Response of soil microorganisms to land-use change in China, Ecuador and Germany

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Abstract

Within different ecosystems of China, Ecuador and Germany the effects of land-use change on i) nutrient turnover, ii) microbial biomass and iii) microbial community structure were assessed. On the Loess Plateau of China accelerated soil erosion, induced by land-use change from forest to agriculture, was the main process leading to soil degradation. Intensified soil erosion significantly decreased the contents of organic matter and microbial biomass in the soils. However, independent of erosion intensity N and C cycling rates were maintained in the bare plots. This might be explained by changes in the structure of the soil microbial community. In the mountain rainforest region of the South Ecuadorian Andes the initial increase in microbial biomass and activity after forest to pasture conversion by slash-and-burn slows down with increasing pasture age and/or increasing dominance of bracken fern and was associated with a significant shift in the phospholipid fatty acid (PLFA) fingerprint of the soil microbial community. A fast response of soil microorganisms to fertilization with urea was detected. At the agricultural study site in NE-Saxony, Germany, land-use effects were visible 6 years after starting the different management systems (intensive agricultural use, fallow) as indicated by the principle component analysis of PLFA data.

Key Words

Soil microbial community, PLFA, SOC mineralization, gross N mineralization, soil erosion, fertilization.

Introduction

Soil microorganisms are important drivers of nutrient cycling processes in soils. Land-use change as well as management practices are known to have impacts on soil microbial community structure and activity. However, extent and direction of land-use and management induced changes are highly variable and seem to depend strongly on the ecosystem considered. Some authors report shifts in soil microbial community structure within 2 years after land-use had changed (Hedlund 2002), others after 45 years (Buckley and Schmidt 2003). The interactions of microbial community dynamics and mineralization processes are complex and up to now not fully understood. For example, only little is known about how microbial communities mediate N cycling rates after disturbance of the soil ecosystem (Smithwick *et al.* 2005). Land-use induced disturbances of soil ecosystems like clear-cutting of forest, slash-and-burn practices and intensive agricultural use frequently occur worldwide often leading to soil degradation. Within the present study the response of soil microorganisms to land-use change in different ecosystems of China, Ecuador and Germany is compared. On the Loess Plateau of China accelerated soil erosion, induced by land-use change from forest to agriculture, is the main process leading to soil degradation. Soils with different degradation and rehabilitation status have been examined. In the mountain rainforest region of the South Ecuadorian Andes natural forests often have been converted to pastures by slash-and-burn. With advanced pasture age the pasture grass (*Setaria sphacelata*) is increasingly replaced by the tropical bracken (*Pteridium arachnoideum*) leading to the abandonment of this unproductive pastures (Beck *et al.* 2008). A sustainable management strategy for already existing pasture land in this mountain rainforest region of Southern Ecuador is one prerequisite to prevent further forest clearing for the establishment of new pastures. Hence, a pasture fertilization experiment was established where urea is used as N-fertilizer. In NE-Saxony, Germany, the effects of agricultural management practices on nitrogen dynamics and the structure of the soil microbial community have been considered depending on season.

Methods

Study sites

The study sites in China were located close to the “Fuxian Observatory for Soil Erosion and Eco-Environment” (Shaanxi Province), in the sole forest region remaining on the Loess Plateau. Annual mean air temperature and precipitation range between 6-10 °C and 600-700 mm. The forest is a 140 years old secondary stand. In 1989 within the forest runoff plots have been established on a hillslope to quantify soil erosion and the associated nutrient loss from the soils after clear-cutting as described in Zheng *et al.* (2005).

A land-use gradient from bare soils without vegetation (Bare), soils under agricultural management (Arable), soils with six year old natural successional vegetation (Succession) and soils under a 140 year old secondary forest (Forest) have been investigated. Additionally, a sequence of increasing erosion intensity along a hill from top to down slope was included on bare and forest sites (gradient: sheet erosion, rill erosion, gully top, gully). Soil samples were taken from 0-20cm depth. Soil type is a Calcaric Regosol developed on loess (Hamer *et al.* 2009a) with a soil pH(H_2O) between 8.5 and 9.0 (Table 1).

The study sites in Ecuador were located close to the "Estacion Científica San Francisco", about halfway between the provincial capitals Loja and Zamora, in the Cordillera Real, an eastern range of the South Ecuadorian Andes at about 2000 m above sea level. The mean annual air temperature is 15.3°C with an average annual rainfall of 2176 mm (Bendix *et al.* 2006). Soil samples were taken from 0-5cm depth of an active and an abandoned pasture site (Pasture, Abandoned Pasture). At both sites the soil type is a Cambisol and soil pH(H_2O) is acidic (5.4-5.6, Table 1). Using ^{14}C- and ^{15}N-labelled urea the effects of urea fertilization on soil organic matter mineralization and microbial community structure were investigated (Hamer *et al.* 2009b).

The study sites in Germany were located in Kreinitz (NE-Saxony) on a former arable site, which had been under fallow between 1996 and 1999. In 1999 the area was ploughed and divided into 12 plots of 50 m * 18 m size. Six out of these 12 plots were randomly chosen for intensive agricultural use (Intensive) and six plots were set aside and left to develop under natural succession vegetation (Fallow). Soil samples were taken from 0-10cm depth in June and September 2005. The soil type is a Cambisol developed on a loamy sand loess overlying a sand-gravel deposit with a soil pH(H_2O) between 5.3 and 5.6 (Table 1). Annual mean air temperature and precipitation vary between 8.4°C to 9.8°C and 550 mm to 600 mm, respectively (Hamer *et al.* 2008, Hamer and Makeschin 2009).

Table 1. Soil pH, soil organic carbon (SOC) content, C/N ratio, total amount of phospholipid fatty acids ($PLFA_{tot}$), mineralization of SOC during 14days of incubation and gross N mineralization rate in soils from China, Ecuador and Germany under different land-use (mean values; nd not determined).

	pH(H_2O)	SOC (g/kg)	C/N	$PLFA_{tot}$ (nmol/g)	SOC mineralization (%)	Gross N mineralization (mg/kg/d)
		China[1]				
Bare Sheet Erosion	8.7	7.5	10.2	11.8	1.1	0.2
Bare Rill Erosion	8.8	6.9	8.8	7.2	1.2	nd
Bare Gully Top	9.0	3.1	8.5	2.3	3.8	nd
Bare Gully	8.9	5.3	8.9	6.0	1.4	0.2
Forest	8.5	20.5	10.9	66.9	1.3	1.1
Forest Gully	8.6	19.8	11.1	44.0	1.0	1.6
Succession	8.8	11.0	9.8	22.6	1.2	0.5
Arable	8.8	5.8	8.6	23.1	2.2	0.5
		Ecuador[2]				
Pasture	5.4	122.3	12.5	322.0	1.2	12.1
Abandoned Pasture	5.6	78.1	15.7	124.0	0.8	0.4
		Germany[3]				
Intensive Agriculture (June)	5.3	8.2	11.6	16.1	0.5	1.1
Fallow (June)	5.6	9.2	11.5	12.0	0.6	1.7
Intensive Agriculture (September)	5.2	7.9	11.4	17.8	1.0	1.1
Fallow (September)	5.6	9.2	11.9	18.9	1.0	1.4

[1] 0-20cm, n = 3; [2] 0-5cm, n = 6; [3] 0-10cm, n = 6

Microbial biomass and community structure

Microbial biomass carbon and nitrogen (MBC, MBN) were determined with the chloroform-fumigation extraction method. The structure of the soil microbial community was assessed using phospholipid fatty acid analysis (PLFA) as described in Hamer *et al.* (2009a,b).

Microbial activity

Mineralization of soil organic carbon (SOC) was determined during 14 days of incubation in the dark at 22°C. During the incubation the CO_2 produced was absorbed in 0.05*M* NaOH solution and quantified by titration. Gross rates of N mineralization were determined using the ^{15}N isotope pool dilution method as described in Hamer *et al.* (2009a,b).

Results and Discussion

At all three investigation sites in China, Ecuador and Germany the respective land-use change did not only affect the activity of soil microorganisms (Table 1) but also their community structure (Figure 1). As observed in laboratory incubations these changes are at least partly triggered by litter quality (Potthast *et al.* 2010) and fertilization regime (Hamer *et al.* 2009b). In the Ecuadorian pasture soils fertilization with urea induced a shift in the microbial community in both examined soils into the same direction: towards a higher relative abundance of PLFA marker characteristic of Gram negative bacteria and fungi (Hamer *et al.* 2009b). Also in the German agricultural soils fertilization seems to be important. However, there seasonal differences between samples taken in June and September were more pronounced (Hamer *et al.* 2008, Hamer and Makeschin 2009). As indicated by the principal component analysis of all PLFA data, there is a clear separation of soil microbial communities of the German and Chinese arable soils along principal component 1 from the other Chinese soils and the Ecuadorian soils with different land-use (Figure 1). The second principal component separates the Ecuadorian soils from the Chinese soils with one exception. The soil taken at the gully top at the bare site in China, a site without vegetation since 10 years, showed a PLFA fingerprint comparable to those of the Ecuadorian soils (Figure 1) and also had the highest mineralization of SOC (Table 1). Intensified soil erosion significantly decreased the contents of organic matter and microbial biomass in the Chinese soils, leading to the lowest SOC and $PLFA_{tot}$ contents observed among all sites investigated (Table 1). However, independent of the intensity of erosion N and C cycling rates were maintained in the bare plots. This might be explained by changes in the structure of the soil microbial community. Gross N mineralization and gross NH_4 consumption rates were significantly highest in forest soils. Within the forest, after 140 years, nutrient contents, microbial activity parameters and the soil microbial community structure were similar, independent of former erosion intensity. Thus, these parameters developed into the same direction during 140 years of secondary forest growth. Even after six years of natural succession a partial re-establishment of soil properties toward forest conditions was detected (Hamer *et al.* 2009a).

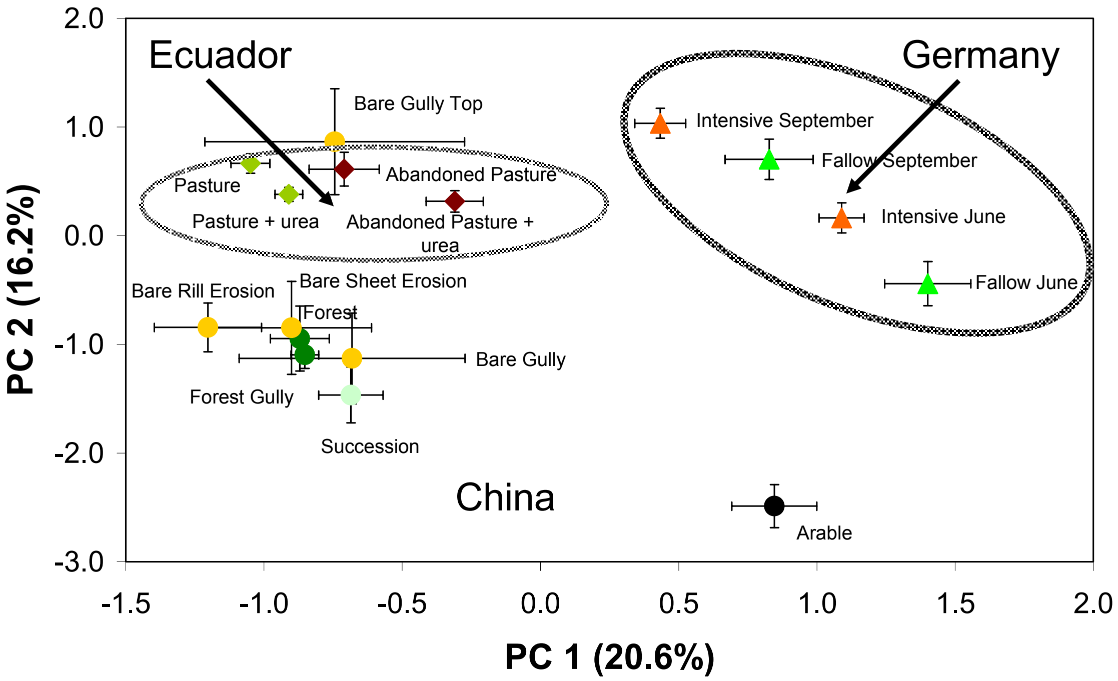

Figure 1. Principal Component (PC) analysis of PLFA data from soils of (◆) Ecuador (pasture and abandoned pasture without and with urea fertilization), of (●) China (bare, forest, succession and arable land with different erosion intensity) and of (▲) Germany (intensive agricultural use and fallow land in June and September) (mean values, bars represent standard error, n=6 for Ecuador and Germany, n=3 for China).

Conclusions

In the different ecosystems considered in China, Ecuador and Germany distinct microbial communities developed as indicated by their PLFA fingerprints. At all three sites land-use change significantly affected the soil microbial community structure and the microbial activity. Six years after land-use change these effects were detectable at the latest as can be seen at the German as well as Chinese sites. They might be detectable even more early. However, here further sites of different age have to be included. In laboratory incubation experiments it was obvious that soil microorganisms reacted immediately to fertilization. A changed microbial community structure was detected one month after urea addition to the Ecuadorian pasture soils.

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