

# Microbial community response to various degrees of pasture soil disturbance

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## Introduction

Commercial dairy farming from planted pasture is commonly practised in the southern Cape region of South Africa. These pastures are established by various methods ranging in degree of disturbance from no-tillage to conventional tillage. Different establishment methods may alter the below-ground ecosystem, and depending on the degree of disturbance, lead to changes in microbial biodiversity and soil health. Disturbance of pasture soil may play an important role in regulating soil microbial community structure. The aim of this study was to investigate changes in soil microbial community-level physiological profiles of kikuyu (*Pennisetum clandestinum*) pastures reinforced with annual ryegrass (*Lolium multiflorum*) by various degrees of soil disturbance.

## Materials and Methods

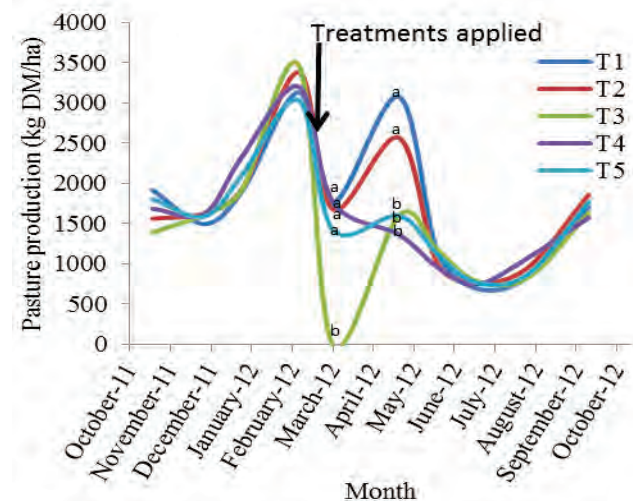
The study was conducted on Outeniqua Research Farm (South Africa) on a deep Podzol soil or Spodosol. The experimental layout was a randomized complete block design with six blocks and five treatments. The land-use before treatments were applied was 19 years of minimum-tillage kikuyu-ryegrass pasture under irrigation and grazed by dairy cows. Five treatments in order of degree of disturbance are described in Table 1 and were applied in March 2012. Pasture was measured with a rising plate meter (Van der Colf 2011). Representative soil samples, sectioned into depth increments of 0-10 cm, 10-20 cm and 20-30 cm were taken 90 days before, 60 days after and 150 days after application of treatments. Whole-community carbon source utilisation (CSU) patterns were assessed using Biolog EcoPlates<sup>TM</sup> (Winding and Hendriksen 1997).

## Results and Discussion

Figure 1 showed that treatments T1 (control) and T2 had similar productions. T2 was designed to reinforce ryegrass with no-tillage planters into the kikuyu base while disturbance is kept to a minimum. Shallow disturbance and deep disturbance resulted in similar pasture productivity, and eradication of kikuyu with glyphosate resulted in the lowest pasture productivity.

**Table 1. Description of treatments applied to soil.**

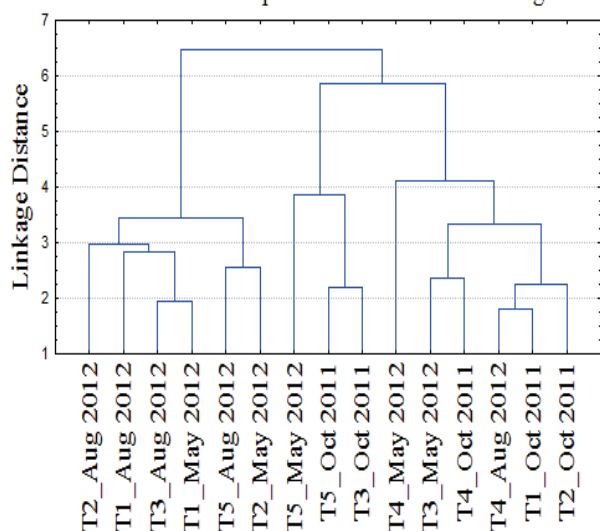
Treatment	Description of treatment/method to reinforce pasture
T1	No soil disturbance or over-sowing (control)
T2	Post-grazing kikuyu stubble mulched; annual ryegrass established with a minimum-till planter
T3	Kikuyu eradicated with glyphosate; annual ryegrass established with a minimum-till planter
T4	Kikuyu pasture soil rotavated (10cm depth); annual ryegrass established with a minimum-till planter
T5	Kikuyu pasture ripped (30cm depth), conventionally tilled (20cm depth); annual ryegrass established with a minimum-till planter



**Figure 1. Monthly pasture production (kg DM/ha) of kikuyu-ryegrass. Significant differences ( $P < 0.05$ ) are only indicated with different letters for months when production was not similar between treatments.**

Similarity in the relationship between T1 and T2 was evident from closely related CSU patterns (Figure 2), clustered with a short linkage distance during October 2011 and August 2012. CSU profiles of T1 and T2 for October 2011 and August 2012 were found on opposites of the dendrogram, illustrating a shift in soil microbial functional diversity. Shortly after treatments were applied, the May 2012 assessment showed that T1 and T2 were located in one main cluster and T3, T4 and T5 in another main cluster. This illustrates a shift in the CSU profile in treatments where more disturbance was

Carbon source utilisation profiles from Oct 2011 to Aug 2012



**Figure 2. Cluster analysis illustrating the influence of different treatments on soil microbial carbon source utilization from October 2011 to August 2012.**

applied. CSU profiles in treatments prior to application (October 2011) grouped together in a main cluster. CSU of all August 2012 treatments except for T4, clustered together, illustrating that the microbial functional diversity has returned to an equilibrium state 150 days after disturbance. CSU patterns of T3 changed the most and occurred in three different clusters, signifying the most change in soil microbial functional diversity

resulted from the effect of glyphosate-based herbicides.

## Conclusion

Soil microbial functional diversity shifted through time, changing from October 2011 to August 2012. Treatments with minimal disturbance changed the least. Pasture productivity of the two treatments with the least disturbance was similar. When pasture soil was treated with glyphosate-based herbicide, most change was observed in the functional diversity of soil microorganisms.

Microbial functional diversity can be used as an indicator of soil quality and health, but is sensitive to changes in various environmental factors, pasture productivity, and soil and agricultural management practices. It is recommended that trends in soil microbial functional diversity should be monitored over time in order to attain more complete reflection that different agricultural practices might have on soil microbial functional diversity as a possible indicator of soil quality and health.

## References

- Van der Colf J (2011) The production potential of Kikuyu (*Pennisetum clandestinum*) pastures over-sown with Ryegrass (*Lolium* spp.). MSc thesis (University of Pretoria: Pretoria)
- Winding A, Hendriksen NB (1997) BIOLOG® substrate utilisation assay for metabolic fingerprints of soil bacteria: incubation effects. In 'Microbial Communities - Functional versus Structural Approaches'. (Eds in: H Insam, A Ranner) pp. 195-205. (Springer-Verlag: Berlin)