Changes in soil bacterial community as affected by soil compaction, soil water content and plant roots

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Abstract. The present study assessed the effects of compaction on temporal dynamics of soil microbial communities and whether these changes were influenced by the presence of plant roots and soil water content. A pot trial comprised three levels of compaction (1.1 g cm⁻³ – uncompacted; 1.25 g cm⁻³ – moderately-compacted; 1.4 g cm⁻³ – heavily-compacted), two levels of irrigation regimes (60 and 80% FC), and two soil conditions (planted soil versus free root soil) was established. Soil microbial attributes investigated included bacterial activity and diversity, which were obtained from five sampling times (5; 10; 15; 20; 30 days). The results showed that bacterial activity and diversity changes over time and were higher in uncompacted soil treatment at day-20. Bacterial activity and diversity were higher in moderately-compacted soil with high soil moisture level (80% FC). Microbial activity and diversity were weakly correlated with the presence of plant roots particularly when soil was heavily compacted. Given the changes of microbial communities that followed changes in soil moisture availability, it was, therefore, concluded that management of the timing of irrigation inputs is needed in order to maintain microbial communities in soil.

1. Introduction

Of the various forms of soil degradation, soil compaction is the most widespread and insidious form confronting agricultural land in a wide range of soils and climates [1, 2]. Soil compaction is recognized to occur more readily in tropical systems as a consequence of wet-dry climatic oscillations in these regions [3].

Soil compaction indicated by increased bulk density is the most soil physical parameter that directly modifies soil environment where crops and diseases exist in, but it might also indirectly cause more disease by affecting the composition of soil microbial communities in the soil [4]. (Hill et al. 2000). The destruction of soil physics potentially causes detrimental effects on soil microbial communities that can eventually impair soil functions mainly in the context of controlling soil-borne disease transmission [5]. Knowledge about the relationships between soil compaction and microbial communities is limited, particularly in association with soil microbial community dynamics and in tropical environments.

Soil moisture has an essential role in regulating soil microbial communities [6] by affecting their biological processes [7]. Soil moisture also plays an important role in the formation of soil compaction, where compaction is exacerbated in soil containing low organic matter [1]. When the soil is wet, tillage operation can lead to severe compaction [8]. However, what is less clear is whether the availability of soil moisture and it’s fluctuation in compacted soil can influence changes in soil microbial communities. Factors that are dominantly involved in the temporal changes in soil microbial communities in
compacted soil have not been clearly defined. In order to gain a greater understanding of the relationships between soil moisture and plant factors, soil compaction and soil bacterial community activity and diversity, the present study was completed. This study assesses soil bacterial communities changed over time in compacted soil and whether enhanced soil moisture availability (common field remedies employed to overcome compaction) were involved in temporal changes in soil bacterial communities in compacted soil.

2. Materials and Methods

In this experiment, the interaction between soil water and compaction, and their combined and individual effects on soil bacterial activity and diversity, was established. Because plant roots are a source of carbon for microorganisms, soils with and without seedlings planted into them were used in this experiment to control for the effect of roots on microbial diversity and activity.

A pot trial was designed with three treatments in a full factorial combination in the Bundaberg region, Queensland, Australia, from January to April 2015. Soil used in the trials was a Red Ferrosol [9]. The first treatment factor was soil compaction: 1.1 g cm$^{-3}$ (‘not compacted’), 1.25 g cm$^{-3}$ (‘moderate compaction’), and 1.4 g cm$^{-3}$ (‘heavy compaction’). The second treatment factor was two levels of moisture content: 60% FC and 80% FC; and the third treatment factor was the presence and absence of plant material, via capsicum seedlings planted at 4 weeks of age. Each treatment combination had four replications. Soil was sampled five times over a 30-day period at: 5, 10, 15, 20 and 30 days.

2.1. Soil water content determination

A method of determining soil water content at 60% and 80% of field capacity (FC) using the gravimetric method was developed for soil samples at each level of compaction. Fresh soil samples with a known volume were prepared at each level of compaction in PVC cylinder pots with a uniform size (90 mm in diameter and 8 cm in length). The units of the values are expressed in gram water per gram soil (g g$^{-1}$). In order to ensure consistency in irrigation throughout the trial, pots and soil were weighed before and after each water addition. For the ‘planted’ treatments, capsicum seedlings were planted with one seedling in each pot. Soil moisture was maintained at 80% FC and 60% FC by irrigation every two to three days or when each level of moisture reduced to around 10 - 20%, which was identified through weighing each pot. The amount of water added at each irrigation was determined by subtracting initial weight from the current weight of pot + soil + water for the bare soil treatments and plus plant for the planted soil treatments.

2.2. Response variables measurement

The following responses to soil compaction, soil moisture content, and presence/absence of plants were assessed at each time period. The attributes of soil bacterial communities assessed included bacterial functional activity and diversity analyzed by community level physiological profiles (CLPP) method.

For determining bacterial community characteristics, three soil samples from each planted compacted soil treatment were used to measure bacterial community using the Biolog Eco-platesTM, where the third soil sample was collected from the mixture of soil samples from replicate 3 and 4. The main reason for using only the Biolog Eco-plate analysis in this experiment was because the aim of this experiment was to assess the dynamics of bacterial community in different compaction level and irrigation regimes that can be represented by bacterial community changes due to their high sensitivity to environmental changes. The 168 h absorbance data were chosen as single-point absorbance readings to be used for determining average well color development (AWCD), richness (R) and Shannon-Weaver index (H).

2.3. Statistical analyses

Responses of soil bacterial community on compaction were determined using Generalised Linear Model (GLM). Analyses were performed using Minitab version 16.
3. Results and Discussion

The present study found that the interaction between soil compaction and irrigation had significant effects on soil bacterial activity and diversity (determined by the values of AWCD, R and H). Bacterial activity was significantly affected by the interaction between compaction, irrigation regimes and time (F(8,89) = 9.87; p = 0.000). Higher bacterial activity within a 5-day period was found in heavily-compacted soil containing high moisture. The activity of bacterial communities across the treatments decreased at a 10-day period of sampling time with higher bacterial activity found in moderately-compacted soil with high moisture content. Bacterial activity remained stable in other treatments at the period of sampling time. An exception to this was bacterial activity in un-compacted soil containing high moisture increased sharply and reached the highest position of activity among the whole sampling time periods. Bacterial activity across the treatments declined at a 30-day period (Figure 1).

The main effect of the interaction between compaction, irrigation regimes and time on bacterial abundance (R) was significant (F(8,89) = 7.51; p = 0.000). At a 5-day period, bacterial abundance was found higher in both heavily-compacted soil with high moisture content and in un-compacted soil with low moisture content. A decline in bacterial abundance across the treatments occurred at a 10-day period with the higher position of bacterial abundance being found in moderately-compacted soil containing high moisture. Bacterial abundance across the treatments returned to increase at day-15 with the higher position of bacterial abundance being found in heavily-compacted soil containing low moisture. The abundance of bacterial communities in some treatments remained stable at day-20 except bacterial abundance in un-compacted soil treatment with high moisture content that showed a sharp increase and reached the highest position of bacterial abundance over the period of sampling time. Bacterial abundance across the treatments then reduced at day-30 with the higher position being found in moderate-compacted soil treatment containing low moisture (Figure 2).

Microbial diversity (H) was significantly affected by the interaction between irrigation regimes and time (F(1,59) = 5.83; p = 0.020). The main effect of soil compaction on bacterial diversity was also significant (F(2,59) = 5.63; p = 0.006). Higher bacterial diversity was found in un-compacted soils with low moisture content at a 5-day period, whilst lower diversity was found in un-compacted soils with high moisture content. At a 10-day period, bacterial diversity across the treatments decreased, except in un-compacted soils with high moisture content that increased at that period of time. The diversity across the treatments increased at day-15 with the diversity in moderately-compacted soils with high moisture content placed in the higher position, whereas the lower position was placed by the diversity in heavily-compacted soils with low moisture content. The diversity in some treatments shows a decline at day-20, except in un-compacted soil with high moisture content where the bacterial diversity placed the highest position over the sampling time period, whereas the lower diversity was found in moderately-compacted soil with high moisture content. Bacterial diversity across the treatments decreased at day-30 with the higher position of bacterial diversity was found in moderately-compacted soils with low moisture content (Figure 3).

The significant effects of soil moisture on compaction and soil bacterial community found in this study were related to the roles of soil moisture. Soil moisture has a dual impact on the relationship between compaction and microbial communities, influencing the severity of compaction when soil is compressed at high soil water contents [8] and regulating soil microbial activity and diversity [7]. A decrease in soil water potential from between – 0.1 bar and – 0.2 bar (wet soil) to -50 bar (dry soil) has previously been shown to reduce microbial activity, and when the dry soil is rewetted a large increase in microbial activity of up to 40-fold is recorded [10].
Figure 1. Temporal changes in AWCD values over 168 h of incubation time for a 30-day period in un-compacted (1.1 g cm\(^{-3}\)), moderately (1.25 g cm\(^{-3}\)) and heavy compacted (1.4 g cm\(^{-3}\)) soil with different soil moisture regimes (60% and 80% FC).
Figure 2. Temporal changes in richness values over 168 h of incubation time for a 30-day period in un-compacted (1.1 g cm\(^{-3}\)), moderately- (1.25 g cm\(^{-3}\)) and heavily-compacted (1.4 g cm\(^{-3}\)) soil with different soil moisture regimes (60% and 80% FC).

Figure 3. Temporal changes in Shannon index of soil bacterial community at 96 h of incubation time over a 30-day period in un-compacted- (1.1 g cm\(^{-3}\)), moderately- (1.25 g cm\(^{-3}\)) and heavily- compacted (1.4 g cm\(^{-3}\)) soil treatment with different soil moisture regimes.
4. Conclusions
Soil moisture regulated soil microbial communities, with soil bacterial activity and diversity following fluctuations in soil moisture availability. Higher bacterial diversity within 20 days was confirmed with higher utilization of C-substrates in un-compacted and moderately-compacted soil within the timeframe. Given the characteristics of the microbial community changed over time in compacted soils, which followed the availability of soil moisture content, it is, therefore, necessary to look further at the important things related to the changes in soil microbial community. Firstly, changes in microbial communities due to compaction might have a potential effect on soil-borne disease development. Secondly, these changes might hinder soil-borne progress as a consequence of the rearrangement of soil moisture content regimes.

References
[1] Hamza, M. A., and Anderson, W. K. 2005. Soil compaction in cropping systems: A review of the nature, causes and possible solutions, Soil and Tillage Research, vol. 82, pp. 121-145.
[2] McGarry, D. 2003. Tillage and Soil Compaction, in L García-Torres, J Benites, A Martínez-Vilela & A Holgado-Cabrera (eds), Conservation Agriculture, Springer Netherlands, http://dx.doi.org/10.1007/978-94-017-1143-2_37.
[3] Soane, B. D. and Van Ouwerkerk, C. 1995. Implications of soil compaction in crop production for the quality of the environment, Soil and Tillage Research, vol. 35, no. 1, pp. 5-22.
[4] Hill, G. T., Mitkowski, N. A., Aldrich-Wolfe, L., Emele, L. R., Jurkonie, D. D., Ficke, A., Maldonado-Ramirez, S., Lynch, S. T. and Nelson, E. B. 2000. Methods for assessing the composition and diversity of soil microbial communities, Applied Soil Ecology, vol. 15, no. 1, pp. 25-36.
[5] Sturz, A. V., Carter, M. R. and Johnston, H. W. 1997. A review of plant disease, pathogen interactions and microbial antagonism under conservation tillage in temperate humid agriculture, Soil & Tillage Research, vol. 41, pp. 169-189.
[6] Dennis P. G., Miller, A. J. and Hirsch, P. R. 2010. Are root exudates more important than other sources of rhizodeposits in structuring rhizosphere bacterial communities?, FEMS Microbiology Ecology, vol. 72, no. 3, pp. 313-327.
[7] Chen, M. M., Zhu, Y. G., Su, Y. H., Chen, B. D., Fu, B. J. and Marschner, P. 2007. Effects of soil moisture and plant interactions on the soil microbial community structure, European Journal of Soil Biology, vol. 43, no. 1, pp. 31-38.
[8] Mosaddeghi, M., Hajabbasi, M., Hemmat, A. and Afyuni, M. 2000. Soil compactibility as affected by soil moisture content and farmyard manure in central Iran, Soil and Tillage Research, vol. 55, no. 1, pp. 87-97.
[9] Isbell, R. 1997. The Australian soil classification, vol. 4, CSIRO publishing.
[10] Orchard, V. A. and Cook, F. J. 1983. Relationship between soil respiration and soil moisture, Soil Biology and Biochemistry, vol. 15, no. 4, pp. 447-453.

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