

How does a cotton production system change the soil biology?

■ By Vadakattu Gupta¹, Oliver Knox² and Andrew Bissett¹

THE role of soil biota in providing ecosystem functions for crop productivity and maintaining our soil and water resources is well recognised in the Australian cotton industry. Crop management practices such as crop rotation, tillage, crop residue retention, fertiliser and agrochemical application have been shown to influence soil biological communities with potential impact on biological functions. This is important because our soil microorganisms along with the fauna, as captured in the eukaryotic analysis, mediate carbon and nutrient cycles and play a critical role in disease suppression, degradation of agrochemicals and the maintenance of overall plant health and soil structure.

Additionally, soil biodiversity has been recognised as a key factor

that affects ecosystem functioning and higher microbial diversity increases resilience of microbial processes. But until recently the majority of attention has been given to only a small percentage (less than 10 per cent) of microorganisms, because the majority were unculturable on laboratory media.

Recent developments in high throughput DNA and RNA-sequencing have allowed detailed analysis of the total microbial community to be undertaken. Currently though there is very little information available comparing the genetic composition of soil biology as represented by the bacteria, archaea[#], fungi and eukaryotes* in cotton soils with that in remnant native bush soils on cotton farms.



Left: Vetch being incorporated in long-term crop rotation experiment at ACRI. Right: A native vegetation site near the ACRI rotational trial.

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As part of the larger Biomes of Australian Soil Environments (BASE) project (<http://www.Bioplatforms.Com/soil-biodiversity/>), soil samples were collected during the summer of 2013 with the assistance of the late Dr Ian Rochester from 0–10 cm and 10–20 cm depths within the long-term field experiment at ACRI from under the Continuous Cotton (CC) and Cotton-Vetch-Cotton (CVC) rotations and nearby remnant bush.

These samples were submitted for microbial (bacteria, fungi and archaea) and eukaryotic genetic analysis. The aim of this scoping study was to obtain detailed information on the genetic diversity of soil organisms in cotton fields compared to remnant bush.

A study comparing the soil biota between Continuous Cotton (CC) and Cotton-Vetch-Cotton (CVC) rotations and nearby remnant bush found a distinct biota community in cotton fields and has highlighted differences in the composition of soil bacterial, archaeal, fungal and eukaryotic communities between soils from cotton fields and remnant vegetation.

What did we find?

- In general there were clear differences in the composition of all soil biological groups between cotton fields and the remnant bush. But the field-based differences varied with depth for different communities. For example, a clear variation in soil fungal communities was seen between rotations, sample site and at both depths (Figure 1), but with archaeal communities the variation was only seen at 10–20 cm depth.
- Bacterial diversity was generally higher in the 0–10 cm soils compared to the 10–20 cm soils, but differed more between samples in the 10–20 cm depth soils (Figure 2).
- There was clear difference in the dominant bacterial groups between cotton fields and remnant vegetation at both depths. The general trends identified in bacterial and fungal communities in the cotton soils were similar to those previously observed (CRDC project CSE1401).
- With regards to the soil archaeal communities, members of Nitrososphaeraceae family accounted for over 99 per cent of total archaeal communities in the surface 0–10 cm soils of the CC, CVC and Remnant veg as well as the 10–20 cm depth soils from CC samples.
- Members of soil fungi belonging to the phyla Ascomycota accounted for the major portion of the fungal community (averaging 80 per cent) in the cotton fields, but in the remnant

vegetation soils they were only 50 and 30 per cent in the 0–10 and 10–20 cm depths.

- Mycorrhizal fungi are known to be more abundant and diverse in the native and undisturbed ecosystems, such as remnant vegetation, which was supported by the data showing higher proportion of Glomeromycota fungi in the remnant bush soils (more than 2.2 per cent) compared to the cotton field soils (under 1.4 per cent, Figure 1).
- Distinct differences were seen in the eukaryotic community in the cotton soils compared to the remnant vegetation, in particular in the surface 0–10 cm soils (Figure 3). There was a limited depth-based effect on the eukaryotic community in the CC field compared to that seen in the CVC rotation and remnant vegetation. This could be partly attributed to variation in the quality and quantity of above and below-ground crop residues, root growth patterns and disturbance from crop management practices.

So what does this mean?

- This study has provided a clear indication of a distinct biota community in cotton fields, highlighting for the first time the differences in the composition of soil bacterial, archaeal, fungal and eukaryotic communities between soils from cotton field soils and remnant vegetation.
- Bacterial diversity in soils has been shown to be influenced both by the soil, environmental and management factors. Therefore, the differences in the composition and diversity of soil bacteria between cotton fields and remnant vegetation could be partly due to the variation in soil chemical properties. For example Organic C, available phosphorus and mineral N were generally higher in the remnant vegetation soils compared to cotton field soils.
- There is increasing evidence that archaea play a significant role in plant-fungal interactions and the cycling of carbon and nitrogen. Previous research has indicated that crop rotation and addition of wheat stubble can significantly impact on the composition and abundance of archaeal communities. But this data only showed crop rotation based differences in the 10–20 cm depth soils. We would speculate that, in the shrink swelling vertosol, wetting and drying events could change soil physical and chemical characteristics, which might impact archaeal communities, but the implications of differences in

FIGURE 1: The composition of soil fungal communities in cropped and remnant soils from ACRI in 0–10 and 10–20 cm deep soil samples

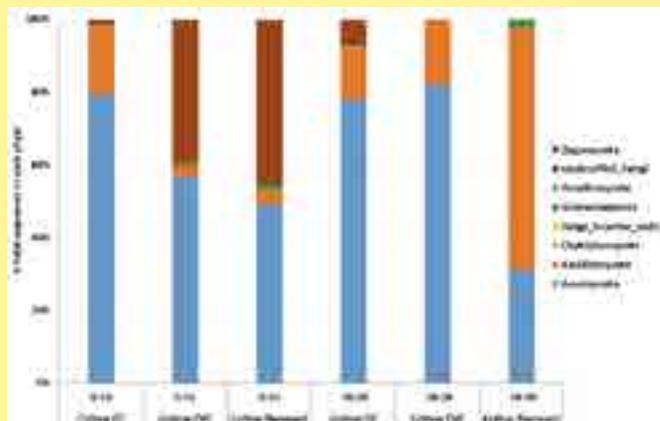


FIGURE 2: The composition of soil bacterial communities in soils from the long-term cropping system experiment and the remnant vegetation at ACRI

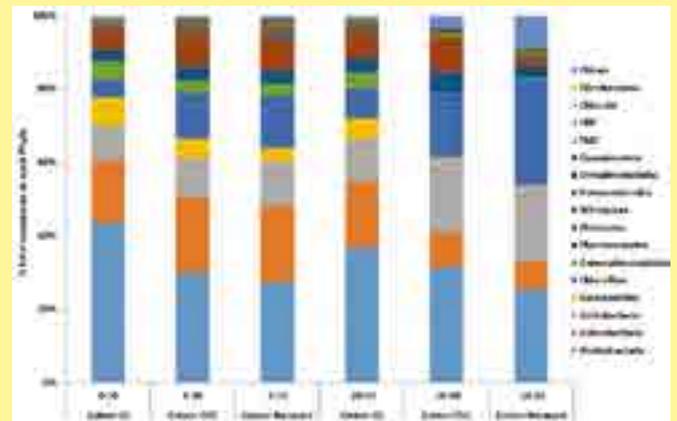
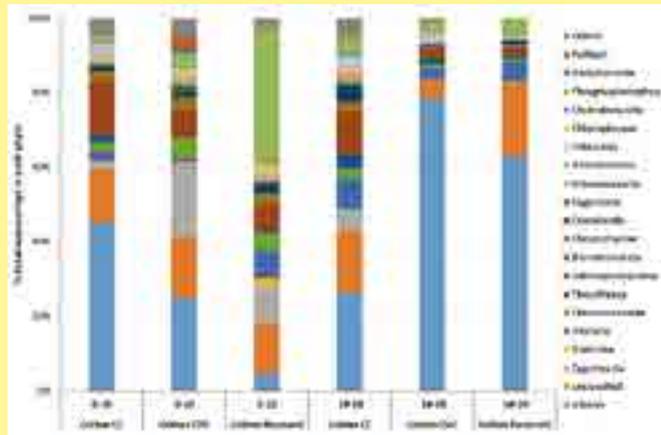


FIGURE 3: The genetic composition of soil Eukaryotic communities in soils from the long-term cropping system experiment and remnant vegetation at ACRI



archaeal community structure observed in this study to soil functions are yet to be fully understood.

- The change in mycorrhizal fungi was mainly attributed to the use of phosphorus fertiliser in cropping fields compared to no P application in the native vegetation, although the continuous presence of plant roots under native vegetation may also be important.
- It has been suggested that the intensive cotton cropping

systems with their higher mechanical disturbance may not provide an ideal habitat for the eukaryotic community and in particular the soil micro, meso and macro-fauna.

- In general the CVC samples appeared more similar to the remnant samples than they were to the CC samples suggesting management based changes.

To sum up

Findings from grain cropping systems have indicated that Actinobacteria generally dominate soil bacterial community, whereas the Proteobacteria were the major group in all the soils in this study. The functional significance of these observations requires further investigation, especially as a number of Proteobacteria have been shown to possess abilities related to plant growth promotion and disease suppression.

There is increasing evidence to show that soil archaea are playing a significant role in the cycling of carbon, nitrogen and plant-fungal interactions, so the presence of archaea from just one family is of note and raises questions about the functional role of this group of organisms and their resilience in cotton soils.

But a note of caution is that the lack of replication at sequencing level doesn't allow statistical evaluation of the differences between fields and there is still more to learn about the total biology in these soils and ways to better harness their functional capability.

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*Archaea are simple single-celled micro-organisms.

*Eukaryotes are more complex organisms with cells which have a nucleus and other membrane-bound structures

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