Bioenergy driven land use change impacts on soil greenhouse gas regulation under Short Rotation Forestry

Kim Parmar [a, b, *], Aidan M. Keith [a], Rebecca L. Rowe [a], Saran P. Sohi [b], Claudia Moeckel [a], M.Gloria Pereira [a], Niall P. McNamara [a]

[a] NERC Centre for Ecology & Hydrology, Lancaster Environment Centre, Library Avenue, Bailrigg, Lancaster, LA1 4AP, United Kingdom
[b] School of Geosciences, University of Edinburgh, Crew Building, The Kings Buildings, Edinburgh, EH9 3JN, United Kingdom

ARTICLE INFO

ABSTRACT

Second-generation bioenergy crops, including Short Rotation Forestry (SRF), have the potential to contribute to greenhouse gas (GHG) emissions savings through reduced soil GHG fluxes and greater soil C sequestration. If we are to predict the magnitude of any such GHG benefits a better understanding is needed of the effect of land use change (LUC) on the underlying factors which regulate GHG fluxes. Under controlled conditions we measured soil GHG flux potentials, and associated soil physico-chemical and microbial community characteristics for a range of LUC transitions from grassland land uses to SRF. These involved ten broadleaved and seven coniferous transitions. Differences in GHGs and microbial community composition assessed by phospholipid fatty acids (PLFA) profiles were detected between land uses, with distinctions between broadleaved and coniferous tree species. Compared to grassland controls, CO_2 flux, total PLFAs and fungal PLFAs (on a mass of C basis), were lower under coniferous species but unaffected under broadleaved tree species. There were no significant differences in N_2O and CH_4 flux rates between grassland, broadleaved and coniferous land uses, though both CH_4 and N_2O tended to have greater uptake under broadleaved species in the upper soil layer. Effect sizes of CO_2 flux across LUC transitions were positively related with effect sizes of soil pH, total PLFA and fungal PLFA. These relationships between fluxes and microbial community suggest that LUC to SRF may drive change in soil respiration by altering the composition of the soil microbial community. These findings support that LUC to SRF for bioenergy can contribute towards C savings and GHG mitigation.

© 2015 Published by Elsevier Ltd.

1. Introduction

The greatest contributors to global greenhouse gases (GHGs) are emissions from fossil fuel use and land use change (LUC) [1]. Land use patterns have changed in response to human needs over time [2], and now in order to meet renewable energy and GHG emissions reduction targets, LUC to bioenergy crops is under serious consideration [3—5]. Estimates suggest that 13—22% of the world's global energy demands by 2050 could be met through biomass [6]. In Europe, bioenergy currently accounts for almost two-thirds of the total renewable energy and much of this comes from energy crops [7] and, furthermore, the European Union has committed to increase the proportion of renewable energy from 9% in 2010 to 20% of total energy consumption by 2020 [8]. Although there are competing land demands from activities such as food production, infrastructure, recreation and biodiversity [9], the rationale remains for converting certain land to bioenergy crop production [10]. For a bioenergy crop to be considered as a viable and sustainable option in the future it must provide GHG savings in comparison to the use of fossil fuels [11,12]. Impacts of LUC on GHG emission reduction are dependent on the land uses involved, but LUC to bioenergy has the potential to deliver GHG emissions savings through soil C sequestration, with the greatest potential following LUC from arable crops to forestry [13,14]. In addition, and linked to changes in soil C, LUC can also influence GHG fluxes between the soil and the atmosphere [15].

Together with other dedicated bioenergy crops, Short Rotation Forestry (SRF) could contribute to biomass requirements for renewable energy targets [16,17]. Short Rotation Forestry is defined as high density plantations of fast-growing tree species, grown on

* Corresponding author. Centre for Ecology & Hydrology, Lancaster Environment Centre, Library Avenue, Bailrigg, Lancaster, LA1 4AP, United Kingdom.
E-mail address: kimpar70@ceh.ac.uk (K. Parmar).

short rotational lengths (greater than 10 years) and harvested at breast height of 10–20 cm for biomass [16,17]. Although not currently widely practised in the UK commercially, a suite of species is under consideration for SRF, including coniferous and broadleaved species types [16–18]. Tree species can influence soil organic carbon (SOC) sequestration and GHG fluxes due to varying rates of rhizodeposition [19], differences in above and below-ground C partitioning [20] and differences in litter inputs and decomposition rates [21].

Litter decomposition rates are generally distinct between coniferous and broadleaved species, with litter decomposition most rapid for deciduous broadleaved species [22–24]. Litter decomposition rates are strongly related to litter qualities including, litter N and lignin content, C/N ratio, and leaf area [21,23,25,26] and these can vary greatly between tree species. Litter quality can also affect soil pH, which in turn can alter soil microbial activity affecting decomposition of soil organic matter [24]. Roots also directly add organic material to the soil through exudation (rhizodeposition), fine root turnover and through coarse root shedding [24]. Root-derived inputs (rhizodeposits) are chemically diverse and range in complexity from labile exudates to senescent material released as a consequence of tissue turnover [27]. These compounds provide a diverse source of substrate to soil microbial communities and are responsible for the stimulation of microbial biomass and activity in the rhizosphere [27]. Soil microbial community composition can be measured by analysis of phospholipid fatty acids (PLFAs). PLFA analysis has become widely used to study soil microbial communities [28,29] and quantifies total soil microbial biomass and the proportions of bacteria and fungi. Total PLFA is well-correlated with other methods for microbial biomass estimation and readily discriminate land use, soil type and land management practises (e.g. Bardgett et al. [30]).

Around half of soil respiration is derived from plant root respiration; the remaining respiration is associated with the decomposition of organic matter by the microbial community [24,27]. In the absence of root respiration, the rate of heterotrophic respiration (the CO_2 mainly derived from soil microbial activity) is largely a function of microbial community composition and organic matter quality, and ultimately organic matter quality is regulated by plant inputs [31,32]. Examining this component of respiration following LUC to SRF may give an indication of how changes in organic matter quality, or differences between species types, influence CO_2 fluxes. As emissions of methane (CH_4) and nitrous oxide (N_2O) contribute to climate change they must also be considered in LUC to forestry [24]. CH_4 has a global warming potential (GWP) 25 times greater than CO_2 [1]. CH_4 is produced under anaerobic conditions and therefore emissions are more likely in wet soils [33]. CH_4 is consumed in aerobic conditions [33] and because of this net CH_4 emissions in any soil depend on both production and consumption rates. It is generally accepted that forests are strong sinks for CH_4 [34]. N_2O is a powerful GHG and has a global warming potential (GWP) 298 times that of CO_2 [1]. Unlike CH_4 and CO_2, N_2O can be produced under both aerobic and anaerobic conditions and can be consumed in wet, nitrogen-poor soils [35]. Recent studies indicate a tendency towards higher N_2O emissions from deciduous than coniferous forest soils [36,37] due to differences in tree litter quality and soil moisture [24].

Our previous work examining changes in soil C stock following the establishment of different SRF species has shown greater litter accumulation, and an overall increase in soil C stock in coniferous soils (relative to agricultural controls) compared to broadleaved soils [38]. Despite broadleaved species having no overall effect on soil C stock, the response was more variable suggesting that individual species influence soil C accumulation differently. When combined with estimates of C stocks in aboveground biomass the

likelihood of C accumulation under conifers was further strengthened [38]. In addition to these findings on soil C, knowledge on GHG fluxes under SRF is needed to contribute to a better understanding of sustainability of this bioenergy land use. Therefore, we examined potential soil GHG fluxes, under standardised conditions, from LUC transitions, and the associated changes in soil physico-chemical and soil microbial community characteristics. The gas flux measurements also yield additional information on the potential for the biological consumption and production of GHGs such as N_2O and CH_4. Specifically, we tested for 1) differences in GHG potential fluxes, soil physico-chemical (pH, C concentration) and microbial community characteristics between land uses (controls and different SRF species types), and 2) whether changes in soil physico-chemical (pH, C concentration) and microbial community characteristics could explain changes in CO_2 flux.

2. Materials and methods

2.1. Site selection and sampling strategy

Sampling was undertaken at six sites across the UK from replicated experimental and commercial SRF sites. A paired plots approach was used where SRF species and adjacent land continuing in former land use could be identified at each location. To confirm that the soil for the control land use was comparable to the transitional SRF land use, data on management history and soil type had been collected and examined (Table 1). Following soil sampling, texture analysis was carried out and was used to confirm similarity in soil type between control land use and transitional land use at each site (Table 1). Expert advice and current literature on potential SRF tree species was also used to make an informed decision regarding suitable site selection [17,18,39]. The tree species chosen for this study, which have been broadly classified as coniferous (7 transitions) and broadleaved (10 transitions), included Alder (*Alnus glutinosa*), Ash (*Fraxinus excelsior*), Downy birch (*Betula pubescens*), Hybrid larch (*Larix x eurolepis*), Poplar (*Populus spp.*), Scots pine (*Pinus sylvestris*), Silver birch (*Betula pendula*), Sitka spruce (*Picea sitchensis*), and Sycamore (*Acer pseudoplatanus*). All sites with the exception of the site in North-West England (20 years into its second rotation; Table 1) are in their first rotation ranging in age from 12 to 24 years.

A hierarchical sampling design was used to capture spatial variability [38]. Five sampling locations were randomly selected within each paired plot (transition) (i.e. control or tree species) using an overlain grid. At each randomly selected sampling location, soil cores were taken from three positions, resulting in 15 spatially nested samples per transition.

Three soil cores (30 cm × 4.8 cm) were taken at each sampling location using a split-tube soil corer (Eijkelkamp Agrisearch Equipment BV, Giesbeek, The Netherlands), at the grid intersect and then at distances of 1 m and 1.5 m in random compass directions. Prior to soil sampling, the litter (L) and fermentation layers (L_f) were removed. Soil cores were divided into 0–15 cm and 15–30 cm sections in the field, bagged, and returned immediately to the laboratory where they were stored at 4 °C.

2.2. Laboratory processing

Soil core sections were quartered lengthways, with quarters being allocated for different subsequent analyses; one quarter was used to derive soil C concentration and pH, and others allocated for microbial analysis and to the controlled GHG potentials laboratory incubation experiment. For further details on the soil processing methods see Keith et al. [38].