

The composition and diversity of prokaryotic and eukaryotic communities from an Australian Vertisol: an experimental study

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Introduction

Soil disturbances caused by natural or human activities have direct impacts on ecosystem properties and function. Soil processes are greatly influenced by bacterial, fungal and faunal community structure, activity, and stability. Studies on detrital food webs in self-mulching Vertisols are rare (Coleman et al. 2004; Bell et al. 2006). Our objective was to measure the prokaryotic and eukaryotic diversity in an Australian Vertisol that had varying land-use history i.e. irrigated cotton-based cropping systems. We hypothesized that treatments under cotton-vetch rotation would have more available organic and inorganic N, and this would be reflected in a more speciose array of bacteria, fungi and soil micro-fauna.

Methods

Surface (0-10cm) soil samples were collected from rotation treatments cotton-fallow-cotton (CWC), and cotton-wheat-vetch-cotton (CWVC), in a field experiment started in 2002 and located at the ACRI (Hulugalle et al. 2009). Samples were collected in 2006 during the cotton phase, sieved through 4 mm mesh, air-dried and used to set-up PVC core microcosms. Treatments included: Soil alone-Wet, Soil+stubble (wheat stubble @1%w/w)-Wet and Soil alone-Wet Dry. Soil moisture was adjusted to field moisture capacity; 'Wet-Dry' samples were exposed to a drying regime during weeks 2, 5 and 7. All samples incubated at 25 °C in dark. Individual cores were sampled after week 3 and 8 for microbial (sequencing or DGGE of SSU rRNA genes) and faunal (MPN or extraction methods) analyses. ANOVA and multivariate statistics were used to determine the significance of treatment effects.

Discussion

Crop residues provide important microsites hosting diverse populations of microflora, protista and mesofauna, particularly in the lower fertility Australian agricultural soils. Proteobacteria were the most abundant phylum and β -proteobacteria were the largest group within all the sequence libraries. In contrast, Actinobacteria were the most abundant phylum in the Horseshoe Bend agroecosystem plots in USA (Upchurch et al. 2008), and in the cereal cropping soils from the rainfed region in South Australia (Gupta et al. 2010).

Fungi were more responsive to short-term experimental manipulations than bacteria in this study. This is consistent with other Australian studies demonstrating a greater response of fungal communities to crop residue management than bacterial communities (Wakelin et al. 2007; Gupta et al. 2010) suggesting that, in self-mulching vertisols, soil habitat characteristics would not allow persistence of stable hyphal networks. Although amoebae were the most abundant protistan group, ciliates responded more to the addition of stubble and exposure to wetting and drying, indicating phyla-level differences in protistan communities. Added stubble contributes to unprotected microsites supporting increased microbial populations and activity thereby stimulating protistan groups with r-type strategies. Nematode communities requiring stable habitable pore structure were negatively influenced by the effects of changing soil structure in response to wetting-drying events.

We therefore hypothesize that the response of bacteria, fungi and faunal populations in vertisols is strongly related to the physico-chemical characteristics, with secondary effects due to stubble management.

Conclusion

In a self-mulching Vertisol, under cotton based farming system from New South Wales, previous site use history (e.g. including vetch in the rotation) had a greater impact on biotic diversity than short-term additions of stubble.

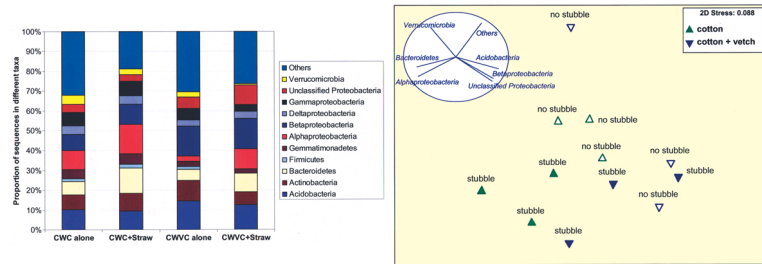


Figure 1: (A) Bacterial diversity data shown by phylogenetic assignment of clones in the 16S rRNA gene libraries in to different phyla (a total of 923 sequences analysed). (B) Non-metric MDS and PERMANOVA analysis showed that crop rotation was the major driver of bacterial diversity (CV=9.8; P=0.043) and the effect of stubble treatment was less (CV 8.3; P=0.072).

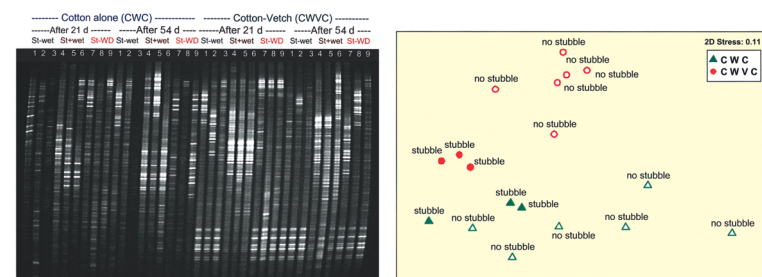


Figure 2: Composition of soil fungal communities as influenced by crop rotation history and incubation treatments (A) 18S rRNA gene DGGE patterns (B) non-metric MDS plot showing similarities between fungal communities after 21 and 54 days of incubation. The major driver of fungal community structure was due to the interaction of crop rotation x stubble incorporation (CV=49; P=0.001), and there was a secondary effect of crop rotation x moisture (CV=29; P=0.021).

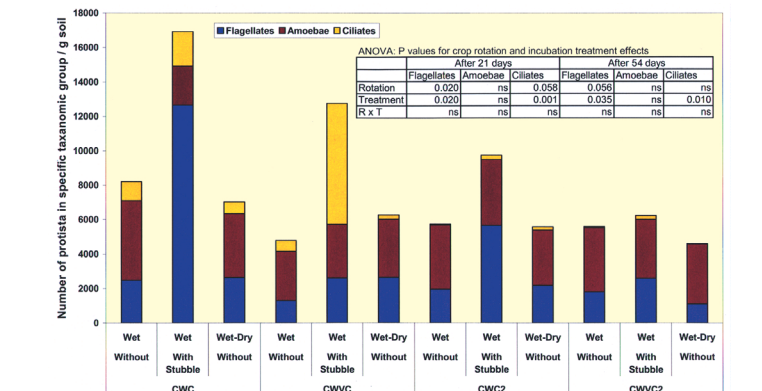


Figure 3: Composition of phenotypic groups of soil protists as influenced by crop rotation history and incubation treatments. Wetting and drying caused significant reduction in ciliate populations and stubble treatment mainly increased Colpoid populations.

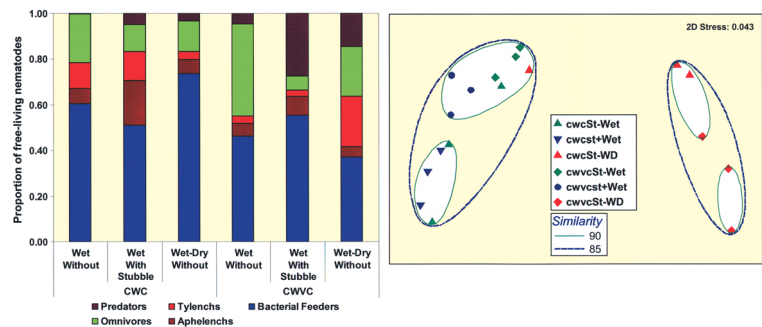


Figure 4: Composition of soil nematode communities at the end of incubation experiment (A) Proportions of various feeding groups and (B) nMDS plot showing similarities between nematode communities.

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Further information

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