

Responses of forest soil fungal communities to management by repeated prescribed burning

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Abstract A repeated prescribed burning experiment (comprising burning every 2 yrs, burning every 4 yrs and unburned control plots) has been maintained at Peachester State Forest, Queensland, Australia for > 30 yrs. We have analysed total soil fungal and basidiomycete communities, along with mycelial communities of ectomycorrhizal fungi using direct DNA extraction and community profiling techniques. Overall the data indicate that, while soil fungal communities in plots burned every 4 yrs were similar to those in unburned control plots, burning every two years significantly altered soil fungal community structure.

Introduction

Fire causes major disturbance in forest ecosystems and can strongly influence above-ground ecology. Despite their importance in forest nutrient and carbon cycling processes, there is relatively little information on responses of soil fungal communities to fire. Much of the published information appears contradictory, largely reflecting differences in experimental methodologies, fire intensity and time-scale of the various studies (Neary et al 1999). Although conducted at various times following fire, most previous studies have considered the effects on soil fungal communities after only single burning events. Since fire-related benefits may last only a few years, repeated prescribed burning can be required for effective forest management. Such repeated burning can reduce surface and soil organic matter content, along with influencing nitrogen availability (Neary et al, 1999; Guinto et al., 2001). The effects of long-term repeated burning on soil fungal communities are, however, largely unknown. In order to address this, we have investigated the influence of repeated prescribed burning on fungal communities and their activities at an experimental site in Peachester State Forest, Queensland Australia. In this talk I will present an overview of the work at Peachester.

Materials and Methods

A repeated prescribed burning experiment has been maintained at Peachester since 1972 and comprises replicated plots that are subjected to biennial burning (2 yr plots), quadrennial burning (4 yr plots) or no burning (control plots). The influence of burning treatments on soil fungal communities has been investigated by direct DNA extraction from soil, coupled with DGGE analysis of partial rDNA ITS sequences for total soil fungi (Bastias et al. 2006a) or T-RFLP analysis of partial rDNA ITS sequences for basidiomycetes (Anderson et al. 2007). For analysis of ectomycorrhizal fungal communities, 50µm nylon mesh bags containing acid-washed sand were buried at the site for seven months, following which DNA was extracted and analysed by DGGE of partial rDNA ITS sequences and cloning of ITS sequences coupled with RFLP and sequence analysis.

Results and Discussion

Canonical analysis of principal coordinates of DGGE profiles of total soil fungal communities in the upper 10 cm of the soil profile grouped the data strongly according to burning treatment, indicating that both burning regimes significantly altered fungal community structure compared to the unburned controls. In contrast, no obvious trend was observed for soil from the upper 10-20 cm of the profile. Detrended correspondence analysis of ITS T-RFLP profiles separated basidiomycete communities in unburned control plots from those in burned plots, with two year plots being the most different from controls. Burning had no effect on

basidiomycete species richness, thus these differences appear to be due to changes in community structure. Basidiomycete communities in the unburned control plots were vertically stratified in the upper 20 cm of soil, but no evidence was found for stratification in the burned plots, suggesting that repeated prescribed burning results in more uniform basidiomycete communities.

Analysis of sequences derived from the hyphal ingrowth bags indicated that 88% were probably derived from ectomycorrhizal fungi. Multivariate analysis indicated that DGGE profiles for two year plots were significantly different to those of four year plots and unburned control plots. Analysis of clone assemblages indicated that this reflected altered ectomycorrhizal fungal community composition.

Overall the molecular data indicate that, while soil fungal communities in plots burned every 4 yrs were similar to those in unburned control plots, burning every two years significantly altered soil fungal community structure. Recent work involving PLFA analysis, Microresp community level physiological profiling (Campbell et al., 2003) stable isotope probing and laccase gene expression (aimed at investigating functional changes in soil microbial communities in response to the burning treatments) will also be discussed.

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