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Impact of biotic and abiotic interaction on soil microbial communities and functions: A field study

Brajesh K. Singh^{*}, Lorna A. Dawson, Catriona A. Macdonald¹, Sarah M. Buckland

Macaulay Institute, Craigiebuckler, Aberdeen AB15 8QH, United Kingdom

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ABSTRACT

Interactions between plants, soils and microbes regulate terrestrial ecosystem functioning. Biotic and abiotic interactions can strongly affect the community structure which in turn will impact on ecological processes. Plant species with different ecophysiological traits can exert strong effects on soil biological properties. Our objective was to investigate and identify the effects of different biotic and abiotic variables on soil microbial community structure and functions and to examine if plant species with different physiological traits support different microbial communities in soils. Here, we show that 3 years of the presence of plants had direct impacts on soil function in terms of total heterotrophic respiration and on microbial biomass and microbial community structure. However, the plant species-specific impact on bacterial community structure was weak, and differences were mainly driven by sample field location. The fungal community analysis gave similar results, with soil location being the most important factor driving fungal community structure. The effect of plant species on fungal community structure was weak but statistically significant. There was a strong concordance between bacterial and fungal communities ($P < 0.001$) which suggested that the bacteria and fungi have an influence on shaping the structure of each other's community. Among the abiotic factors, moisture had a comparatively higher impact on bacterial communities compared to soil N and C. However, the fungal community was not affected by the soil moisture but soil N and C had a stronger impact than on the bacterial community. These results indicate that the microbial community structure in the natural environment is influenced by interactions between both biotic and abiotic factors.

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1. Introduction

Microbial community structure and ecological functions are influenced by interactions between above and belowground biota (Wardle et al., 2002). These interactions can have positive, negative or neutral impact on diversity and community structure of plants and soil microbes (Singh et al., 2004). It has been observed that many plants select beneficial groups of microorganisms via rhizodeposition (loss of carbon due to root exudation, leakage or root decomposition), and litter decom-

position, which may represent a positive association where plants supply carbon for microbial growth and microorganisms in return provide major elements such as N and P, as well as protection against pathogen and parasite attacks (Singh et al., 2004). It is believed that the carbon source made available by plants drives many complex chemical and biological interactions in the soil (e.g. Jones et al., 2004). These include sustaining a complex food web of prokaryotes and eukaryotes, the composition of which is thought to be regulated by complex signalling (Phillips et al., 2003). However,

^{*} Corresponding author. Tel.: +44 1224 498200; fax: +44 1224 498207.

E-mail address: b.singh@macaulay.ac.uk (B.K. Singh).

¹ Present address: Rothamsted Research, Harpenden AL5 2JQ, UK.
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it is not known if plants actively select for beneficial soil microbial communities. Significant change in soil microbial community structures has been reported with change in vegetative cover. These vegetation-induced changes have been observed both at the universal bacterial group level (Grayston et al., 1998, 2004; Nusslein and Tiedje, 1999) as well as at the functional group level (Singh et al., 2007a). However, another study reported similar microbial community structure in soils which shared similar agricultural management practices despite differences in above-ground community composition (Buckley and Schmidt, 2001). Similarly, Girvan et al. (2003) found that soil type is the primary determinant of the composition of the total bacterial community in arable soils. Most of the previous studies focused only on the bacterial community (Buckley and Schmidt, 2001; Girvan et al., 2003; Nunan et al., 2005), while a few exclusively studied universal fungal communities (Smit et al., 1999; Marcial-Gomes et al., 2003). There are only few reports of investigations on the impact of both plant species and soil type on both fungal and bacterial communities (Mougel et al., 2006; Costa et al., 2006; Singh et al., 2007b). To our knowledge none has investigated the concordance between bacterial and free-living fungal communities. With the growing evidence for the linked ecological functions of bacterial and fungal communities in processes such as decomposition and nutrient cycling, it is important to understand whether both communities are influenced by the same environmental factors (Costa et al., 2006).

The influence of the plant community on ecosystem functions is well known (Horner-Devine et al., 2003; Tilman et al., 2006). Furthermore, it is well established that plant species which dominate different stages of succession have different sets of ecophysiological traits (Aber et al., 1990; Van Vuuren et al., 1992; Grime et al., 2007) and that these sets of traits can exert strong effects on soil biological properties (Wardle et al., 1998; Bardgett et al., 1999; Hobbie, 2002; Garnier et al., 2004) such as selecting for decomposer food webs with certain basic attributes (Wardle et al., 2002). There are evidences that plant species differ considerably in the composition of soil biota that they support (Grayston et al., 1998; Wardle et al., 1998; Marilley et al., 1998; Bardgett et al., 1999; Johnson et al., 2003; Vandenkoornhuysen et al., 2003). Other studies found mainly mycorrhizal fungi (Van der Heijden et al., 1998a,b) or bacteria (Van der Heijden et al., 2006) to be key determinants of ecosystem diversity and functions. Although soil ecologists have long recognised the need to understand the mechanisms by which community structure is shaped and ecosystem functions are maintained, study on multi-community and multi-trophic interactions between above and belowground communities and their impact on ecosystem function is lacking. In the present study, we studied the impact of grass species with differential physiological traits (in monoculture and as a natural mixed community) and soil abiotic factors (soil C, N and moisture) on soil bacterial and fungal communities under field conditions. We also investigated the interactions between bacterial and fungal communities and the impacts on shaping microbial community structure. Soil functional capabilities under different grass species were also measured in terms of respiration rate and total microbial biomass.

2. Materials and methods

2.1. Site, soil properties and plant species

This study was carried out at an experimental site at Sourhope, Scotland (55°28'32"N 2°14'43"W), a semi-natural *Festuca ovina*–*Agrostis capillaries*–*Galium saxatile* grassland, determined as a *Luzula multiflora*–*Rhytidiadelphus loreus* sub-community (National Vegetation Classification (NVC) U4d), also the location of the recent NERC Soil Biodiversity Programme (Usher et al., 2006). The site is a long-term (>200 year old) grassland, and in 1998 a fence was erected to exclude grazing animals (e.g. livestock, deer, rabbits and hares). It is situated at 309 m above sea level and varies in slope from 8° at the top to 4° at the foot and has a northerly aspect, mean annual rainfall is 954 mm. The soils are developed on a drift locally derived from andesitic lavas of old red sandstone and are characterised as acid brown forest soil belonging to the Sourhope series (SH 74711) (pH 4.5–5.0) (Grayston et al., 2004).

In 1999, the site was fenced to prevent sheep grazing and set out in five replicate blocks, each block being placed along the contour of the slope. Experimental plots (1 m²) were arranged in a randomised block design with nine treatments in each of the five blocks. Nine treatments involved creating monocultures, eight of which were common herbaceous species at the Sourhope site: *Agrostis capillaris* (Ac), *Anthoxanthum odoratum* (Ao), *Festuca ovina* (Fo), *Festuca rubra* (Fr), *Nardus stricta* (Ns), *Luzula multiflora* (Lm), *Trifolium repens* (Tr), *Rumex acetosa* (Ra); and a ninth species which was present in the improved areas of pasture, *Lolium perenne* (Lp). These species also represent a broad range of physiological and functional types, illustrated by the contrasted values in key plant traits (Table 1). The monoculture plots were created by removing the surface 2–3 cm of turf and inserting vegetative specimens collected from the surrounding natural vegetation contained in the Sourhope enclosure, washing and brushing off as much soil as possible, before transplanting into their respective plots. Monocultures of *L. perenne* were established by sowing in seed (60 g per plot). A 10th treatment included plots of undisturbed, natural (N) turf, to provide data on the natural soil community in the absence of turf removal. A 11th treatment comprised bare (B) plots, to provide data on the effect of turf-stripping without reintroduction of transplants. The plots were maintained by regular hand-weeding to promote ongoing establishment of the monocultures and to prevent vegetation colonization on the bare plots. Plots were mown monthly between May and September, following the management design implemented on the NERC soil biodiversity experiment.

2.2. Measurement of soil respiration, microbial biomass, soil N, soil C and moisture

Three years after the treatments were established, soil samples were collected from each field-block by a (3.5 cm diameter × 8 cm depth) corer. Roots were removed by hand picking. From each plot, four cores were taken and stored in plastic bags at 4 °C until analyses were completed. For molecular work, sub-samples were frozen at –20 °C until

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