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Life at the interface: above- and below-ground responses of a grazed pasture soil to reforestation



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ABSTRACT

Conversion of agricultural lands to mixed species woody plantings is increasingly being undertaken as a means of sequestering C and increasing biodiversity. The implications of such changes in land use for soil communities, and the ecosystem services they provide (e.g., nutrient and C cycling), are relatively little understood. Results of a detailed study of vegetation, soil physicochemical properties and soil communities (primarily microbial) to reforestation of a pasture (15 years post reforestation), and its immediately adjacent un-restored pasture, are presented. Whereas the reforested portion of the site had significantly higher levels of tree canopy cover and a well-developed litter layer than the immediately adjacent pasture, the reverse was true for grass biomass. Although there were no differences in total root biomass between the sampling zones, the pasture zone was dominated by fine roots and the reforested zone by coarse roots. Reforestation had a significant impact on soil physicochemical properties, with soil C, C:N and mineral N being higher than in the pasture. The reforestation also supported a greater microbial PLFA, a higher Fungal: Bacterial PLFA ratio and a different microbial community (based on PLFA profiles) from that of the adjacent pasture. There were also differences in earthworm abundance, with earthworms present and absent in soils from the pasture and reforested zones, respectively. All of the changes in vegetation, soil physicochemical properties and biotic communities occurred abruptly at the interface between the land-use types, with no evidence of an interaction between side of fence (reforested versus pasture zones) and distance from the fence. Results are discussed in the context of changes in land-use on soil ecology and their potential functional significance.

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1. Introduction

There is great potential to sequester C in the soil (Lal, 2004). This can be achieved in many ways, including the addition of C-rich materials to the soil, changes in specific farming practices, and land-use change (Cunningham et al., 2015a; Minoshima et al., 2007; Ng et al., 2014; Paul et al., 2002; Quilty and Cattle, 2011). One approach that is receiving increasing attention is the conversion of agricultural lands, especially those that are marginal or are expected to become so under climate change, to mixed species woody plantings (Cunningham et al., 2015b). This approach to C sequestration can also provide additional environmental benefits, such as the provision of habitat, improving soil stability, and reducing the risk of point source pollution (Bradshaw et al., 2012; Burger et al., 2010; Cunningham et al., 2015b).

Reforestation can have a profound impact on soil properties. For example, soil N levels are generally lower following reforestation compared to agricultural lands due to the addition of fertilizers in

http://dx.doi.org/10.1016/j.apsoil.2015.12.002 0929-1393/© 2015 Elsevier B.V. All rights reserved. fields (Garten and Ashwood, 2002), and the large N demand of growing trees (Berthrong et al., 2009). In contrast, P mineralization and availability can be higher in tree plantings than in agricultural lands (Chen et al., 2008; Wilson et al., 1997). Increases in the amounts and stability of soil C have also been reported following reforestation of agricultural lands (Cunningham et al., 2015a; de Alcântara et al., 1996; Smith et al., 2012). These changes in soil C are likely due differences in the amount and chemical nature of plant litter inputs from trees compared to crop and pasture species (Aerts and Chapin, 2000). Soil C:N ratios can also increase following reforestation of pastures (Berthrong et al., 2009; Cunningham et al., 2015a; Cunningham et al., 2012). These changes in soil chemistry are often associated with changes in soil microbial communities and their functioning.

Shifts in microbial community composition following reforestation have been reported (e.g., Bossio et al., 2005; Hedlund, 2002; Wu et al., 2013). An increase in soil fungal:bacterial (PLFA) ratios, as high as 50%, has also been found following reforestation of pastures (MacDonald et al., 2009). These increases in fungal: bacterial (PLFA) ratios can be explained by a positive relationship between soil fungal:bacterial (PLFA) and soil C:N ratios (Busse

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et al., 2009; Högberg et al., 2007; Waring et al., 2013). Together, such changes in soil microbial community composition and bacterial and fungal biomass can have implications for soil nutrient and C cycling as soil microbes play an important role in these processes (Bardgett and Wardle, 2010; Jackson et al., 2008; Paul, 2006).

Although soil ecological responses to reforestation of agricultural lands have been studied (e.g., Bossio et al., 2005; Hedlund, 2002; Singh et al., 2007), relatively little is known about patterns of change at the interface between these land-use types. However, some insights have been gained. For example, in a study of soil and vegetation properties at the interface between a reforested pasture and its immediately adjacent un-restored pasture, an abrupt change in both the amounts and forms of C (by ¹³C solid-state NMR) was found (Smith et al., 2012). The same was also true for rates of nutrient cycling processes (specifically potential N mineralization), which were higher in the reforested zone. Impacts on soil communities were not considered in this earlier work. Given their importance in soil C and nutrient cycling (see Bardgett and Wardle, 2010; Jackson et al., 2008; Paul, 2006 for detailed review), this is an important knowledge gap.

Here results of a study of soil ecological responses of a pasture soil to reforestation are presented. The study focused on the interface between an area that had been converted from a pasture to a tree planting 15 years prior to sampling, and a contiguous pasture of a similar size that had been managed in the same way as the tree planting prior to its establishment. Particular emphasis was placed on changes in soil microbial community composition, soil C stocks and aspects of soil N cycling. It was hypothesized that planting trees on the pasture would result in:

- 1. An abrupt change in soil physicochemical properties at the interface between the two land-uses;
- 2. An increase in the fungal:bacterial (PLFA) ratio in the reforested portion of the site compared to the pasture; and
- The development of microbial community in the reforested portion of the site that was different from that of the pasture.

2. Materials and methods

2.1. Field site and survey design

Soils were collected from a grazed (sheep) pasture farm in Archie's Creek, in the West Gippsland region of Victoria, Australia. The region has a temperate climate with a mean maximum temperature in the hottest month of 23.4 °C, and a mean minimum temperature in the coolest month of 5.9 °C, and an annual mean rainfall of 1095 mm/year (http://www.bom.gov.au/climate/, last accessed June, 2015). Prior to European settlement, this region was covered predominantly in woodlands and forests dominated by *Eucalyptus* species. These woodlands and forests have been extensively cleared since the 1840 for pasture and stock production.

The field site included an area that had been converted from a pasture to a tree planting 15 years prior to sampling. The tree planting was 2 ha in size, and was immediately adjacent to a pasture (3 ha in size) that had been managed in the same way as the tree planting prior to its establishment (i.e., previously part of the same field). The tree planting was established by fencing out grazing stock and hand planting tubestock seedlings into furrows/ rip-lines at 3 m spacing. The site contained a mixture of native plant species and was dominated by *Eucalyptus globulus* spp. *globulus* and *Eucalyptus obliqua*, with a tree density of 690 trees ha⁻¹ and a basal area of 23.8m² ha⁻¹ (Cunningham, unpublished).

Patterns in soil properties at the pasture/tree-planting interface were studied at the site in September 2013 (Austral Spring). A 36 m × 36 m plot that (equally) spanned both sides of the fence line dividing the pasture and the tree planting was established (Fig. 1); this spatially explicit sampling design is based on that of Smith et al. (2012). Importantly, the main plot was located on the site where all sampling zones were in a similar topographical position so as to avoid any gradients that may have existed across the site prior to reforestation. The main plot was divided into six contiguous sampling zones (referred to as zones A–F, hereafter), each of which was 36 m long (parallel to the direction of the fence line), and 6 m wide (perpendicular to the direction of the fence line). Thus, each sampling zone was divided into six equally sized (i.e., 6 m × 6 m) sampling plots, giving a total of 36 plots across the site.

2.2. Sample collection and analysis

Tree canopy cover (i.e., extent) was quantified in the center of each plot (following Burger et al., 2010). Surface litter was collected from each plot from a centrally located $0.25 \text{ m} \times 0.25 \text{ m}$ quadrat. Grass biomass was also collected from within each of the litter sampling quadrats. Litter and grass dry weights were determined (separately) after drying of the samples at 60 °C for 48 h.

After collection of grass and litter, three soil cores were collected from within each litter sampling quadrat by gently tapping metal cores (7.2 cm diameter) of known volume (203 cm³) into the soil to a depth of 5 cm. This sampling zone was selected as this soil layer is where biological activity is greatest in these soils (Cavagnaro, un-published). The first core was used for measurement of bulk density and root biomass as follows. All soil was removed from the core and divided into two sub-samples. The first sub-sample was used to determine soil gravimetric moisture content following drying at 105 °C for 48 h, and calculation of bulk density (see Smith et al., 2012), and the second for determination of root biomass. Roots were carefully washed from the soil, separated into to fine (<2 mm diameter) and coarse (>2 mm diameter) roots, dried for 48 h at 60 °C, and root biomass per g dry soil determined. The remaining two soil cores were immediately

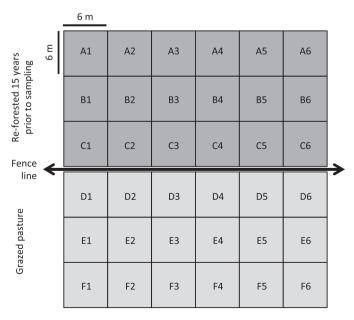


Fig. 1. Schematic diagram of field site and sampling regime. All soil and vegetation samples were taken from the center of each plot. N.B. diagram not drawn to scale. The fence was a barbed wire fence 1 m in height and the width of a single line of wire.

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