for the site show an increase in CQ values (thus a reduction in abundance) for almost all major nitrogen cycle genes in the 20-30 cm soil layer. This does not appear to be linked with any particular soil chemical parameters.

5.3 Site 3. MH

Soil physical and chemical data (Table 11) for MH site 3 shows reduced bulk density following the deep ripping treatment in the 0-10 layer on the modified site. There appears to be no residual bulk density benefits from the ripping treatment (40 months earlier) in the 10-20 cm layer. Although OC levels were higher on the modified site compared to the control, MBC and soil respiration values

showed no significant differences between the control and modified areas (Table 12). Bacteria levels were higher and fungi levels and lower on the ripped treatment on this site compared to the control 0-10 cm layer (Table 13). There was no significant difference between CQ values for major N cycling genes at this site at the surface (Table 14).

5.4 Site 4. TY

At this site pH values were higher in the 0-20 cm layers on the modified plot than the control. This is likely to be due to the introduction of alkaline material in the clay spread on this site. OC values were also generally higher in the modified plot than the control (Table 15). Despite the difference in OC, there was no difference between microbial biomass carbon or basal soil respiration levels on either the control or modified plot. (Table 16). There was higher levels of bacteria and fungi on the modified plots than the control in the 10-20 cm layer however there was no difference in the 0-10 cm layer (Table 17). There was no difference between the control and the modified site in abundance of major N cycling genes at sampling in September 2017 (Table 18)

5.5 Site 5. JH

Soil bulk density values were lower in the 10-20 and 20-30 cm layers on the modified site compared to the control. The control and modified sites had almost identical OC for comparative depths (Table 19). Lime application resulted in significant increases in pH throughout the profile which has resulted in large increases in both microbial biomass carbon and soil respiration (Table 20). When comparing the absolute abundance values bacterial rDNA values were higher in both the 0-10 and 10-20 cm layers as a result of liming (Table 21).

5.6 Satellite sites 6 (SM) and 7 (JP)

Soil chemical and physical data was not gathered for the two satellite sites SM and JP. PCR assays on the sand over clay site at Mt Hill (S6 – SM) show lower levels of bacteria in the 0-10 cm layer on the treated area compared to the control. There were also lower levels of fungi at all depths (Table 23). The CQ data shows no difference between the control and modified site in relative abundance of genes for nitrogen cycling (Table 24) on the sand at Mt Hill (Site 6). However although there were higher levels of both bacteria and fungi in the 0-10 cm and 20-30 cm layers in the modified plot on the heavier textured site at Ungarra (S7-JP) (Table 25), this did not result in increased abundance of the organisms responsible for nitrogen cycling (Table 26).

Although the absolute abundance data for bacteria, fungi and nematodes indicated higher levels of microbe following soil modification, there is currently little data linking increased microbial biomass or microbial activity (soil respiration) directly to crop and pasture yield response. The aim of the relative abundance analysis was to identify whether an increase in soil microbial biomass might result in increased function of nitrogen cycling pathways. However, the results from this analysis show that at most sites there was little difference between the control and the modified for QPCR N and C cycling genes despite large differences in microbial biomass carbon.

Dr Hayden in an email communication (28th June 2018) advised that *"coarse measures of soil biology like microbial biomass and respiration are easier to interpret because they measure almost the whole community (all aerobic organisms that released CO_2) and are known to be more closely related to pH, OC, salinity and soil texture".* She states that the QPCR of the N and C cycling genes are harder to interpret as they;

- Target a very small and specific group of bacteria and archaea that use niche substrates for their energy source e.g. NH4 for amoA
- Are complex relationships that which depend on and can be heavily impacted by crop type, management, soil type, and climatic conditions.
- All act independently of each other and can present in a number of very different microbes.

- In lower pH soils archaeal amoA rather than bacterial amoA might be the functional gene converting NH_4 to NO_2 and as such might not have been measured in the amoA assay (there are different assays for archaeal and bacteria amoA)

Dr Hayden suggests that confidence in the interpretation of these results might be improved with more sampling replicates for both soil biology and nitrogen.

6 PHASE II. UNDERSTANDING SOIL BIOLOGY WORKSHOPS

Three 1/2 day workshops were held in March 2018 at Streaky Bay (WEP), Rudall (EEP) and Ungarra (LEP) to present the results of soil sampling back to local landholders, and to provide them with the opportunity to engage in discussion around soil management options for improved soil biological health through presentations by local landholder's trialling practices on their properties.

These workshops were intended to be an 'Introduction to Soil Biology 101' for landholders, with experts in soils and soil biological function providing participants with information about;

- What organisms should we expect to find in our soils and in what (relative) abundance?
- What roles/functions do these organisms play in plant production?
- What conditions favour beneficial organisms over pathogenic ones?
- What management practices increase/decrease these levels? e.g. seed treatments, in row insecticides, heat, waterlogging.

The workshops were facilitated by Sharon Honner (Spectra Coaching) who drafted a report following the workshop which summarised the,

- Workshop objectives and speakers,
- Key messages and ideas participants took away from the workshops?
- What surprised/challenged participants,
- What will be the impact of these ideas?
- If the workshops were run again, what could be done differently?

Brett Masters (PIRSA Soils Consultant) presented the results from EP soil sampling providing local context behind the presentations of the other guest presenters. Dr Helen Hayden (Soil microbiologist, Agriculture Victoria) and co-author of 'Soil biology, soil health, soil borne diseases and sustainable agriculture') presented an overview of soil biology functional groups and processes, abundance in dryland cropping system, and disease suppressive soils. Dr Michael Rose (Soils project officer, NSW DPI) presented on soil biology/plant interactions and potential impacts of pesticides on soil biology.

In addition the workshops aimed to provide a farmer narrative by having local and "outside the district" farmers present their experiences with trying to improve soil biological health. Paul Oxbrow (Wimmera Farmer and past president of Vic No Till Farmers Association) spoke on his trials in recent years with mixed species cover crops to improve soil biological function on his property. At each location one to two local farmers were invited to speak about the things that they were trialling to manage a constraint and improve soil biological health on their property. The speakers at each location were.

- Streaky Bay - Simon Patterson 'Carbon flows – A farmers take'
- Rudall – Paul Bammann 'Using summer cover crops to dry out mallee seeps in winter cropping paddocks'. Tuckey Ag Bureau held an afternoon crop walk following the Rudall workshop which included visits to a number of paddocks where landholders sowed summer forage crops in early summer, which provided significant livestock feed during extremely dry summer.
- Ungarra - Bruce Morgan and Jamie Phillis 'Exploring where winter and summer cover cropping fit on Lower Eyre Peninsula'

The dot points below contain a brief summary of some of the key points from each speaker.

6.1 Brett Masters (Soils Consultant, PIRSA, Port Lincoln)

- EP soil results showed big differences in respiration and microbial biomass carbon on sites where there were large differences in organic carbon or pH.
- Soil sampling should aim to provide a comparison - either in time or differences in production in the paddock.
- Results of soil biology analysis should not try to be interpreted in isolation of soil chemical and physical characteristics.
- Soil biology tests are not cheap. It is important to work out which tests will provide meaningful information for changing management practices and ensure samples are taken and delivered according to lab requirements

6.2 Dr Helen Hayden (Soil Microbiologist, Agriculture Victoria)

- Soil biology makes up 2-7% of organic carbon in soil with 25% of soil biology concentrated in 0-2 cm layer.
- Pore size is critical in determining the types of organisms that can live in a soil. Compacted soils with pore size <3 um will dominated by fungi.
- Bacteria are the key in formation of soil micro aggregates through secretion of lipopolysaccharides.
- Disease suppressive soils have a more diverse active bacterial community than non-suppressive soil with some bacteria in the soil producing a range of antibiotics which can be both beneficial and pathogenic to other organisms.

6.3 Dr Michael Rose (Soils project officer, DPI NSW)

- Herbicide impacts on bulk soil biota and functions are minimal at label rates (small impacts at >5x label rates). However fungicides have a much higher impact on soil biota. There is limited data on the impact of insecticides on soil biota but given relative abundance of fungi and insects in soil it is expected that the impact would fit somewhere between herbicides and fungicides
- Trial data indicates that other soil factors and management practices (i.e. OC% and pH) have more significant and longer lasting impacts than pesticides.
- Although long term tillage trial data showed increase in SOC by 25% in under no-till with annual tillage reduced soil C by ~4% with reduced microbial biomass at 0-5 cm there may not be a net microbial benefit from minimum tillage but rather a stratification effect in the 0-5 cm layer. Trial data showed no difference in soil biota between no-till and minimum tillage at 5-10 cm.

6.4 Farmer Speakers

- Cover cropping can be incorporated profitably in systems which contain livestock.
- It is important to leave control strips to enable comparison and to see if your treatment is providing a benefit or costing you.
- Summer forage crops have provided much needed feed for livestock producers in a year where the biomass in stubbles and pasture residues over summer has been extremely low.
- Two farmer presenters were continuous croppers (no livestock) and there was a great deal of discussion around the value of growing summer cover crops in systems where there is no grazing benefit returned. One of the landholders used summer cover crops to successfully dry out Mallee seeps which was of benefit to his winter cropping program. The other grower stated that although he wanted to improve soil health, in his situation there was 11 to 30% penalty to his winter crop yields (presumably due to moisture deficit) on areas where he had grown a cover crop over summer.

7 SUMMARY AND CONCLUSIONS

Soil sampling under this project was useful in gathering introductory soil microbe parameters in a range of cropping soils on Eyre Peninsula.

It is important to be clear about what you want to find out and why.

- Are you just wanting to test for an abundance of different biota? Or do you also want to know what the potential activity of those biota are?
- How will the test help you make management decisions?

There is limited calibration of soil biological tests for South Australian dryland agricultural soils, therefore it is important that samples taken are able to be compared against an equivalent site to explain any differences in the results. This may be a control vs treated area or where there is a difference in crop and pasture growth on the same soil type within a paddock.

It is important to take, process and deliver samples to the laboratory according to the laboratory requirements. Find out the requirements of the lab that you are sending to.

- How much sample do they need?
- Should the sample be refrigerated or dried?
- Avoid sampling immediately after major management intervention i.e. sowing or spraying.
- Sample a representative part of the paddock and stay away from fence lines, animal camp or uneven ground.

If samples are not collected and treated correctly, the information will be of no use.

Results showed that the abundance of soil microbes (MBC) and microbial activity (soil basal respiration) were increased where the bulk density was low, soil pH was in the optimum range for plant growth and where soil organic carbon levels were increased. To put it in simple terms ‘create a friendly environment, build a house and provide food for the microbes’. The data showed that the treatments imposed were appropriate for achieving these goals at a number of sites.

However while the abundance and activity of microbes could be improved by modification it is still unclear as to whether this has a direct impact on crop and pasture production.

8 ACKNOWLEDGEMNTS

This project was supported by Natural Resources Eyre Peninsula with funding from DEWNR’s ‘Healthy Soils for premium food’ Program and the Australian Government’s National Landcare Program. The author wishes to gratefully acknowledge;

- All landholders involved in this project for allowing us to sample their paddocks and their ongoing interest in the results.
- Dr Helen Hayden (Agriculture Victoria, DEDJTR) for generously and enthusiastically giving of her time and extensive knowledge to review and interpret laboratory the analysis results, make comment on them in plain language for use in presentations and this report, and present at Eyre Peninsula workshops. Her knowledge and experience has been invaluable to the success of this project.
- Dr Ashley Martin and team (Microbiology Laboratories Australia) for analysis of soil samples and for their advice on soil sampling and sample delivery protocols to ensure that the results were meaningful and useful.
- Professor Enzo Lombi, Dr Barbara Drigo, Dr Cathy Dandie and team (Future Industries Institute, University of South Australia) for their advice on soil sampling protocols and suggested assays and for undertaking analysis of soil samples.

- Ms Mary Crawford (NREP) for her enthusiasm to develop this sampling and extension project plan and tireless work organising guest speakers and logistics for the EP workshops.
- Dr Mick Rose, Mr Paul Oxbrow and all landholder (Presenters) as well as Mrs Sharon Honner (Workshop Facilitator) for their willingness to share their time, knowledge and experiences with EP landholders at the three workshops in March 2018.

9 ABBREVIATIONS USED IN THIS DOCUMENT.

C- Carbon

$CaCl_2$ – pH in calcium chloride

CEC - Cation Exchange Capacity

CFI AOG- Carbon Farming Initiative: Action on the Ground

Col. - Colwell

CQ - Relative quantification

DEDJTR – Department of Economic Development, Jobs, Transport and Resources

DEWNR- Departments of Environment, Water and Natural Resources.

DNA - Deoxyribonucleic Acid

EEP - Eastern Eyre Peninsula

EP – Eyre Peninsula

EPARF- Eyre Peninsula Agricultural Research Foundation

g - Gram

K - Potassium

kg/ha - kilograms per hectare

LEP - Lower Eyre Peninsula

MBA - Microbiology Laboratories Australia

MBC - Microbial Biomass Carbon

mg/kg - milligrams per kilograms

N - Nitrogen

NH_3 - Ammonia

NO_2^- - Nitrite

NO_3^- - Nitrate

NLP - National Landcare Program

NREP - Natural Resources Eyre Peninsula

NSW DPI- New South Wales Department of Primary Industries -

OC - Organic Carbon

P - Phosphorus

PBI - Phosphorus Buffering Index

PCR – Polymerase Chain Reaction

pH - Potential Hydrogen (measure of soil acidity/alkalinity)

PIRSA - Primary Industries and Regions South Australia

RNA - Ribonucleic acid

UniSA - University of South Australia

WEP - Western Eyre Peninsula

10 REFERENCES, TOOLS AND FURTHER READING

Honner, S (2018) '*Natural Resources Eyre Peninsula: What lies beneath the surface? Soil biology workshops'*. Project Report, Spectra Coaching

Stirling, G., Stirling, M., Hayden, H. and Pattison, T (2016) 'Soil health, Soil biology, Soil borne diseases and Sustainable agriculture' *CSIRO Publishing.*