— Stabile Isotope in der Bodenkunde —
DBG-Workshop in Göttingen

Am:
27. und 28. September 2010
Beginn: 27.09.10, 13^{15} ; Ende: 28.09.10, ca. 13^{30}

Veranstaltungsort:
Universität Göttingen (Bereich Forstwissenschaften)
Büsgenweg 2, Hofgeschoss,
Raum F O2 und FSR 2.1

Anreise:
siehe http://www.uni-goettingen.de/kosi

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Technische Ausstattung

Vorträge im Hörsaal F O2 Beamer, XP-Notebook
Die Vorträge sollen maximal 15 Minuten lang sein, damit mindestens 10 Minuten Diskussionszeit zur Verfügung steht.

Poster
Die Poster werden in dem benachbarten Raum **FSR 2.1** aufgestellt. In diesem Raum sind Posterstellwände für DIN A0-Poster vorgesehen.
Jeder Aussteller erhält zudem Gelegenheit sein Poster kurz in max. 5 Minuten vorzustellen, vorzugsweise über Beamer.

Stabile Isotope in der Bodenkunde — Programm

	Montag, 27. Sepember 2010
13:15 h	**Begrüßung**
13:30 h	Martin Köstler Automatische Analyse von Bodenproben/Bodenzusatzstoffen anhand der $^{13}CO_2$ Emission
13:55 h	Mirjam Helfrich Modelling of subsoil C dynamics using simple models
14:20 h	**Pause**
14:50 h	Christian Knoblauch Methane oxidation associated to submerged brown-mosses reduces methane emissions from Siberian polygonal tundra
15:15 h	Susanne Kramer C-Assimilation von Bodenmikroorganismen - Einfluss der Qualität und Verfügbarkeit von Ressourcen
15:40 h	Juergen Esperschuetz Microbial food web dynamics along a chronosequence of a glacier forefield
16:05 h	**Pause**
16:30 h	Stefan Lukas, Martin Potthoff, R.G. Jörgensen Auswirkungen des Klimawandels auf Mikroorganismen und Streuumsatzraten im Boden
16:55 h	Mario Schenck zu Schweinsberg Rhizodeposition C and N: Impact on microbial growth and C and N turnover within the rhizosphere
17:20 h 18:00 h	**Pause/Postervorstellung**
19:00 h	Option: gemeinsames Abendessen

	Dienstag, 28.September 2010
9:00 h	Caroline Indorf, Rainer Georg Jörgensen, Jens Dyckmans Aminozucker-spezifische $\delta^{13}C$-Analyse zur Bestimmung der Bildung und der Nutzung von mikrobiellen Residuen in Böden
9:25 h	Michael Zech, Bruno Glaser, Björn Buggle, Roland Werner, Dieter Juckelka Sustanzspezifische $\delta^{18}O$ Analysen an Monosacchariden mittels GC-Py-IRMS: Potential, Probleme und Lösungsvorschläge
9:50 h	**Pause/ Poster**
10:20 h	Meik Meißner The sources of water transpired by single and mixed tree groups in a temperate deciduous forest
10:45 h	Evgenia Blagodatskaya Assessment of ^{13}C fractionation and preferential substrate utilization by microbial turnover based on C3 – C4 vegetation change
11:10 h	Juvia Sueta, Marife D. Corre Estimates of (de)nitrification contributions to N_2O fluxes from tropical montane and lowland forests using short-term ^{15}N tracing
11:35 h	**Pause**
12:00 h	Wolfram Eschenbach ^{15}N-Tracer studies on denitrification activity of aquifer material from two sandy aquifers in northern Germany – laboratory incubation experiments in relation to influencing sediment parameters
12:25 h	Reinhard Well Eignet sich die Isotopomersignatur von N_2O als Indikator für bakterielle Denitrifikation?
12:50 h	**Abschlussdiskussion**

Automatische Analyse von Bodenproben/Bodenzusatzstoffen anhand der $^{13}CO_2$ Emission

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Um das Abbauverhalten von Bodenkohlenstoff bzw. von in den Boden eingebrachten Kohlenstoffquellen (Bodenzusatzstoffe) zu untersuchen, wurde durch uns eine automatisierte Messanlage für Bodenproben entwickelt. Die Anlage umfasst, neben der selbstkonzipierten Steuerelektronik, Ventile und einen Wavelength Scanned-Cavity Ringdown Spectroscope (WS-CRDS) als Gasanalysator. Die homogenisierten Bodenproben befinden sich unter kontrollierten Bedingungen in Glasgefäßen. Es sollen sowohl der Aufbau als auch Messergebnisse vorgestellt werden.

Modelling of subsoil C dynamics using simple models

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Soil C dynamics below the plough layer have been little studied, despite a suspected large C stabilization potential of subsurface horizons. The objective of this study was to test two simple models (model A: single compartment for C3- and for C4-derived C; model B: division of C3- and C4-derived C into active and passive compartments) in their ability to simulate the C dynamics in subsoil horizons of a Haplic Phaeozem after conversion from C3- (rye) to C4-cropping (maize). The models were calibrated on an unfertilized maize soil and then validated on a maize soil with NPK-fertilization. Both models simulated well C3-C and C4-C dynamics in the investigated soil depths (20–40 cm and 40–60 cm). In all cases, the model efficiency EF was > 0, which indicated that the simulated values described the trend in the measured data better than the mean of the observations. However, we observed some inconsistency in the obtained parameter set (e.g. a higher proportion of passive C for C4-derived than C3-derived C or a very low decomposition rate constant for passive C4-C in 40–60 cm), which we assume to result from data restrictions on the investigated soils. Detailed data, which is needed for the evaluation of complex subsoil models (e.g. pool sizes, turnover rates and C inputs to subsoils) is still limited for most long-term experiments. As even the simple models applied here suffered from a lack of data, we assume more detailed information on subsoil C dynamics is vitally needed – especially for applying more complex models.

Methane oxidation associated to submerged brown-mosses reduces methane emissions from Siberian polygonal tundra

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First evidence for microbial methane oxidation associated to submerged brown-moss species from polygonal tundra environments of the Siberian Arctic is presented. We combined biogeochemical and molecular approaches and revealed that moss associated methane oxidation (MAMO) in polygonal ponds exceeds potential methanotrophic activity in semi-terrestrial soils of the same environment by up to two orders of magnitude. Polygonal ponds covered by the brown-moss Scorpidium scorpioides became a net sink for atmospheric methane (-1.7 mg CH4 m^{-2} d^{-1}) when exposed to sun-light but a methane source (21.6 mg CH4 m^{-2} d^{-1}) in the absence of light, indicating that methane oxidation benefits from oxygen produced by moss photosynthesis. Stable isotope probing with $^{13}CH_4$ and $^{13}CO_2$ revealed a symbiotic relation between methanotrophic bacteria and brown mosses. Carbon derived from CH4 oxidation was incorporated into the common methanotrophic fatty acids 16:1ω7 and 18:1ω9/ω7 and into phytol, sitosterol, and 24-ethyl-cholestanol highly abundant in moss biomass. The capacity of CH_4-C incorporation into the brown moss Scorpidium scorpioides was almost 60 % of the CO_2-C assimilation capacity. Methanotrophic bacteria living in close association with mosses are thus not restricted to Sphagnum species and low pH temperate peatlands. Rather is the process of moss associated methane oxidation a very effective buffer for CH_4 emissions from permafrost affected tundra, a region that is of high importance for the global green house gas budget. Considering that submerged mosses are widely abundant in polar-regions and require long-term stable environmental conditions, climate change may have a major impact on the carbon turnover in Arctic freshwater environments.

C-Assimilation von Bodenmikroorganismen - Einfluss der Qualität und Verfügbarkeit von Ressourcen

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Im Rahmen des DFG-Projekts „Carbon flow in belowground food webs assessed by isotope tracers“ wurde im Jahr 2009 auf einer bislang mit C3-Pflanzen agrarwirtschaftlich genutzten Fläche in Göttingen durch Anbau der C4-Pflanze Zea mays ein Feldversuch etabliert. Bei Körnermaisanbau erfolgt der Eintrag von C aus über- sowie unterirdischen Quellen (Streu / Rhizodeposition) und stellt so eine rekalzitrante und labile C-Quelle dar. Beim Futtermaisanbau wird C vor allem über die Rhizodeposition in den Boden eingebracht und stellt somit eine leicht verfügbare C-Quelle für die Bodenorganismen dar, während Maisstreu, die auf Weizenplots aufgebracht wird, mehr stabilere Verbindungen enthält. Ziel dieses Teilprojekts ist es, die mikrobielle Nutzung und C-Assimilation von Ressourcen unterschiedlicher Qualität zu untersuchen. Hierzu wurden im Jahr 2009 drei Probenahmen durchgeführt und die mikrobielle Biomasse, die Gemeinschaftsstruktur über Phospholipidfettsäuren (PLFA) und Enzymaktivitäten in drei unterschiedlichen Bodentiefen bestimmt. Über den Einbau des ^{13}C-Signals in die mikrobielle Biomasse, Ergosterol und in einzelne PLFAs wird die Nutzung der unterschiedlichen C-Quellen durch Bakterien und Pilze quantifiziert. Unsere bisherigen Ergebnisse haben gezeigt, dass bereits nach der ersten Vegetationsperiode das ^{13}C-Signal der Maisflächen in der gesamten mikrobiellen sowie der pilzlichen Biomasse nachgewiesen werden konnte. Dies ist die Basis für die geplante Untersuchung der Nahrungsnetze im Boden und die spätere Modellierung unserer Ergebnisse.

Microbial food web dynamics along a chronosequence of a glacier forefield

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Microbial food webs determine the functionality and stability of ecosystems, since an efficient budget of nutrients is the basis for the initiation and stabilisation of ecosystem processes. However the successional development of microbial food webs and their role in young ecosystems is unclear. Due to a continuous glacier retreat since mid of the 19th century, glacier forefields provide an excellent opportunity to study food web development along a chronosequence of differently developed soil ecosystems. In the present study, litter degradation and the corresponding carbon fluxes were measured along the forefield of the Damma glacier (Switzerland). ^{13}C enriched litter of the pioneering plant Leucanthemopsis alpina L. (+90‰ $\delta^{13}C$ vs V PDB) was applied at sites that have been free of ice for approximately 10, 60 and 100 years; furthermore a site outside the forefield (> 700 years of ecosystem development) was used as reference. Structure and function of microbial communities were identified by ^{13}C analyses of phospholipid fatty acids (PLFA) and phospholipid ether lipids (PLEL). Surprisingly, litter degradation rates were similar at all investigated sites at the end of the vegetation period, although total microbial biomass increased with growing stage of soil age and development. In contrast, at sites that have been free of ice for a shorter period, a high microbial activity was observed which might have compensated the lower biomass values. Once the plant derived carbon has entered the soil, a fast C-turnover and C-cycling through the microbial food web was observed in less developed ecosystems. Concerning litter degradation, a progressive specialization of the microbial community structure was detected with increasing ecosystem development.

Auswirkungen des Klimawandels auf Mikroorganismen und Streuumsatzraten im Boden

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Ein Inkubationsexperiment wurde für 56 Tage bei -3 °C, +4 °C und zwei verschiedenen Gefrier-Tau-Behandlungen durchgeführt, um eine differenzierte Nutzung von Ernterückständen durch Bodenmikroorganismen bei verschiedenen Winterklimaverläufen zu untersuchen. Hierfür wurde auf 5 mm zerkleinertes Maisstroh äquivalent zu 1,2 mg C und 31,5 µg g^{-1} Boden in Bodenmesokosmen eingearbeitet. Die Maiszugabe führte in allen Temperaturbehandlungen zu einem signifikanten Anstieg der mikrobiellen Biomasse. Mit einer Zunahme von 99 % im Vergleich zu den Kontrollproben trat der stärkste Anstieg bei Bodenproben auf, die einem einzelnen Frost-Tau-Zyklus ausgesetzt waren. Dauerfrost führte zu einem Anstieg von lediglich 31 %. Weder ein einzelner, noch multiple Frost-Tau-Zyklen führten zu signifikanten Unterschieden in der mikrobiellen Biomasse zwischen den Kontrollproben der vier Temperaturbehandlungen. Mit rund 10 % maisbürtigem Kohlenstoffanteil in der mikrobiellen Biomasse wurde durch die Behandlung der Bodenproben mit nur einem Frost-Tau-Zyklus im Vergleich zur +4 °C Behandlung (5,5 %) annähernd doppelt soviel Kohlenstoff in die mikrobielle Biomasse inkorporiert. Dauerfrost und häufige Frost-Tau-Zyklen führten zu einer Inkorporation von 4 % bzw. 7 %. Umgekehrt ergaben die Berechnungen des CO_2, dass im Vergleich zu einem einzelnen (11 %) bzw. mehreren Frost-Tau-Zyklen (12 %) bei konstanten +4 °C mit 21 % annähernd doppelt soviel

maisbürtiger Kohlenstoff mineralisiert wurde. Bei Dauerfrost wurden lediglich 3 % des zugegebenen Kohlenstoffes veratmet. Im Durchschnitt konnten 100 % des Maisstrohkohlenstoffes in den Fraktionen wieder gefunden werden. Die Ergebnisse zeigen einen deutlich messbaren mikrobiellen Abbau des maisbürtigen Kohlenstoffes bei Temperaturen um den Gefrierpunkt. Höhere Durchschnittstemperaturen bedingen hierbei eine stärkere Mineralisation, während Frost-Tau-Zyklen und damit verbundene niedrigerere Mitteltemperaturen zu einer signifikant höheren Inkorporation und dem Aufbau eines größeren Pools an mikrobieller Biomasse führen.

Rhizodeposition C and N: Impact on microbial growth and C and N turnover within the rhizosphere

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Two greenhouse rhizobox experiments were carried out to investigate the fate and turnover of ^{13}C- and ^{15}N-labelled rhizodeposits within a rhizosphere gradient from 0-8 mm distance to the roots of oat and wheat. Rhizosphere soil layers from 0-1, 1-2, 2-3, 3-4, 4-6 and 6-8 mm distance to separated roots of oat and wheat were analysed after a period of 27 and 53 days of roots affecting the rhizosphere soils, respectively. The soil samples from different distances to the separated roots of oat and wheat were investigated in incubation experiments (42 days, 15°C) for changes in total C and N and C and N derived from rhizodeposition in total soil, in soil microbial biomass and in 0.05 M K_2SO_4-extractable soil fraction. Additionally, the CO2-C respiration in total and that derived from rhizodeposition were measured from the rhizosphere soil samples up to 6 mm distance to the previously separated roots during the soil incubation. In total, 36% less C and 39% less N derived from rhizodeposition were found in the rhizosphere soil of oat in comparison to wheat within the rhizosphere gradients. Significant amounts of rhizodeposition C were revealed in rhizosphere soil up to 4-6 mm distance from the separated roots of oat and wheat. Rhizodeposition N was only revealed in the rhizosphere soils up to 1-2 mm and 3-4 mm distance from the roots of oat and wheat, respectively. Microbial biomass C and N increased significantly with increasing proximity to the separated roots in both experiments. In the rhizosphere soil of oat, the net increase of microbial biomass C close to the separated roots was smaller than the amount of incorporated rhizodeposition C. In contrast, the net increase of microbial biomass C in the soil close to roots of wheat accounted for only 82% of C derived from rhizodeposition. However, these values changed with increasing distance to the roots. During soil incubation, microbial biomass C derived from rhizodeposition decreased by about 50% and 22% of the previously incorporated C derived from rhizodeposition in oat and wheat soil samples, respectively. Beside rhizodeposit N, large amounts of unlabelled soil N (native SOM) were incorporated into the growing microbial biomass towards the roots in both experiments, indicating a distinct acceleration of soil organic matter decomposition and N immobilisation into the growing microbial biomass, even under the competition of plant growth. C decomposition of native soil organic matter was enhanced within the entire investigated rhizosphere gradients. This effect was less distinctive in the rhizosphere samples of oat. The data indicate differential microbial response to the rhizodeposit input at a high spatial resolution from the roots. These relations indicate a complex interaction between microbial growth and turnover as well as substrate input derived from rhizodeposition and accelerated decomposition of native soil organic matter (i.e. rhizosphere priming effects). The effects were different between the experiments with oat and wheat, presumably due to different amounts of rhizodeposits previously entering the rhizosphere soils during plant growth.

Aminozucker-spezifische $\delta^{13}C$-Analyse zur Bestimmung der Bildung und der Nutzung von mikrobiellen Residuen in Böden

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Aminozucker sind Bestandteile von Mikroorganismen insbesondere der Zellwände von Bakterien und Pilzen. Sie kommen nicht in höheren Pflanzen vor und können somit als Indikatoren mikrobieller Produkte in Böden verwendet werden. Die wichtigsten Aminozucker sind Glucosamin, Muraminsäure, Galaktosamin und Mannosamin.
Um in Tracerexperimenten die Umsatzdynamiken sowohl von Pilzen als auch Bakterien erfassen zu können, ist die substanzspezifische ^{13}C-Analyse der Aminozucker notwendig.Die bestehenden Verfahren zur Analyse von Aminozuckern ermöglichen entweder keine Möglichkeit zur Isotopenanalyse oder nur nach Derivatisierung und gaschromatographischer Trennung. Nachteil der GC-Trennung nach Derivatisierung ist allerdings, dass die Messgenauigkeit durch das Einbringen zusätzlicher C-Atome drastisch reduziert wird und außerdem Fraktionierung auftreten kann.
Ziel des Projektes ist die Anpassung der verfügbaren Methodik zur Messung von Aminozuckern, um $^{13}C/^{12}C$- Verhältnisse mit einem Isotopenratio-Massenspektrometer (IRMS) messen zu können. Mit dieser Methodik ist es möglich die Bildung und Nutzung von mikrobiellen Residuen zu untersuchen und zu bewerten. Dafür wurde zunächst die Hochleistungsflüssigkeitschromatographie(HPLC)- Umkehrphasen(RP)-Methode auf der Basis von APPUHN et al. (2004) modifiziert und an die verfügbare HPLC adaptiert. Nach erfolgreicher Validierung dieser RP-Methode wurde eine weitere Methode zur Bestimmung von Aminozuckern an einer Hochleistungs-Anionen-Austauschchromatographie (HPAEC) optimiert und validiert.
Die Einführung der HPAEC-Methodik ist erforderlich, um einen Eluenten ohne organische Beimischungen verwenden zu können, da ansonsten für die spätere Messung der $^{13}C/^{12}C$-Verhältnisse der Aminozucker am IRMS der Hintergrund-Kohlenstoff zu hoch ist. Die Messung der Aminozucker mittels der HPAEC-Methodik erfordert separate Analysen für die basischen bzw. den sauren Aminozucker Muraminsäure. Nach der Kalibrierung der HPAEC-Methoden sollen diese mit der Umkehrphasen-HPLC-Methode verglichen werden. Weiterhin wurde der Versuch unternommen, eine Methode basierend auf der Kationenaustausch-chromatographie (HPCEC) in Hinblick auf die Bestimmung aller 4 Aminozucker mit nur einer Methode zu entwickeln.
Die vorgestellte Methode soll die Analytik von Aminozuckern mit bisher unerreichter Genauigkeit und damit die Bestimmung der Bildung und Nutzung von mikrobiellen Residuen in Böden in Hinblick auf ein besseres Verständnis für die Bedeutung der mikrobiellen Residualmasse im Boden ermöglichen.

Sustanzspezifische $\delta^{18}O$ Analysen an Monosacchariden mittels GC-Py-IRMS: Potential, Probleme und Lösungsvorschläge

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Seit etwa 10 Jahren sind Gaschromatographie-Pyrolyse-Isotopenmassenspektrometer Kopplungen (GC-Py-IRMS) für substanzspezifische Isotopenmessungen auf dem Markt. Während δD-Analysen, beispielsweise an pflanzenwachsbürtigen Alkanen bei paläoklimatischen Fragestellungen, mittlerweile von vielen Arbeitsgruppen weltweit durchgeführt werden, hat die substanzspezifische $\delta^{18}O$ Analytik bisher kaum Eingang in die Stabil-Isotopengemeinschaft gefunden.
In unserem Vortrag stellen wir als mögliche Anwendung dieser Analytik die Paläoklima-rekonstruktion mittels pflanzenbürtiger Monosaccharide aus Baumringen, Seesedimenten und Paläoböden vor. Wir diskutieren Probleme und bieten Lösungsvorschläge an.

Literatur:
Zech, M. and Glaser, B., 2009. Compound-specific $\delta^{18}O$ analyses of neutral sugars in soils using GC-Py-IRMS: problems, possible solutions and a first application. Rapid Communications in Mass Spectrometry 23, pp. 3522-3532.
Zech, M., Werner, R., Juckelka, D., Buggle, B. and Glaser, B., 2010. Absence of oxygen isotope fractionation/exchange of (hemi-) cellulose-derived sugars during litter decomposition and soil organic matter formation. Organic Geochemistry, submitted.

Water uptake depth of single and mixed tree groups in a temperate deciduous forest

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The aim of this study was to investigate how soil water dynamics are influenced by tree groups with different species combination, in particular during times of summer drought. Furthermore we analyzed whether soil water resources are vertically partitioned among tree species. For this purpose 16 tree clusters were selected in the Hainich National Park, Germany, each consisting of three co-dominant trees and their surrounding neighbours. Observed species were beech (*Fagus sylvatica*), ash (*Fraxinus excelsior*) and lime (*Tilia cordata*) combined in single- and three-species (n=4). Volumetric soil water content was measured with FDR sensors (at 0.1 - 0.7 m soil depth), soil water potential with tensiometers (at 0.1, 0.3 and 0.5 m soil depth) and throughfall with four collectors per cluster. A stable isotope analysis was conducted to assess the natural abundance of ^{2}H and investigate on the soil water uptake depth of the different species. Hence, soil samples were taken from the soil profile in 0 - 0.1, 0.1 - 0.2, 0.2 - 0.3, 0.3 - 0.5 and 0.5 - 0.7 m depth in addition with stem samples from the cluster trees. Soil water isotopic values for ^{2}H declined with depth in the soil profile from the topsoil to 0.5 m levelling off at 0.5 to 0.7 meters. Single species clusters showed similar water uptake patterns with the main extraction source at 0.3 to 0.5 and 0.5 to 0.7 meters. However, the mixed clusters showed a broader range of water uptake depth, additionally utilizing 0.2 - 0.3 m in the soil profile. This is because lime showed a change in water uptake patterns utilizing a broader range of the soil profile as water source in the mixture as compared to lime in single species clusters.

Assessment of ^{13}C fractionation and preferential substrate utilization by microbial turnover based on C3 – C4 vegetation change

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Two processes contribute to changes of the $\delta^{13}C$ signature in soil pools: 13C fractionation per se and preferential microbial utilization of various substrates with different $\delta^{13}C$ signature. These two processes were disentangled by simultaneously tracking $\delta^{13}C$ in three pools: soil organic matter (SOM), microbial biomass, dissolved organic carbon (DOC), and in CO_2 efflux during incubation of 1) soil after C3 – C4 vegetation change, and 2) the reference C3 soil. The study was done on the Ap horizon of a loamy Gleyic Cambisol developed under C3 vegetation. Miscanthus giganteus – a perennial C4 plant – was grown for 12 years, and the $\delta^{13}C$ signature was used to distinguish between 'old' SOM (> 12 years) and 'recent' Miscanthus-derived C (< 12 years). The differences in $\delta^{13}C$ signature of the three C pools and of CO_2 in the reference C3 soil were less than 1.5‰, and $\delta^{13}C$ of microbial biomass was significantly different compared to other pools. In contrast to the reference soil, the $\delta^{13}C$ of all pools in the soil after C3 – C4 vegetation change was significantly different. Old C contributed only 20% to the microbial biomass but 60% to CO_2. This indicates that most of the old C was decomposed by microorganisms catabolically, without being utilized for growth. Based on $\delta^{13}C$ changes in DOC, CO_2 and microbial biomass during 54 days of incubation in Miscanthus and reference soils, we concluded that the main process contributing to changes of the $\delta^{13}C$ signature in soil pools was preferential substrate utilization (causing an up to 8‰ shift in $\delta^{13}C$ values) and not ^{13}C fractionation per se. Based on the $\delta^{13}C$ changes in SOM, we showed that the estimated turnover time of old SOM increased by two years per year in 9 years after the vegetation change. This confirms preferential utilization of available recent C versus the old C. The relative increase in turnover rate of recent microbial C was 3.7 times faster than that of old C. Combining long-term field observations with soil incubation reveals that the turnover time of C in microbial biomass was 200 times faster than in total SOM. Our study clearly showed that estimating the residence time of easily degradable microbial compounds and biomarkers should be done at time scales reflecting microbial turnover times (days) and not those of bulk SOM turnover (years and decades). We conclude that comparing the $\delta^{13}C$ signature of linked pools helps calculate the relative turnover of old and recent pools.

^{15}N-Tracer studies on denitrification activity of aquifer material from two sandy aquifers in northern Germany – laboratory incubation experiments in relation to influencing sediment parameters

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In NO_3^- contaminated aquifers containing reduced compounds like organic carbon or sulfides, denitrification is an intense process. Its characterization is of interest because NO_3^- consumption improves water quality and N_2O production can cause emission of this greenhouse gas to the atmosphere. The amount and spatial distribution of reduced compounds within denitrifying aquifers is not well known. Recent findings from parallel investigations on in situ denitrification and reactive compounds suggests that single-well ^{15}N tracer tests might be suitable to characterize the stock of reduced compounds in aquifers (Konrad 2008), but an evaluation of this approach has not been realized until now. The overall objective of our studies is to measure the spatial and long-term dynamics of denitrification within two sandy aquifers in northern Germany. Here we present the first

results of these long-term incubation experiments to investigate the stock of reactive material present in these sediments and its denitrification activity. In these batch experiments we filled the aquifer material from different depths between two and 68 m below ground in glass bottles, supplemented it with $K^{15}NO_3$ solution, sealed the bottles airtight with rubber septa and flushed the headspace with pure N_2. Afterward the bottles where stored in the dark by 10°C to obtain aquifer like conditions. The labeled denitrification products ($^{15}[N_2O+N_2]$), N_2, N_2O, CO_2, Nitrate, Sulfate and pH were analyzed six times during the experiment. In order to study the stock of reduced compounds within the incubated sediments we also performed other laboratory measurements with the aquifer material. We measured its capability to reduce potassium permanganate and the concentrations of extractable sulfate, dissolved organic carbon, hot water soluble organic matter and total C, N and S per kilogram sediment. Results up to now show for most of the incubated glass bottles with sediments an almost linear increase of the denitrification products over time. The measured denitrification rates for aquifer material from the zone of heterotrophic denitrification and for sediments from the zone of autotrophic denitrification range from 0.2 to 42 µg N $kg^{-1}d^{-1}$ and from 22 to 120 µg N $kg^{-1}d^{-1}$, respectively. The relationships between denitrification rates and the parameters of the reduced compounds will be discussed.

Eignet sich die Isotopomersignatur von N_2O als Indikator für bakterielle Denitrifikation?

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Fluxes of nitrous oxide (N_2O) from soils result from its production by nitrification and denitrification and reduction during nitrification. The dual isotope and isotopomer signatures of N_2O such as $\delta^{18}O$, average $\delta^{15}N$ ($\delta^{15}N^{bulk}$) and ^{15}N site preference (SP = difference in $\delta^{15}N$ between the central and peripheral N positions of the asymmetric N_2O molecule) have been used to estimated the contribution of partial processes to net N_2O fluxes to the atmosphere. However, the use of this approach to study N_2O dynamics in soils requires knowledge of isotopic signatures of N_2O precursors, isotopologue fractionation factors (ε) of N_2O production by nitrification or denitrification, and N_2O reduction by denitrification. SP is a promising parameter here, because in contrast to $\delta^{18}O$ and $\delta^{15}N^{bulk}$, SP is independent of precursor signatures. It is assumed that SP of produced N_2O is almost exclusively controlled by the enzymatic isotope effects of NO reductases (NOR), which are known to be structurally different among certain classes of N_2O producers with each class causing different isotope effects.

The aim of our study was to determine site specific fractionation factors of the NO_3-to-N_2O step (ε_{SP}) for several species of denitrifiers representing each of the known NOR-types of bacteria, i.e. cNOR, qNOR and qCu_ANOR. Pure cultures where amended with NO_3^- and incubated anaerobically until all NO_3^- was reduced to N_2O while N_2O reductase was blocked by adding C_2H_2. Gas samples were collected from incubation vessels and analysed for $\delta^{18}O$, $\delta^{15}N^{bulk}$ and SP using isotope ratio mass spectrometry.

Our results show that the ε_{SP} range of gram-negative bacteria (cNOR-type) is larger than previously estimated. Moreover, ε_{SP} of the qNOR type tends to be even more negative. Overall this suggests that SP of N_2O produced by soil bacteria may be more negative than previously estimated. This needs to be taken into account when using isotopomer signatures to estimate other processes such as fungal denitrification, nitrification and N_2O reduction by denitrifiers.

Short-term transformation of alanine in soil assessed by position-specific labeling

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Transformation of low molecular weight organic substances (LMWOS) in soil is one of the most important processes in the turnover of organic matter as all high molecular substances pass the stage of LMWOS during decomposition. We suggested using a unique feature of isotope applications – the position-specific labeling – to get a closer look on LMWOS fate in soil. This tool allows to distinguish the flux of the complete molecule from the splitting of the substance into metabolites and tracing these metabolites within any pools. We assessed short-term turnover of the different positions of the amino acid alanine: Position-specifically labeled ^{14}C-alanine were mixed with soil and ^{14}C activity was measured at increasing time steps. Different sterilization treatments ($HgCl_2$ or NaN_3) of the soil-mixture allowed to differentiate between the potential mechanisms of a declining ^{14}C activity in the solution: sorption, exoenzyme activity and microbial activity. An additional factor with considerable influence on the fate of LMWOS in soil is their concentration. We simulated the concentration typical for hot spot nearby dying root cells with a 5 mM alanine solution, rhizosphere conditions with a 0.5 mM alanine solution and conditions typical nearby degraded proteinogenous plant material with a 50 µM alanine solution. We used a 5 µM concentration as this is the mean concentration in soil solution and 0.5 µM concentration for simulating root free soil. The LMWOS concentrations lead to a different fate of single C atoms. Desorption of the LMWOS from the soils revealed to which extent alanine is irreversibly bound to the mineral surfaces and thus stabilized by mineral-LMWOS-interactions. We showed that the application of position-specifically labeled substances opens a new way to investigate the LMWOS-transformations in soil. The transformations of single C atoms allow conclusions about the individual transformation steps and improve our understanding of soil carbon fluxes.

Effect of grazing on C partitioning in Tibetan montane pasture revealed by $^{13}CO_2$ pulse labeling

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Since 1959 settle programs have changed the grazing activity on the Tibetan Plateau (TP). Near the villages grazing pressure increases, leading to land degradation. In remote areas grazing pressure decreases and thus leads to changes in vegetation pattern. To clarify the effect of land use changes on the carbon (C) cycle on the TP, it is necessary to characterize differences in belowground C allocation and sequestration of both grazed and ungrazed grassland. In situ $^{13}CO_2$ pulse labeling was accomplished on 1) a montane Trigonella-Kobresia grassland, used as winter pasture for yaks, and 2) on a grazing exclosure, where yaks have been excluded since 2002, both on the Qinghai-TP in 3440 m a.s.l. The average partitioning pattern of assimilated C was chased from July 27th until August 22nd, 2009. ^{13}C incorporated into structural shoot components did not differ significantly after 27 days (43% of recovered 13C and 38% in the grazed and ungrazed plots, respectively). However, in the grazed plots significantly less C was lost by shoot respiration (17% of recovered 13C compared to 42%), but significantly more was translocated to belowground pools (40% compared to 20%). Within the belowground pools, the smallest proportion of 13C (< 2%) was incorporated into structural root components in both cases. 13C not decomposed but remained in soil and 13C mineralized to CO2 was about twice as much in the grazed plots (about 20%). C content in the soil layer 0 - 5 cm under grazed grassland was significantly higher than in the ungrazed grassland. Concluding, a positive effect of grazing on C input and sequestration in soil was revealed, since belowground 13C allocation, the amount of 13C remaining in the soil and the soil C content in the layer 0 – 5 cm were significantly higher in the grazed than in the ungrazed plots.

Soil organic carbon dynamics in northwestern Vietnam

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The majority of people in the northwest of Vietnam live in poor conditions and depend on lowly modernized slash-and-burn agriculture. Thus, reduced yields as a consequence of soil degradation are a serious threat. For quantification of the dramatic soil fertility decline and the potential carbon sequestration in the steep slope lands of northwestern Vietnam we investigated soil organic carbon (SOC) dynamics. SOC content and ^{13}C abundance were measured in soils with varying ages of maize cultivation since deforestation of primary forest. Our aims were to quantify (1) the SOC loss due to cultivation, (2) the newly established SOC as well as (3) carbon turnover rates of bulk SOC. Three chronosequences (each including one reference site under primary forest) have been established in slopes on limestone, clayey shale and marl. Soils have been sampled in 0–10, 10–20 and 20–30 cm depth, as well as horizon wise in soil pits. The results show that the maize derived SOC is low , while soil erosion by water is leads to high losses of SOC derived from both maize as well as forest. With increasing soil depth bulk SOC declines, while ^{13}C increases. Compared to forest soils, SOC pools are enriched in ^{13}C due to maize cultivation.

Carbon and nitrogen transformation during decomposition of ^{13}C- and ^{15}N-labelled beech and ash leaf litter

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Turnover and distribution of C and N in forest soils are affected by tree species, in particular over the controlling factor of litter quality. In December 2008, we established a field experiment to detect tree species induced differences in C and N translocation and transformation processes during litter decomposition in Hainich National Park. Mesocosms with intact soil cores (thickness 5-10cm; diameter 24cm) were installed and original litter layer was replaced by ^{15}N- and ^{13}C-labelled beech (Fagus sylvatica) and/or ash (Fraxinus excelsior) leaf litter or unlabelled reference litter. A first set of mesocosms was collected in May 2009. Another set remained in the forest for measurements of CO_2 emissions and δ13C of CO_2-C until December 2009. Organic carbon (Corg), total nitrogen (Nt), microbial biomass (Cmic, Nmic) and their isotopic compositions were analysed in the mineral soil (1-cm sections). A higher proportion of litter-N (0.5-5%) than of litter-C (0-1%) was translocated to the top centimeter of mineral soil. The absolute amount of litter-N decreased with increasing soil depth. Down to a depth of 4 cm higher proportions of ash litter derived C (3% of litter-C input) and N (7% of litter-N input) compared to beech litter (1.5% of litter-C input, 3% of litter-N input) were found in Corg and Nt. Litter-C and -N that was translocated to the mineral soil was preferentially incorporated into microbial biomass. While the Cmic:Corg-ratio was ~1%, 10-16% of the translocated litter-C was found in microbial biomass. The Nt:Nmic-ratio was 2-3% and 7-11% of the translocated litter-N was incorporated into microbial biomass. Mineralization of ash litter was significantly faster than of beech litter. After one year, ~20% of beech litter-C and ~35% of ash litter-C was emitted as CO_2. Our results indicate that litter quality is one major factor controlling C and N translocation and transformation processes in soil.