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A robust relationship is found between monthly and annual mean daily surface CO_2 concentration drawdown and CO_2 flux measured by eddy covariance above several forested sites across a wide range of latitudes. The finding implies that surface concentrations can be quantitatively related to mean boundary layer concentrations, a result supported by investigation of tall tower data. We conclude that concentration data are regionally representative, and surface concentration drawdown (daily minimum minus daily average) averaged at monthly or annual resolution may be used at isolated sites for regional flux estimates, or in a network of sites for larger scale flux estimates. Estimation of monthly mean boundary layer concentrations from the relationship found here have an associated error that is comparable to that at continental sites within the Globalview-CO_2 network. Surface concentration measurements at flux towers can therefore potentially be incorporated into regional and global scale atmospheric inversion models for improved resolution of longitudinal flux partitions.

B71C-10 1105h

Measurements of Regional-Scale Isotopic Discrimination and CO_2 Flux for the North-Central U.S.

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Here we describe a method to estimate regional-scale ^{13}C isotope discrimination and CO_2 flux using the mean gradients in CO_2 isotopes and concentration between the planetary boundary layer and the free troposphere. Using monthly flask measurements from a 400 m tall tower in Wisconsin and a mountain top in Colorado, in concert with continuous environmental measurements from the tower, we constructed monthly and annual estimates of the net isotopic signature and CO_2 flux imparted to the free troposphere. Furthermore, the resultant flux weighted isotope signatures allowed us to constrain natural versus anthropogenic contributions to the annual CO2 budget for the region.

B71C-11 1120h

Results from the stable isotope sampling network in Carboeuroflux

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Integrating stable isotopic measurements of canopy air and ecosystem organics with flux tower and ecophysiological data provides a powerful tool to differentiate between carbon sources and sinks, and scale-up processes from plant to ecosystem levels.

During the 2001 and 2002 growing-seasons monthly flask samples of nocturnal canopy air and ecosystem organics were collected from selected forest flux sites within the Carboeuroflux network (13 sites in 2001 and 18 in 2002). Flask air was analysed for CO_2 concentration ($[CO_2]$), and the carbon and oxygen isotopic compositions ($\delta^{13}C$ and $\delta^{18}O$) of this CO_2. The $\delta^{18}O$ of waters distilled from leaf, stem and soil samples, and the $\delta^{13}C$ and $\delta^{18}O$ of these dried, homogonised organic samples were also measured. Analytical precisions were $\pm$0.1ppmv for $[CO_2]$, $\pm$0.1 permil and $\pm$0.2 permil for the $\delta^{13}C$ and $\delta^{18}O$ of atmospheric CO_2, $\pm$0.05 permil for water $\delta^{18}O$ and $\pm$0.1 permil for both the $\delta^{13}C$ and $\delta^{18}O$ of organics.

The $\delta^{13}C$ of ecosystem respired CO_2 ($\delta^{13}C_R$) was determined for each sampling period and location using a Keeling plot approach. Ecosystem discrimination ($\Delta^{13}C_E$) was estimated as the difference between the δ^{13}Cs of background atmospheric CO_2 and ecosystem respired CO_2. The seasonal and spatial variation in these variables, and the $\delta^{13}C$ and $\delta^{18}O$ compositions of the organic samples are examined relative to meteorological and ecophysiological conditions. We assessed the potential for using the $\delta^{18}O$ of ecosystem respired CO_2 ($\delta^{18}O_R$) together with that of soil and leaf waters to partition between the soil and above-ground respired CO_2 sources. At sites where soil $\delta^{13}C$ varied significantly from leaf $\delta^{13}C$, we also assessed the partitioning potential in using the $\delta^{13}C$ data. More intensive sampling campaigns, including incubations in branch-bags, and leaf, trunk and soil chambers, were also conducted at specific sites to examine the partitioning and scale relationships between individual source CO_2 contributions and $\delta^{13}C_R$. These experiments are still being conducted and their final results will be presented.

Significant variations are observed in $\Delta^{13}C_E$ and $\delta^{13}C_R$ spatially, seasonally and between years. The observed variations in $\Delta^{13}C_E$ and $\delta^{13}C_R$ follow a general trend with daytime average temperature, such that the most enriched compositions are typically observed during the mid-season and in warmer, more continental climatic locations. The average seasonal range in $\delta^{13}C_R$ at individual sites is 5 permil, between -26 permil and -21 permil, although, the average range between sites is also 5 permil.

The average $\delta^{18}O$ compositions of soil and twig waters for both years were 6.6 permil and 6.0 permil respectively (SD=2.5 permil). Throughout each season and between sites these compositions varied from 0 permil to 10 permil.

The results of this network highlight some of the applications of stable isotope monitoring for assessing local and regional-scale terrestrial ecosystem dynamics. In particular, the observed regional variations in $\Delta^{13}C_E$ may have implications for modelling regional carbon sources and/or sinks from measurements of the $\Delta^{13}C$ of atmospheric CO_2, as these estimates currently assume constant $\Delta^{13}C_E$.

URL: http://www.weizmann.ac.il/ESER/wp5/

B71C-12 1135h

Modeling Forest Productivity in a Complex Forested Landscape Using High Spectral Resolution Remote Sensing and Extensive Field Data

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Spatial estimates of forest carbon fluxes are needed for a growing number of environmental issues that range from local to global scales. Although integration of ecosystem models and remote sensing data has become a relatively common approach, prediction accuracy is often limited by a lack of detailed input data for important physiological variables such as plant photosynthetic capacity, as well as errors within the models themselves. However, understanding the various sources of prediction error can be challenging in areas that lack extensive field data for rigorous model validation.

Previous work with high spectral resolution remote sensing has suggested that the ability to remotely-detect biochemical properties of a plant canopy, most notably leaf N concentrations, may improve our ability to derive high-quality productivity estimates. In this study, we evaluated the effectiveness of this approach in a topographically-complex forested landscape in New Hampshire's White Mountain National Forest. Spatial estimates of net primary productivity were generated by combining an ecosystem model (PnET) with a canopy nitrogen coverage derived using NASA's Airborne Visible/Infrared Imaging Spectrometer (AVIRIS). Model predictions were compared with field-measured productivity data from an extensive network of forest inventory plots, as well as with predictions derived using directly-measured canopy nitrogen. Results showed that model predictions using remotely-sensed canopy N were improved substantially over those generated using input data that were aggregated by cover type. However, remaining prediction error was mostly related to error in the remote sensing coverage, indicating that model accuracy was largely a function of input data quality and that future improvements can be achieved through improved methods for canopy N detection.

B72A MCC: Hall C Sunday 1330h

Using Microbial Community Structure, Activity and Reaction Modeling to Evaluate Biogeochemical Cycles in Sediment and Soil Environments I Posters *(joint with H, OS)*

Presiding: **L Proctor,** University of Maryland Biotechnology Institute and U.S. Geological Survey**; E Roden,** University of Alabama

B72A-0744 1330h POSTER

Microbial Dynamics in Shallow Peat in Calcareous Fen

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This paper presents the results of fine-scale vertical investigation of pore water geochemistry and anaerobic microbial communities present in the upper humified peat in the McLean Fen (NY). Equilibrium diffusion chambers were used to collect anoxic pore waters at every 2cm depth from the land surface to approximately 50 cm depth at two sites along a groundwater flow path. One site, with a degraded vegetation assemblage, was at the edge of the wetland and adjacent to a farmer's field which had been fertilized in the past. The second site was down gradient in a pristine part of the wetland. Peat cores were also taken and subsampled every 2 cm. The upper peat near the edge of the wetland has an average bulk density 5 times greater than that in the pristine area. Strong downward vertical gradients of Fe and Mn at the degraded site suggest concurrent reduction of these two elements in the upper peat, whereas the absence of similar vertical gradients at the pristine suggests an absence of much Fe and Mn reduction. At both sites, concentrations of NO3- and SO42- indicate nitrogen reducers in the upper 5-10 cm layers and sulfate reducers in the lower part of the measured peat profile. Molecular biology techniques were used to quantify the abundance of nitrogen-reducers, iron-reducers, sulfate-reducers, and methanogens. Preliminary results indicate that the anaerobic microbial communities within the peat are highly complex and that different microbial groups coexist within the same peat zones.

B72A-0745 1330h POSTER

Effect of Forest Conversion Practices on the Composition of Soil Microbial Key Populations Involved in N-Cycling

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Investigations on the effect of forest conversion practices on composition of soil microbial populations involved in N-cycling were performed at the Hglwald Forest site (Southern Germany, near the city of Augsburg: 100 year old spruce stand) and at 4 forest sites in the Northeastern German Lowlands (pine forests, pine forests mixed with beech and a beech forest, respectively). While at the Hglwald Forest, the short term effects of forest conversion practices on microbial populations were studied (thinning of a spruce stand, and clear cutting of a spruce stand, respectively), in the Northeastern German Lowlands a chronosequence of forests was studied consisting of different stages of pine forest conversion to mixed pine-beech forests (pure pine stand: c. 80 years old; pine stand with 10 year old beech; pine stand with 40 year old beech) and results were compared with those obtained at a 130 year old beech stand.

At the Hglwald Forest, one year after clear cutting, this forest management practice had lead to a dramatic increase of cell numbers of denitrifiers (c. 8-fold) in the mineral soil as compared to cell numbers observed (a) before clear cutting had been performed and (b) in the soil of an untreated spruce control site. In contrast to clear cutting, thinning of a spruce stand had no significant effect on cell numbers of denitrifiers. Besides denitrifiers, cell numbers of chemolithotrophic nitrite oxidizers had also significantly increased in the mineral soil of the clear cutted site. The increase in cell numbers of both denitrifiers as well as nitrite oxidizers was in excellent agreement with enormous losses of N2O and N2 at the clear cutted site as compared to the untreated spruce control site.

The long term studies at the Northeastern German Lowland forest sites revealed that cell numbers of denitrifiers as well as of heterotrophic nitrifiers in the soil of the beech stand were c. 20 times and 10-times, respectively, higher as compared to cell numbers of the pure 80 years old pine stand. Cell numbers of these microorganisms in the soil of the mixed pine-beech stands showed intermediate values as compared to the pure pine and beech stands, respectively, indicating that tree species has a direct impact on magnitude of cell numbers of these important microbial populations involved in N-cycling.

B72A-0746 1330h POSTER

N-Cycling in N-Saturated Forests: New Aspects Towards in situ Soil Microbial N-Transformations

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Long term studies on in situ net and gross rates of ammonification and nitrification in forest soils of different coniferous forest sites in Southern and Northeastern Germany were performed using the burried bag method for determination of net rates and the 15N-pool dilution technique for both gross ammonification as well as gross nitrification. Gross nitrification was simultaneously also determined using the barometric process separation method (BaPS). Results obtained using both methods were in excellent agreement. The studies revealed that gross ammonification and nitrification rates in these soils were up to 20 times higher as compared to net rates. At the Northeastern German Lowland forest sites (pine stands) mean annual gross ammonification was appr. 90 kg N ha-1 a-1, whereas mean annual gross nitrification was appr. 70 kg N ha-1 a-1. At the Höglwald Forest site (N saturated spruce stand) mean annual gross ammonification rates were > 500 kg N ha-1 a-1 and mean annual gross nitrification rates were > 300 kg N ha-1 a-1. Since at the Hglwald site nitrate is not taken up by the trees and losses of nitrate to the atmosphere in form of N2O, NO and N2 are 16 kg N ha-1 a-1 and nitrate leaching to the groundwater is 21 kg N ha-1 a-1, appr. 260 kg nitrate-N must be immobilized by the microbial biomass per year. Thus, nitrate immobilization via microbial biomass has to be regarded as an important process of N retention in forest ecosystems. The microbial biomass N at the Hglwald Forest site is appr. 54 kg N ha-1; at the Northeastern German Lowland pine sites the value is 35 kg N ha-1. In view of the demonstrated extremely high rates of gross microbial N-turnover rates the conclusion is that within the soil an enormous internal N-cycling (consisting of ammonification, nitrification, N-immobilization and remineralization) via the microbial biomass must exist in which the microbial biomass functions as an intermediate N-storage pool and, in consequence, must underly a severalfold quantitative turnover within one year.

B72A-0747 1330h POSTER

Shifts in microbial communities and soil nutrients along a fire chronosequence in Alaskan boreal forest

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Fires are important pathways of carbon loss from boreal forests, while microbial communities form equally important mechanisms for carbon accumulation between fires. We used a chronosequence in Alaska to examine shifts in microbial abundance and community composition in the several decades following severe fire, and then related these responses to soil characteristics in the same sites. The sites are located in upland forests near Delta Junction, Alaska, and represent stages at 3-, 15-, 45-, and over 100-yr following fire. Plant communities shift from herbaceous species in the youngest site, to deciduous shrubs and trees (e.g. *Populus tremuloides* and *Salix*) in the intermediate sites, to black spruce (*Picea mariana*) forest in the oldest site. Soil organic matter accumulated 2.8-fold over time. Potential mineralization was highest in the intermediate-aged sites, as was nitrification and standing pools of inorganic nitrogen. In contrast, inorganic phosphorus pools were highest immediately following fire, and then decreased nine-fold with age. As measured with Biolog^{TM} plates, bacterial diversity and abundance were greatest in the oldest sites. Plant roots in the intermediate-aged sites displayed higher colonization by ecto- and arbuscular mycorrhizal fungi than those in the youngest and oldest sites. Likewise, glomalin, a glycoprotein produced by arbuscular mycorrhizal fungi, was most abundant in the 14-yr old site. Glomalin is believed to contribute to the formation of water-stable aggregates in the soil. However, water stable aggregates were most abundant in the younger sites and did not follow the pattern of glomalin or arbuscular mycorrhizal abundance. Our results indicate that fire may maintain landscape-level diversity of microbial functional groups, and that carbon sequestration in microbial tissues (e.g. glomalin and fungal biomass) may be greatest in areas that have burned several decades earlier. Changes in soil structure may not be directly attributable to microbial activity.

B72A-0748 1330h POSTER

Shifts in Fungal and Bacterial Community Structure During Tallgrass Prairie Restoration

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The cycling of carbon through the microbial community of soils results in both the storage of freshly added carbon in the soil and the release of greenhouse gases such as carbon dioxide to the atmosphere. It is hypothesized that fungi and bacteria cycle carbon differently, and result in different proportions of carbon stored and evolved. The intensive management of a soil will affect these proportions and thus, may also affect the terrestrial carbon cycle. The soil microbial community was monitored in four soils that form a tallgrass prairie restoration chronosequence. The chronosequence was composed of: 1) native tallgrass prairie, 2) farmland restored to tallgrass prairie in 1979, 3) farmland restored to prairie in 1993, and 4) farmland still in production with row crops. The structure of the microbial community was determined by terminal restriction fragment length analysis (T-RFLP) and we focus here on comparing bacterial and fungal domains from agriculture to native conditions. Shifts in the fungal and bacterial communities were detected that indicate that the bacteria recovered faster from changing the land use from farmland back to prairie, while the fungi are more sensitive to the perturbations of invasive agriculture and appear to be taking longer to revert to their original prairie composition. However, it must also be considered that assays of the activities of these two communities indicate that as the restoration progresses, the fungi dominate the degradation of freshly added carbon (the ratio of fungal-to-bacterial activity was 13.5:1 in the 1979 restoration, but only 0.85:1 in the farmland). Identification of this shift in community structure offers insights into monitoring ecosystem restoration and may also suggest opportunities for enhancing carbon storage by allowing marginal lands to revert to a natural condition.

B72A-0749 1330h POSTER

Microbial Mediation of Carbonate Precipitation: Biogeochemistry of Stromatolitic Mats of Lagoa Vermelha, Rio de Janeiro, Brazil

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Contemporary microbial mats are organosedimentary constructions, which have a structure similar to ancient stromatolites. However, only a few marine and hypersaline microbial mats have been found to precipitate carbonates. In addition, the formation of continuous laminae of carbonates has been observed only in Shark Bay (Western Australia) and Highborne Cay (Bahamas). Here, we describe microcrystalline carbonate precipitation in microbial mats of the moderate hypersaline lagoon, Lagoa Vermelha (RJ, Brazil), where precipitation of dolomite at ca. 15 cm depth in the sediments has been previously reported. The Lagoa Vermelha mats sustain high rates of photosynthesis, aerobic respiration, sulfate reduction and fermentation, resulting in large pH fluctuations in the upper 5-8 mm. Several discrete lithified calcium carbonate layers are present, in which the Mg content increases with depth. The first lithified layer (Ca:Mg of 11:1) in the mats is found beneath a 2-mm-thick biofilm which contains Gloeocapsa. Below the underlying dense Microcoleus layer, the second micrite deposit (Ca:Mg of 8:1) is observed at 4-5 mm depth. Successive micritic laminae (Ca:Mg of 3:1 and lower) are found in the layer of decaying cyanobacteria that harbors large numbers of heterotrophic microbes and purple sulfur bacteria. This is the first report of microbial-mediated Ca-Mg carbonate precipitation in discrete laminae. Observations in this particular environment will undoubtedly offer clues to understand complex ancient conditions involved in stromatolite formation, as well as provide information about the role played by microorganisms during high-Mg calcite and dolomite precipitation. As dolomitic stromatolites are abundant from the Precambrian, understanding the mechanisms driving microbial dolomite precipitation in this microcosm will lead to insights about one of the oldest biomineralization processes.

B72A-0750 1330h POSTER

Microbial Community Structure and Enzyme Activities in Semiarid Agricultural Soils

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The effect of agricultural management practices on the microbial community structure and enzyme activities of semiarid soils of different textures in the Southern High Plains of Texas were investigated. The soils (sandy clay loam, fine sandy loam and loam) were under continuous cotton (Gossypium hirsutum L.) or in rotations with peanut (Arachis hypogaea L.), sorghum (Sorghum bicolor L.) or wheat (Triticum aestivum L.), and had different water management (irrigated or dryland) and tillage (conservation or conventional). Microbial community structure was investigated using fatty acid methyl ester (FAME) analysis by gas chromatography and enzyme activities, involved in C, N, P and S cycling of soils, were measured (mg product released per kg soil per h).

The activities of b-glucosidase, b-glucosaminidase, alkaline phosphatase, and arylsulfatase were significantly ($P<0.05$) increased in soils under cotton rotated with sorghum or wheat, and due to conservation tillage in comparison to continuous cotton under conventional tillage. Principal component analysis showed FAME profiles of these soils separated distinctly along PC1 (20 %) and PC2 (13 %) due to their differences in soil texture and management. No significant differences were detected in FAME profiles due to management practices for the same soils in this sampling period. Enzyme activities provide early indications of the benefits in microbial populations and activities and soil organic matter under crop rotations and conservation tillage in comparison to the typical practices in semiarid regions of continuous cotton and conventional tillage.

B72A-0751 1330h POSTER

Carbon Accumulation and Microbial Community Structure in Reclaimed Mine Soils

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The objective of this study was to investigate the potential for soil amendments to increase accumulation of carbon in reclaimed soils and the relationship between carbon and microbial community structure. Changes in community structure were determined by signature lipid biomarkers (SLBs) or phospholipid fatty acid methyl esters. PLFA provide estimates of the viable biomass, diversity of prokaryotic and eukaryotic diversity, and indications of physiological stress to the microbial community. Artificial neural network (ANN) analysis has been used to examine the relationship between microbial community structure and soil geochemistry. It was hypothesized that (1) soil amendments would cause changes in the structure of the microbial community and carbon content (2) changes in the structure of the microbial community would be vary between the types of amendments, and (3) analysis of the SLB with an artificial neural network (ANN) would distinguish treatment and provide a insight in to the relationship between changes in soil geochemistry and microbial community. Twenty soils samples from different field plots and at different soil horizon depths were analyzed. Biomass as estimated by PLFA analysis, ranged from 1.9 to 265 nmol/g, which corresponded to cell densities of 4.8 x10^7 to 6.6 x10^9 cells/g. In the Wall's Farm and Jenkin's Farm samples the microbial biomass decreased with depth. A horizon soils had biomass values of greater or equal to 120 nmol/g, followed by the A2 horizon,(70 to 100 nmol/g) and the weak B horizon at and (40 to 80 nmo/g). The A2 and B horizon samples showed higher relative abundance of mid-chain branched saturates that are indicative of gram positive prokaryotes and actinomycetes. At Well's Farm, the polyunsaturates indicative of eukaryotes were observed at higher abundances. These changes were related to both the prokaryotic and eukaryotic influences in the microbial community in response to the soil amendments. The correlation between microbial biomass and percent carbon and percent nitrogen for the Walls Farm and Jenkins Farm samples was 0.72 and 0.84, respectively. In addition, the PLFA profile was explored for certain PLFA ratios that are indications of physiological or toxic stress. One sample from the Walls Farm showed high stress values for both the cyclopropyl to monoenic ratio and the trans to cis ratio, indicated that there were nutrient limitations and potentially toxic or inhibitory conditions present. In samples from a site with sawdust and two levels of biosolids added, the microbial biomass was not correlated with percent carbon. The microbial biomass was highest in the sawdust treatments, followed by the high and then low biomass treatments. The community structure was similar for the control and low biosolid plots. The high biosolid plot had elevated levels of terminally branched saturates and branched monoenoics (indicative of gram positive prokaryotes and actinomycetes) and reduced levels of polyunsaturates.. ANN was used to more fully assess the relationship between changes in microbial community structure and changes in soil geochemistry.

B72A-0752 1330h POSTER

Diversity of Arbuscular Mycorrhizal Fungi and its Influence on Soil Dynamics

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The diversity of arbuscular mycorrhizal fungi (AMF) has been correlated with increased plant biodiversity, productivity, and fecundity. However, the influence of AMF diversity on below-ground ecosystem characteristics has yet to be determined. A greenhouse experiment was conducted to examine these interactions. Pot cultures containing equal numbers of four common grass species were either inoculated with one of four AMF species, a mixture of all four species, or were not inoculated, for a total of six different community compositions. After two months of growth, the pot cultures were harvested. Results indicated both individual species effects and diversity effects on factors controlling ecosystem-level processes. Bacterial abundance, bacterial diversity, glomalin concentration, hyphal colonization of roots, and above ground plant biomass exhibited significant differences among treatments. However, N mineralization rates, nitrification rates, and levels of organic matter did not respond significantly to treatments. Bacterial diversity, bacterial abundance, and above ground biomass displayed a similar pattern across treatments, and this may indicate potential interactions among AMF, bacteria, and plants. Specifically, the non-mycorrhizal treatment produced the highest values for all three of these characters while the *Glomus intraradices* monoculture produced the lowest values. Species also varied in production of glomalin, a compound associated with carbon sequestration, with *Gigaspora gigantea* producing the highest concentration of 1.67mg/g soil and *Glomus etunicatum*producing the lowest concentration of 0.63 mg/g soil. Arbuscular mycorrhizal diversity significantly effected the total amount of fungal root colonization (high diversity: 70.9 percent; monocultures: 46.1-63.3 percent) and fungal fecundity and had a marginally significant influence on the abundance of external hyphae. This increased fungal abundance suggested niche complimentarity and positive species interactions within the high-diversity AMF community, resulting in diversity affects on ecosystem processes. Our results indicate that AMF diversity influences below ground dynamics just as previous studies have found AMF diversity effects on above ground dynamics.

B72A-0753 1330h POSTER

Bromus tectorum Invasion Alters Soil Microbial Carbon and Nitrogen Cycling in an Arid Colorado Plateau Grassland

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Invasion by the C_3 annual grass *Bromus tectorum* has significantly increased the amount of relatively low quality (high lignin:nitrogen) plant litter deposited in arid Colorado Plateau grasslands. Our objectives were to determine what effects these changes have on microbial utilization of carbon (C) and nitrogen (N). We measured net C and N mineralization, and the δ^{13}C of bulk organic matter, mineralized C, and bacterial fatty acids from soils of invaded and non-invaded C_3 (*Stipa hymenoides*) and C_4 (*Hilaria jamesii*) native grasslands. Carbon mineralization was greater in invaded compared to non-invaded sites (1.25 $\pm$ 0.09 and 1.52 $\pm$ 0.18 g CO_2-C kg^{-1} soil h^{-1} respectively). Rates of net inorganic N mineralization were lower in invaded compared to non-invaded C_3 grasslands (-0.32 $\pm$ 0.03 and 1.04 $\pm$ 0.11 mg N kg^{-1} soil d^{-1} respectively). The δ^{13}C values of two bacterial fatty acids: i15:0 and i16:0 (-20.9 $\pm$ 0.1 and 22.5 $\pm$ 2.3 $^o/_{oo}$ respectively), were not different from the bulk soil organic C (-21.5 $\pm$ 0.5 $^o/_{oo}$) across all sites. The δ^{13}C of mineralized C was greater in soils from non-invaded C_4 grasslands (-20.3 $\pm$ 0.8 $^o/_{oo}$) compared to invaded C_4 (-22.0 $\pm$ 0.3 $^o/_{oo}$) and both non-invaded and invaded C_3 grasslands, (-22.1 $\pm$ 0.4, and 21.9 $\pm$ 0.1 $^o/_{oo}$ respectively). Greater C and lower net N mineralization in invaded plots suggests greater microbial activity and immobilization of inorganic N with *Bromus* invasion. Isotopic data suggests that microbes in C_4 grasslands invaded by *Bromus* are utilizing a significantly greater proportion of lower quality C_3 organic matter than in C_4 non-invaded sites. These results show that invasion by *Bromus* has significantly altered patterns of microbial utilization of soil organic matter and the cycling of C and N in these arid grasslands.

B72A-0754 1330h POSTER

Methane in Sediments From Three Tropical, Coastal Lagoons on the Yucatan Peninsula, Mexico

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Tropical wetlands are significant sources of methane (CH_4) to the atmosphere, and the majority of research on methane flux and cycling in the tropics has been conducted in fresh-water wetlands and lakes. However, several previous studies have shown that tropical coastal ecosystems can produce significant methane flux to the atmosphere despite the presence of moderate to marine salinities. Information regarding methane cycling within the sediments is crucial to understanding how natural and anthropogenic changes may influence these systems.

We measured methane concentrations in sediments from two tropical coastal lagoons during different seasons, as well as in a third, heavily polluted, lagoon (Terminos) during the rainy season. These three lagoons, Celestun, Chelem, and Terminos, have similar vegetation, seasonal temperature and rainfall patterns, and substrate geology, but very different levels of ground water discharge and pollution. Methane concentrations in Celestun and Terminos lagoon showed high spatial variability($>$ 0.001 to 5 mmol kg^{-1} wet sediment), while sediments in Chelem Lagoon, which has near marine salinities and little sewage discharge, showed much lower variability of methane concentrations. Methane concentrations in Celestun sediments displayed two predominant patterns: some profiles contained a peak in methane concentration (1 to 2 mmole methane kg^{-1} wet sediment) between 5 and 15 cm below the surface while the other sediment profiles instead displayed a steady or monotonic increase in methane concentration with depth to approximately 0.025-0.080 mmol kg^{-1} at 10-15cm below surface followed by stable methane concentrations to the bottom of the cores (20-45 cm below the surface). A subsurface peak in methane concentrations was also found in some locations in Chelem, however, the concentrations were much lower than those measured in Celestun.

Previous studies have shown that sewage pollution may drastically increase methane production in tropical coastal ecosystems. Laboratory experiments using sediment from the upper 20 cm in Celestun lagoon resulted in high rates of biogenic production of methane from the addition of trimethylamine, hydrogen, and, while additions of formate and acetate stimulated methane production to a lesser extent. This indicates that methane production in these sediments may be highly responsive to natural or anthropogenic changes in substrate availability. By synthesizing laboratory data and extensive field measurements from the lagoons, we hope to shed light on the factors controlling methane cycling in these sediments, and to better estimate methane flux to the atmosphere from these ecosystems.

B72A-0755 1330h POSTER

Biogeochemical Processes and Microbial Characteristics Across Groundwater-Surface Water Boundaries

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The flux of contaminants from ground water to surface water is spatially and temporally dynamic and a function of the variability of the hydrogeology, geochemistry, and biology within the boundary between groundwater and surface waters (i.e., the hyporheic zone). Currently, there lacks a basic understanding of processes within this interaction zone, and consequently, it is not possible to accurately predict the transport and fate of contaminants to sensitive surface water biota. A study was conducted on the U.S. Department of Energy's Hanford Site in southeast Washington State to develop and evaluate methods for collecting samples from ground water - surface water mixing zones and to characterize microbiological, geochemical, and hydraulic gradients between the Columbia River and the adjacent unconfined aquifer.

During 2002 we sampled the hyporheic zone using passive multilevel samplers (MLS) deployed in riverbed piezometers to determine fine-scale geochemical variations. MLS units were deployed at four locations in the Hanford Reach of the Columbia River, one near an area where contaminant chromate is known to enter the river and the other three near areas where salmon spawn. MLS units were used to collect ambient water samples in 10 cm intervals to depths ranging from 114 cm to 123 cm below the riverbed. MLS results reflected ambient water conditions integrated over an approximately 10 hour period prior to removal (equilibration

time between the MLS and ambient hyporheic water was approximately 10 hours). MLS units were recovered following periods of relatively high and low diurnal fluctuation of river stage. The period of maximum stage occurred at a river discharge of 192,000 ft^3/s (median river discharge over 10 hours prior to removal = 192,000 ft^3/s); the minimum at 52,000 ft^3/s (median river discharge over 10 hours prior to removal = 52,000 ft^3/s). The median vertical hydraulic gradient (VHG) was larger at all sites during minimum discharge, with values 1.02 to 1.24 times larger than during maximum discharge, suggesting more upward movement of hyporheic water during periods of low river stage. At three of the four sites VHG was inversely correlated with river stage (r<-0.5, P<<0.0001).

Ambient water samples were tested for specific conductance, inorganic nutrient ions including chloride, phosphate, nitrate, and sulphate, and organic and inorganic dissolved carbon. Specific conductance ranged from 138 μS/cm to 571 μS/cm. At the salmon spawning sites specific conductance did not exceed 153 μS/cm, however at the site where chromium enters the river (100D Area) values increased with increasing depth below the riverbed, suggesting upwelling groundwater (r=0.88). Chloride (range=0.95 mg/L to 14.97 mg/L), nitrate (range= undetectable to 15.86 mg/L), and sulfate (range= 9.44 mg/L to 164.36 mg/L) were all positively correlated with depth (r>0.8) and had relatively high concentrations at the 100D Area. No phosphate was detected. Dissolved organic carbon (range=0.76 mg/L to 144.46 mg/L) and inorganic dissolved carbon (range=14.44 mg/L to 39.56mg/L) were greater near the surface at all sites, and were not correlated with depth when sampled below the surface. Analytes collected at high stage and contaminant chromate for high and low stage periods have not been determined and will be available during fall 2002.

B72A-0756 1330h POSTER

Microbial Communities Associated with Biogenic Iron Oxide Mineralization in Circumneutral pH Environments

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Lithotrophic growth on iron is a metabolism that has been found in a variety of neutral pH environments and is likely important in sustaining life in microaerophilic solutions, especially those low in organics. The composition of the microbial communities, especially the organisms that are responsible for iron oxidation, and carbon and nitrogen fixation, are not known, yet the ability to recognize these contributions is vital to our understanding of iron cycling in natural environments. Our approach has been to study the microbial community structure, mineralogy, and geochemistry of 20 cm thick, 100s meters long, fluffy iron oxide-encrusted biological mats growing in the Piquette Mine tunnel, and to compare the results to those from geochemically similar environments. In situ measurements (Hydrolab) and geochemical characterization of bulk water samples and peepers (dialysis sampling vials) indicate that the environment is microaerobic, with micromolar levels of iron, high carbonate and sulfate, and typical groundwater nitrate and nitrite concentrations. 16S rDNA clone libraries show that the microbial mat and water contain communities with considerable diversity within the Bacterial domain, a large proportion of *Nitrospira* and *Betaproteobacteria*, and no Archaea. Because clone library data are not necessarily indicative of actual abundance, fluorescence in-situ hybridization (FISH) was performed on water, mat, and sediment samples from the Piquette mine and two circumneutral iron- and carbonate-rich springs in the Oregon Cascade Range. Domain- and phylum-level probes were chosen based on the clone library results (*Nitrospira*, *Beta-* and *Gammaproteobacteria*, *Acidobacteria*, *Actinobacteria*, *Chloroflexi*, and *Planctomyces*). FISH data reveal spatial associations between specific microbial groups and mineralized structures. The organisms responsible for making the mineralized sheaths that compose the bulk of the iron oxide mat are *Betaproteobacteria* (probably *Leptothrix* spp.). However, only a small proportion of the cells in the mat reside within the sheaths. Most are located on or around the sheaths, which provide a physical framework for the community. Preliminary results from FISH experiments on the iron-rich spring samples show some similarities, including an abundance of *Betaproteobacteria*. Enrichment and isolation experiments are being performed to identify the iron-oxidizing organisms. Iron-oxidizers have been enriched from all sites. In some cultures it has been difficult to isolate the iron-oxidizing organisms from a non-iron-oxidizing heterotroph, possibly indicating codependence. Knowledge of the microbial community structure and the metabolic activities of key members will enable us to better understand the processes and chemical conditions which generate iron oxide deposits found in the geologic record on Earth and possibly extraterrestrial habitats.

B72A-0757 1330h POSTER

Microbial Influences on Trace Metal Cycling in a Meromictic Lake, Fayetteville Green Lake, NY

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Microorganisms can exist in aquatic environments at very high cell densities of up to $10^{1}1$ cells/L, and can accumulate significant quantities of trace metals. Bacteria actively take up bioactive trace metals, including Fe, Zn, Mn, Co, Ni, Cu, and Mo, which function as catalytic centers in metalloproteins and metal-activated enzymes involved in virtually all cellular functions. In addition, bacteria may catalyze the release of trace metals from inorganic substrates by processes such as the reduction of iron and manganese oxides, suggesting that trace metal distributions within a natural environment dominated by microbial processes may be controlled primarily by microbial ecology. Fayetteville Green Lake (FGL), NY, is a permanently stratified meromictic lake that has a well-oxygenated surface water mass (mixolimnion) overlying a relatively stagnant, anoxic deep water mass (monimolimnion). A chemocline separates the water masses at around 20m depth, where oxygen concentrations decrease and sulfate and methane concentrations increase. In addition, previous studies have indicated that trace metals such as V, Cr, Co, Mn, and Fe reach elevated concentrations at the chemocline. Using fluorescent in situ hybridization (FISH) of FGL samples from depths of up to 40m with bacterial and archaeal probes, we have shown that fluctuating redox conditions within the FGL water column correlate with significant variations in the composition and distribution of microbial populations with depth. The mixolimnion is dominated by Eubacteria, with increasing concentrations of Archaea in the lower anoxic zone. Increases in microbial cell densities coincide with increases in trace metals at the chemocline, suggesting microbial activity may be responsible for trace metal release at this boundary. 16S rRNA PCR cloning techniques are currently being used to identify dominant microbial populations at various levels within the FGL water column. Future studies will focus on the potential for these dominant microorganisms to influence trace metal cycling and bioavailability in the FGL water column.

B72A-0758 1330h POSTER

Microbial Activity in the Subseafloor Sediments of ODP Leg 201

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Ocean Drilling Program Leg 201 was the first ocean drilling expedition dedicated to the study of life deep beneath the seafloor. Its equatorial Pacific and Peru Margin sites were selected to represent the general range of subsurface environments that exists in marine sediments throughout most of the worlds oceans. In water depths as great as 5300 meters and as shallow as 150 meters, the expedition drilled up to 420 meters into oceanic sediments and the underlying basaltic crust. The sediments ranged in temperature from 1°C to 25°C and in age from 0 to almost 40 million years. Leg 201 scientists found biogeochemical evidence of metabolic activity throughout the sediment column at every site. This activity is supported at all sites by the diffusion of sulfate down from the overlying ocean, as well as by the dissolution of iron- and manganese-bearing minerals. At the open ocean sites, metabolic activity deep beneath the seafloor is also supported by the transport of sulfate, nitrate and oxygen from water circulating through the underlying basaltic crust. At both the open ocean sites and the Peru margin sites, multiple metabolic activities (sulfate reduction, iron reduction, manganese reduction and methanogenesis) co-occur. Chemical flux estimates suggest that sulfate is generally the principal terminal electron acceptor in these subseafloor sediments. However, at the open ocean sites with the lowest rates of microbial respiration, manganese may rival sulfate as a terminal electron acceptor. The recovered sediments and fluids are being studied further to document the controls on rates of subsurface activity, the influence of past oceanographic conditions on current activity in deeply buried sediments, and the effects of subseafloor biogeochemical processes on Earths surface world.

B72A-0759 1330h POSTER

Vertical distribution of the subsurface microorganisms in Sagara oil reservoir

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The recent microbiological studies reported that active microbial habitat for methanogen, sulfate reducers (Archaeoglobus, d-Proteobacteria, gram positives), fermenters (Thermococcus, Thermotogales, gram positives etc.) and other heterotrophs (g-Proteobacteria etc.) are in subsurface petroleum oil reservoirs. However, microbial distribution at vertical distances in depth has not been demonstrated since the samples in previous studies are only to use oil and the formation water. Here, we show the vertical profile of microbial community structure in Japanese terrestrial oil reservoir by a combination of molecular ecological analyses and culture dependent studies. The sequential WRC (Whole Round Core) samples (200 mbsf) were recovered from a drilling project for Sagara oil reservoir, Shizuoka Prefecture, Japan, conducted in Jar. -Mar. 2002. The lithology of the core samples was composed of siltstone, sandstone, or partially oil containing sand. The major oil components were gasoline, kerosene and light oil, that is a unique feature observed in the Sagara oil reservoir. The direct count of DAPI-stained cells suggested that the biomass was relatively constant, 1.0x104cells/g through the core of the non-oil layers, whereas the oil-bearing layers had quite higher population density at a range of 1.0x105 ? 3.7x107cells/g. The vertical profile of microbial community structures was analyzed by the sequence similarity analysis, phylogenetic analysis and T-RFLP fingerprinting of PCR-amplified 16S rDNA. From bacterial rDNA clone libraries, most of the examined rDNA were similar with the sequence of genera Pseudomanas, Stenotrophomonas and Sphingomonas within g-Proteobacteria. Especially, Pseudomonas stutzeri was predominantly present in all oil-bearing layers. From archaeal rDNA clone libraries, all rDNA clone sequences were phylogenetically associated with uncultured soil group in Crenarchaeota. We detected none of the sequences of sulfate reducers, sulfur dependent fermenters and methanogens that have been previously detected as dominant microbial components in other oil reservoir environments. The absence of methanogen was consistent with the results from the stable isotopic analysis that major hydrocarbon components including methane in Sagara oil reservoir are thermogenic origin. In this presentation, we will also show the activity of the subsurface microbial components by the cultivation assays and discuss about the relationship between the microbial community structure and the formation process of petroleum in Sagara oil reservoir.

B72A-0760 1330h POSTER

Microbial population, activity, and phylogenetic diversity in the subseafloor core sediment from the Sea of Okhotsk

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Subseafloor environments has already been recognized as the largest biosphere on the planet Earth, however, the microbial diversity and activity has been still poorly understood, even in their impacts on biogeochemical processes, tectonic settings, and paleoenvironmental events. We demonstrate here the evaluation of microbial community structure and active habitats in deeply buried cold marine sediments collected from the Sea of Okhotsk by a combined use of molecular ecological surveys and culturing assays.

The piston core sediment (MD01-2412) was collected by IMAGES (International Marine Global Change Study) Project from the southeastern Okhotsk Sea, June 2001. The total recovered length was about 58m. The lithology of the core sediment was mainly constructed from pelagic clay (PC) and volcanic ash layers (Ash). We collected aseptically the most inside core parts from 16 sections at different depths for microbiological study. The direct count of DAPI-stained cells revealed that the cells in Ash samples were present 1.2 to 2.2 times higher than in PC samples. The quantitative-PCR of 16S rDNA between bacterial and archaeal rDNA suggested that the increased population density in Ash layers was caused by the bacterial components. We studied approximately 650 and 550 sequences from bacterial and archaeal rDNA clone libraries, respectively. The similarity and phylogenetic analyses revealed that the microbial community structures were apparently different between in Ash layers and PC samples. From bacterial rDNA clone libraries, the members within gamma-Proteobacteria such as genera Halomonas, Shewanella, Psychromonas and Methylosinus were predominantly detected in Ash layers whereas the Dehalococcoides group and delta-Proteobacteria were major bacterial components in PC samples. From archaeal libraries, the sequences from Ash and PC samples were affiliated into the clusters represented by the environmental sequences obtained from terrestrial and deep-sea environments, respectively. We evaluated the activity of microorganisms in subseafloor environments by the culturing assay. The colony forming unit (CFU) counts on three kinds of media and at four different incubation temperatures (5, 15, 25, 35 deg.C) revealed that the bacteria in Ash layers were in fact alive even at around in-situ temperature (<15 deg.C). In addition, the rDNA phylogenetic analysis of these isolates indicated the consistency results of environmental rDNA analyses.

In conclusion, the permeable ash layer buried in subseafloor environments is significant for discrete microbial habitat, and at least most of bacteria in ash layers within 60 m are indeed alive and may impact on the biogeochemical circulations in subseafloor environments.

B72B MCC: Hall C Sunday 1330h

Biogeochemical Reaction Modeling in Sediment and Soil Environments Posters *(joint with H, OS)*

Presiding: **E Roden,** University of Alabama**; W Burgos,** Pennsylvania State University

B72B-0761 1330h POSTER

Reaction-based modeling of quinone-mediated bacterial iron(III) reduction

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This paper presents and validates a new paradigm for modeling complex biogeochemical systems using a diagonalized reaction-based approach. The bioreduction kinetics of hematite by the dissimilatory metal-reducing bacterium (DMRB) Shewanella putrefaciens strain CN32 in the presence of the soluble electron shuttling compound anthraquinone-2,6-disulfonate (AQDS) is used for presentation/validation purposes. Experiments were conducted under nongrowth conditions with H2 as the electron donor. In the presence of AQDS, both direct biological reduction and indirect chemical reduction of hematite by bioreduced anthrahydroquinone-2,6-disulfonate (AH2DS) can produce Fe(II). Separate experiments were performed to describe the bioreduction of hematite, bioreduction of AQDS, chemical reduction of hematite by AH2DS, Fe(II) sorption to hematite, and Fe(II) biosorption to DMRB. The independently determined rate parameters and equilibrium constants were then used to simulate the parallel kinetic reactions of Fe(II) production in the hematite-with-AQDS experiments. Previously determined rate formulations/parameters for the bioreduction of hematite and Fe(II) sorption to hematite were systematically tested by conducting experiments with different initial conditions. As a result, the rate formulation/parameter for hematite bioreduction was not modified, but the rate parameters for Fe(II) sorption to hematite were modified slightly. The hematite bioreduction rate formulation was first-order with respect to hematite free surface sites and zero-order with respect to DMRB based on experiments conducted with variable concentrations of hematite and DMRB. The AQDS bioreduction rate formulation was first-order with respect to AQDS and first-order with respect to DMRB based on experiments conducted with variable concentrations of AQDS and DMRB. The chemical reduction of hematite by AH2DS was fast and considered to be an equilibrium reaction. The simulations of hematite-with-AQDS experiments were very sensitive to the equilibrium constant for the hematite-AH2DS reaction. The model simulated the hematite-with-AQDS experiments well if it was assumed that the ferric oxide surface phase was a non-crystalline hydroxide rather than hematite. This is the first reported study where a diagonalized reaction-based model was used to simulate parallel kinetic reactions based on rate formulations/parameters independently obtained from segregated experiments.

B72B-0762 1330h POSTER

Kinetic Modeling of Biogeochemical Processes in Subsurface Environments: Coupling Transport, Microbial Metabolism and Geochemistry

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Microbial reactions play an important role in regulating pore water chemistry (e.g., pH and Eh) as well as secondary mineral distribution in many subsurface systems and therefore directly control trace metal migration and recycling in those systems. In this paper, we present a multicomponent kinetic model that explicitly accounts for the coupling of microbial metabolism, microbial population dynamics, advective/dispersive transport of chemical species, aqueous speciation, and mineral precipitation/dissolution in porous geologic media. A modification to the traditional microbial growth kinetic equation is proposed, to account for the likely achievement of quasi-steady state biomass accumulations in natural environments. A scale dependence of microbial reaction rates is derived based on both field observations and the scaling analysis of reactive transport equations. As an example, we use the model to simulate a subsurface contaminant migration scenario, in which a water flow containing both uranium and a complexing organic ligand is recharged into an oxic carbonate aquifer. The model simulation shows that Mn and Fe oxyhydroxides may vary significantly along a flow path. The simulation also shows that uranium (VI) can be reduced and therefore immobilized in the anoxic zone created by microbial degradation.

Sandia is a multiprogram laboratory operated by Sandia Corporation, a Lockheed Martin Company, for the United States Department of Energy (US DOE) under Contract DE-AC04-94AL85000.

B72B-0763 1330h POSTER

Moving from Batch to Field Using the RT3D Reactive Transport Modeling System

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The public domain reactive transport code RT3D (Clement, 1997) is a general-purpose numerical code for solving coupled, multi-species reactive transport in saturated groundwater systems. The code uses MODFLOW to simulate flow and several modules of MT3DMS to simulate the advection and dispersion processes. RT3D employs the operator-split strategy which allows the code solve the coupled reactive transport problem in a modular fashion. The coupling between reaction and transport is defined through a separate module where the reaction equations are specified. The code supports a versatile user-defined reaction option that allows users to define their own reaction system through a Fortran-90 subroutine, known as the RT3D-reaction package. Further a utility code, known as BATCHRXN, allows the users to independently test and debug their reaction package. To analyze a new reaction system at a batch scale, users should first run BATCHRXN to test the ability of their reaction package to model the batch data. After testing, the reaction package can simply be ported to the RT3D environment to study the model response under 1-, 2-, or 3-dimensional transport conditions. This paper presents example problems that demonstrate the methods for moving from batch to field-scale simulations using BATCHRXN and RT3D codes. The first example describes a simple first-order reaction system for simulating the sequential degradation of Tetrachloroethene (PCE) and its daughter products. The second example uses a relatively complex reaction system for describing the multiple degradation pathways of Tetrachloroethane (PCA) and its daughter products.

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B72B-0764 1330h POSTER

Reactive Iron deposition and ground water inflow control neutralization processes in acidic mine lakes

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The controls on the internal neutralization of highly acidified waters by iron sulphide accumulation are yet poorly understood. To elucidate the influence of ground water inflow on neutralization processes, inventories of solid phase iron and sulphur, pore water profiles and rates of ferrous iron and sulphate production and consumption were analyzed in different areas of an acidic mine lake. Ground water inflow had previously been determined by ground water modelling and chamber measurements (Knoll et al., 1999). The investigated sediments adjacent to mine tailings, which were subject to the inflow of groundwater (10-30 L d-1 m-2), were richer in dissolved ferrous iron iron (30 vs. 5 mmol L-1) and sulphate (30 vs. 10 mmol L-1) and showed higher pH values (6 vs. 4) than the sediments in areas of the lake not being influenced by groundwater inflow. Sediments adjacent to the mine tailings also showed higher rates of sulphate reduction and iron sulphide accumulation (Fig. 1). From these data it is suggested that neutralization processes in iron rich, acidic mine lakes neutralization processes primarily occur in areas influenced by the inflow of acid mine groundwater. These waters usually have considerably higher pH values than the surface waters in the lakes due to buffering processes in the tailings. The seepage of this water through the sediment might thus lead to higher pH values and thus to a higher thermodynamic competitiveness of sulfate reduction vs. iron reduction (Blodau and Peiffer 2002). This causes increased neutralization rates. These findings have consequences for remediation measures in highly acidic lakes. In areas influenced by the inflow of mine drainage increases in carbon availability, for example by the deposition of particulate organic matter, should enhance iron sulphide formation rates, whereas in other areas increases in carbon availability would only result in enhanced rates of iron reduction without a lasting gain in alkalinity.

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