

From an ecophysiological perspective, canopy *A_{max}* should scale with absorbed radiation and this relationship should be conservative because of the conservative variation in the quantum yield of photosynthesis. That is, the magnitude and seasonality of canopy *A_{max}* can be explained by acclimation to growth irradiance, temperature and moisture. Specifically, *A_{max}* can be modeled using the functional constraint of co-limitation between light-limited (electron transport) and light-saturated (carboxylation) rates of photosynthesis. In contrast to optimality approaches, this allows for resource use efficiency rather than carbon gain to be maximized in a given environment. Further, this constraint is functionally more realistic, consistent with observations, and testable at leaf to landscape scales.

Based on eddy flux data in arctic, boreal, temperate, and tropical ecosystems, the magnitude and seasonality of canopy *A_{max}* is consistent with acclimation to absorbed radiation in a wide range of ecosystems as predicted by the functional constraint of co-limitation by electron transport and carboxylation. A unique aspect of the approach is the use of a recursive filter for calculating photosynthetic acclimation based on the temporal integration of environmental conditions. Overall, the model provides a process-based link between canopy physiological status and canopy biophysics (e.g. FPAR). As such, the model can be applied at canopy to global scales using remote sensing observations of absorbed photosynthetically active radiation (APAR).

B12B-0827 1330h POSTER

Solar Radiation, Microclimate, and Water Balance in Complex Terrain

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Incoming solar radiation (insolation) is the major source of energy at the earth's surface, and is a primary driver of water flux. In particular, insolation directly affects local temperature, which in turn affects evapotranspiration rates. Three components of topography determine local insolation: 1) elevation, with greater insolation at higher elevations; 2) surface orientation, with decreased insolation at larger angles of incidence; and 3) surrounding obstruction, with decreased insolation when sky obstruction increases. We are using GIS-based approaches to evaluate landscape patterns of insolation, microclimate, and water balance for the Los Alamos National Environmental Research Park and surrounding lands. Using an upward-looking viewshed insolation model (the Solar Analyst), which requires a digital elevation model (DEM) and estimates of transmissivity for input, we calculated variation in direct and diffuse insolation as a function of landscape position and time of year. Then we used an insolation-modified adiabatic model, calibrated with ground-based meteorologic measurements, to calculate climatic surfaces (temperature, precipitation, potential evapotranspiration, and actual evapotranspiration) for the study site. In keeping with findings for other topographically diverse sites, topography has a strong and predictable influence on evapotranspiration through its effect on insolation.

URL: <http://gislab.lanl.gov>

B12C MCC: 132 Monday 1330h

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

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

B12C-01 1335h INVITED

Structure and diversity of functional guilds in the microbial nitrogen cycle of estuarine sediments

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Denitrification is a major flux of nitrogen in Chesapeake Bay, an estuary with a long residence time and high organic and inorganic nutrient inputs from the large surrounding watershed. The estuarine system spans a complex gradient of salinity and many correlated chemical constituents, from its upper bay and river freshwater end members to its nearly full strength seawater lower Bay. Denitrification rates in sediments, computed from net nitrogen fluxes in simulated *in situ* core incubations, show distinct reproducible patterns along the Bay. Highest rates are observed in sediments from the low salinity, high nitrate upper stations in the Bay and Choptank River. Lower rates occur in the low nitrate, oxygen depleted mid bay sediments and in the metabolically less active south Bay sediments. Gene sequences for nitrite reductase, the key enzyme in denitrification, show very high diversity in Bay and River sediments. On the basis of clone library sequences alone, however, there are distinct clades and patterns indicating highest diversity in the upper Bay and River sediments and lower diversity in the lower Bay sediments. Using a DNA microarray containing many individual nitrite reductase sequences, we investigated the population structure of denitrification genes along the estuarine gradient. Evaluation of gene expression patterns, in addition to presence/absence or abundance of individual genes, will allow a direct assessment of the links between diversity and biogeochemical transformation rates for particular functional guilds. The rate of denitrification and its regulation by environmental variables may be reflected in patterns of guild composition and activity.

B12C-02 1350h INVITED

The Role of Reactive Transport Modeling in Understanding Biogeochemical Processes Associated With Iron Oxide Reduction

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In a series of column and batch experiments, we are investigating mineral phase transformations during microbially mediated reduction of the iron oxide ferrihydrite. Quantification of the solid phase over time, using XAS and HRTEM, indicates that the primary sinks during iron oxide reduction, for both Fe (II) and Fe (III), are the secondary iron phases goethite and magnetite. While goethite is the dominant secondary phase when dissolved Fe (II) concentrations are low, magnetite is the dominant sink at higher concentrations. The specific secondary mineral phase assemblage changes with time and is very sensitive to initial conditions. Reactive transport modeling using MIN3P has been an essential tool in our interpretation of the experimental data and has assisted in developing and testing of our conceptual model of this system. Early simulations highlighted the potential importance of dissolved Fe (III) (a parameter often ignored in aqueous systems at near neutral pH) and helped to guide later experimental design. In particular, simulations illustrated the necessity of rapid aqueous mass transfer of dissolved Fe (III) from ferrihydrite to goethite, despite very low dissolved Fe (III) concentrations. These observations have implications for mechanisms of microbial iron reduction, secondary phase formation, the availability of ferric iron to reduction, and the sequestration of metals and nutrients. The modeling results were realized prior to achieving simulations that closely matched the laboratory data, emphasizing the utility of reactive transport modeling as a research tool.

B12C-03 1405h

Bacterial Production and Enzymatic Activities in Deep-Sea Sediments of the Pacific Ocean: Biogeochemical Implications of Different Temperature Constraints

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The deep-sea bed, acting as the ultimate sink for organic material derived from the upper oceans primary production, is now assumed to play a key role in biogeochemical cycling of organic matter on global scale. Early diagenesis of organic matter in marine sediments is dependent upon biological processes (largely mediated by bacterial activity) and by molecular diffusion. Organic matter reaching the sea floor by sedimentation is subjected to complex biogeochemical transformations that make organic matter largely unsuitable for direct utilization by benthic heterotrophs. Extracellular enzymatic activities in the sediment is generally recognized as the key step in the degradation and utilization of organic polymers by bacteria and a key role in biopolymeric carbon mobilization is played by aminopeptidase, alkaline phosphatase and glucosidase activities. In the present study we investigated bacterial density, bacterial C production and exo-enzymatic activities (aminopeptidase, glucosidase and phosphatase activity) in deep-sea sediments of the Pacific Ocean in relation with the biochemical composition of sediment organic matter (proteins, carbohydrates and lipids), in order to gather information on organic matter cycling and diagenesis. Benthic viral abundance was also measured to investigate the potential role of viruses on microbial loop functioning. Sediment samples were collected at eight stations (depth ranging from 2070-3100 m) along two transects located at the opposite side (north and south) of ocean seismic ridge Juan Fernandez (along latitudes 33° 20' - 33° 40'), constituted by the submerged volcanoes, which connects the Chilean coasts to Rapa Nui Island. Since the northern and southern sides of this ridge apparently displayed small but significant differences in deep-sea temperature (related to the general ocean circulation), this sampling strategy allowed also investigating the role of different temperature constraints on bacterial activity and biogeochemical processes and to define possible scenarios dealing with climate induced changes in deep-sea conditions.

B12C-04 1420h

Relationships Between Denitrifier Abundance, Denitrifier Diversity and Denitrification in Gulf of Mexico Hypoxic Zone Sediments.

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The largest zone of anthropogenic bottom water hypoxia in the Western Hemisphere occurs seasonally in the northern Gulf of Mexico. This hypoxic zone reaches its greatest extent in the summer months and is a consequence of seasonal stratification of the water column combined with the decomposition of organic matter derived from accelerated rates of primary production. The enhanced primary production is driven by inorganic nitrogen input from the Mississippi River and these conditions would seem ideal for supporting high levels of denitrification. Yet sediment denitrification exhibited a wide range, even at the height of the seasonal hypoxia. Therefore, we compared benthic denitrifier abundances and denitrifier diversity at several stations over two seasons exhibiting extremes in denitrification to evaluate the relationship between abundances, diversity and denitrification levels. Sediment denitrification ranged from 20 to 100 $\mu\text{mol m}^{-2} \text{h}^{-1}$, with rates in July, 2000 approximately half that observed in July, 2001. The highest rates were generally observed at stations with bottom water DO concentrations between 1 and 3 mg l^{-1} . Relative denitrifier abundances, using *nirS* and *nirK* as proxies for denitrifiers, suggested a direct relationship between abundances and denitrification while denitrifier diversity, measured by

T-RFLPs of nirS and nirK, suggested an inverse relationship between diversity and denitrification. These results suggest that several factors are important in understanding what controls denitrification in Gulf of Mexico hypoxic zone sediments.

B12C-05 1435h

Reactive Transport Modeling of the Long-term Performance of Column Experiments for the Remediation of Acid Mine Drainage

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Reactive transport modeling was used to evaluate the long-term performance of two similar column experiments (Waybrant et al., 2002, ES&T, 36, 1349-1356), which were designed to simulate the treatment of acid mine drainage by an organic carbon permeable reactive barrier through microbially mediated sulfate reduction and subsequent sulfide mineral precipitation. Principal reactions considered in the simulations include reduction of sulfate by organic matter, mineral dissolution/precipitation reactions and aqueous complexation. Simulations of Column 1, containing composted leaf mulch, wood chips, sawdust, and sewage sludge as an organic carbon source, accurately predicted sulfate concentrations in the column effluent throughout the duration of the experiment using a single fixed rate constant for sulfate reduction of $8\text{E-}09 \text{ mol L}^{-1} \text{ s}^{-1}$. The same reduction rate was used for Column 2 which contained only composted leaf mulch and sawdust as an organic carbon source. In this case, sulfate concentrations at the column outlet were over-predicted at late times suggesting that sulfate reduction rates increased over the duration of the column experiment and that microbial growth kinetics may have played an important role. These modeling results suggest that the reactivity of the organic carbon treatment material with respect to sulfate reduction does not significantly decrease over the duration of the fourteen-month experiments. However, the simulations over-predicted the attenuation of ferrous iron at late time for both experiments, which suggests that the overall rate of sulfide production and/or the overall rate of iron monosulfide formation decrease with time.

B12C-06 1450h INVITED

A Role for Antibiotics in Mineral Dissolution and Biofilm Physiology

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Respiration by bacteria is remarkable due to their ability to use a variety of compounds, including insoluble minerals, as terminal electron acceptors. How bacteria solve the problem of breathing something that is solid is poorly understood, but recent evidence points to the role of redox active natural products in shuttling electrons between microbes and minerals. Given the ubiquity of these substances in natural waters and soils, we must now revisit previous conclusions about whether direct contact between microbes and minerals is necessary to promote reductive mineral dissolution. To explore the degree to which extracellular electron transfer catalyzes important biogeochemical processes, we are studying the types of molecules that function as electron shuttles, including redox active antibiotics. I will discuss my laboratory's current understanding of how interspecies exchange of these molecules promotes mineral dissolution, as well as our emerging hypotheses regarding their function in biofilms.

B12C-07 1525h INVITED

Evaluation of Microbial Communities in Soil Using a Mixed Functional and Phylogenetic Array

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As part of a study of the potential for carbon sequestration in degraded mine lands we examined the effects of different soil amendments (e.g., fly ash and biosolids) on soil carbon. In addition we examined the relationships among some aspects of the nitrogen cycling, carbon content, and microbial community structure in the reclaimed mine soils. Nitrogen is a concern due to the potential release of nitrous oxide from microbial activity following the addition of biosolids. We extracted total community DNA from 22 soil samples obtained from reclaimed mine lands amended with fly ash and biosolids. Samples from unamended locations were included as controls. We ran a Terminal Restriction Fragment Length Polymorphism (TRLFP) analysis on 18S rDNA from a PCR amplification using primers specific for fungi. Diversity was much lower and dominance was higher than often seen for bacteria in soil. Using the DNA extracted from 8 soil, we also cloned and sequenced the fungal 18S rDNA. In this more thorough examination of fungal diversity, we examined between 50 and 100 fungal 18S clones per site. The cloning and sequencing indicated that along with the few dominant clones there was a surprising diversity of fungal clones. The diversity based on sequence analysis of the 18S clones was much higher than that indicated by the TRLFP-based analysis. Rarefaction analysis of the cloning data indicated that the total diversity was even higher than we were able to measure with this level of effort (up to 100 clones per site). However, it was clear that we were able to effectively sample the dominant populations.

We also used population statistics and ordination techniques to assess the relationships among the sites and the fungal community structure. Based on the dominant fungal clones, there were two major groups of sites and one intermediate group. We are examining these groups in relation to soil carbon and nitrogen characteristics. We have started to apply microarray methods to characterize the samples. An oligonucleotide-based microarray has been developed jointly with other projects. The array was designed using the information developed by our cloning and sequencing effort, cloning and sequencing efforts with other projects, and sequence database information from Genbank. The oligo array was designed to deal with a diversity of functional genes involved in nitrogen cycling (amoA, pmoA, nirS and nirK) and with the dominant 18S clones from the fungal community analysis. We used the array on several soil samples and have preliminary data showing that we can obtain both the functional information (nitrogen genes) and the phylogenetic information from the same samples using one array. However, it appears that the signals from the 18S genes are weaker than those from the functional genes. Thus, we are experimenting with different labeling steps and different dyes for the phylogenetic and functional genes. In the next stage of the study, we will include an array designed to measure functional aspects of carbon metabolism. Thus, we will determine if the differences in carbon content related to the original treatments, e.g., fly ash treatments had higher levels of carbon after regrowth of vegetation, are also related to differences in the microbial community.

B12C-08 1540h

Nitrogen Deposition Reduces Decomposition Rates Through Shifts in Microbial Community Composition and Function

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Atmospheric nitrogen (N) deposition may alter soil biological activity in northern hardwood forests by repressing phenol oxidase enzyme activity and altering microbial community composition, thereby slowing decomposition and increasing the export of phenolic compounds. We tested this hypothesis by adding ¹³C-labelled cellobiose, vanillin, and catechol to control and N fertilized soils (30 and 80 kg ha⁻¹) collected from three forests; two dominated by Acer Saccharum and one dominated by Quercus Alba and Quercus Velutina. While N deposition increased total microbial respiration, it decreased soil oxidative enzyme activities, resulting in slower degradation rates of all compounds, and larger DOC pools. This effect was larger in the oak forest, where fungi dominate C-cycling processes. DNA and ¹³C-phospholipid analyses showed that N addition altered the fungal community and reduced the activity of fungal and bacterial populations in soil, potentially explaining reduced soil enzyme activities and incomplete decomposition.

B12C-09 1555h

Genetic diversity and relative activity of denitrifying bacteria in stream bed sediments

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In order to understand the controls on sediment denitrification rates, the vertical distribution and potential activity of denitrifiers were evaluated on sediment cores collected from two streams in an agricultural watershed, where nitrogen loads are elevated. Denitrifiers were detected by PCR and the community structure was evaluated by T-RFLP analysis of the nitrite reductase gene nirS, the enzyme which catalyzes the first committed step in the denitrification pathway. A comparative analysis of nirS profiles down core and between sites demonstrated a relationship between abundance and genetic diversity of nirS and geochemical and physical properties of the streambed environment. Denitrifiers tended to be more abundant, diverse and active in surface sediments (upper 3cm) and in sediments with a low C/N. Fine grain sediments or sediments with high C/N exhibited poorly developed and less active denitrifying communities. This study revealed the influence of environmental gradients on denitrifier abundance and diversity and may explain differences in denitrification rates under varying environmental conditions.

B12C-10 1610h INVITED

Modeling Denitrification in Agroecosystems of Central Illinois: Investigations at Field and Watershed Scales

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Midwestern agriculture-dominated watersheds containing artificially-drained soils are known to contribute disproportionately to nitrate loadings in the Mississippi-Atchafalaya River basin. The need to manage non-point nitrogen loads has led to an intense interest in quantifying and modeling nitrogen sinks in these watersheds. That such sinks may be significant is suggested by the summertime depletion of nitrate to less than one-tenth the mean spring levels, which can exceed 1 mM. Due to the change in dominant hydrologic flowpath from drainage tiles to shallow groundwater over the same period, however, it has proved difficult to determine how much of the denitrification occurs in stream sediments versus in shallow groundwater.

To investigate this question at the farm (100-ha) scale, we have developed a 3-dimensional model of the hydrology and biogeochemistry of tile-drained agricultural fields. The hydrology module simulates surface runoff, tile flow, and shallow groundwater flow using

a mechanistic approach. The biogeochemistry module uses operator splitting to solve the coupled reaction and transport equations for solutes, gases, and soil components. Among the key questions we are examining is the appropriate level of complexity, e.g., which nitrogen species, terminal electron acceptors, and bacterial populations, to incorporate into the rate laws for microbial redox processes. The model is employed to investigate the nitrate levels in groundwater entering streams from different flowpath end-members and the dependence of these levels on temporal variables such as flow rate and season.

At the watershed scale, we are employing a data-intensive, inverse approach to estimate nitrogen sources and sinks using 20-year long water quality data records from Illinois. Using a simple mechanistic model of nitrogen sinks within the NHD stream network and a dynamic nitrogen balance for the soil system, we are able to accurately model the observations and generate estimates of denitrification in the streams. These estimates, of course, depend on the rate laws for streambed denitrification and assumptions about denitrification in shallow groundwater that are employed. Parameter collinearity makes it difficult to separately define the absolute magnitudes of the nitrate inputs from mineralization of soil organic matter and sinks due to denitrification.

By combining insights from the two models, we aim to 1) elucidate the spatial location of the predominant denitrification sink at the watershed scale, 2) quantify nitrogen sinks and sources at the watershed scale, and 3) provide insights into improved methods of modeling this significant biogeochemical process.

B12C-11 1625h

Interactions Among Grassland Plant Species, Microbial Communities, and Soil Processes

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Plant-microbial interactions are thought to be an important determinant of ecosystem processes, yet we do not know whether impacts of plant species on soil microbial community composition translate to impacts on function. We established field plots in a California annual grassland of five plant monocultures for two years to determine the effects of different plant species on the composition of the bulk soil microbial community and selected soil processes. Plant species were associated with distinct ecosystem process rates such as net nitrogen mineralization, nitrification, decomposition and soil respiration. Bacterial community substrate utilization profiles differed among different plant species and were related to labile soil C. DNA-based fingerprints of bacterial, ammonia oxidizer, and fungal communities did not generally differ in soils planted to different species; however, these microbial community profiles did strongly correlate to rates of decomposition. Terminal Restriction Fragment Length Polymorphism (TRFLP) analysis of soil microbial communities showed that the lupine community was distinct from the other four plant-associated communities. Phospholipid fatty acid (PLFA) patterns also failed to distinguish differences in the overall microbial communities associated with the five different monocultures. Interestingly, PLFA biomarker 16:1w5, indicative of AM fungi, differed among plant species treatments. This PLFA biomarker and bacterial TRFLP patterns were related to decomposition rates of a common litter. In summary, large functional differences were found between field plots with different plant species and the composition of the microbial communities was closely related to some of the functions assessed, independent of plant species. Only small plant-induced changes in microbial community composition were detected, yet apparently these changes had significant impact on function. Our analyses were not specifically targeted to microsites with high activity (such as rhizosphere soil) and our DNA and PLFA-based analyses included a potentially huge dormant community of soil microorganisms. While our analyses could detect little impact of plant species on overall microbial community profiles, a smaller active-fraction of the soil microbial community may have been more significantly affected.

B12C-12 1640h

Multiple Pore Region Model of Uranium(VI) Reductive Immobilization in Structured Subsurface Media

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A numerical simulation model of bacterial U(VI) reduction in fractured subsurface sediments was developed and used to test the potential feasibility of biomineralization at the fracture/matrix interface as a mechanism for immobilization of uranium in structured subsurface media. The simulations depict flow of anaerobic groundwater, with and without acetate as an electron donor for stimulation of U(VI) reduction by dissimilatory metal-reducing bacteria (DMRB), within mobile macropores along a 1-dimensional flow path. As the groundwater moves along the flow path, U(VI) trapped in the immobile mesopore and micropore domains (the sediment matrix) becomes desorbed and transferred to the mobile macropores (fractures) via a first-order exchange mechanism. By allowing bacterial U(VI) reduction to occur in the mesopore domain (assumed to account for 12 % of total sediment pore volume) according to experimentally-determined biomass-dependent kinetic parameters and an assumed DMRB abundance of 107 cells per cm³ bulk sediment, the concentration of U(VI) in the macropore domain was reduced ca. 10-fold compared that predicted in the absence of mesopore DMRB activity after a 6-month simulation period. Our results suggest that input of soluble electron donors over a period of years could lead to a major redistribution of subsurface uranium contamination in fractured subsurface sediments, converting potentially mobile sorbed U(VI) to an insoluble reduced phase (i.e. uraninite, UO₂(s)) in the mesopore domain that is expected to be permanently immobile under sustained anaerobic conditions.

B21A MCC: Hall C Tuesday 0830h Geophysical Disturbances, Climate, and Ecosystem Patterns I Posters (joint with H, OS, GC)

Presiding: L Alexander, Harvard University; J Florsheim, University of California, Davis

B21A-0700 0830h POSTER

Streambed Mobility and Dispersal of Aquatic Insect Larvae: Results from a Laboratory Study.

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Three series of flume experiments were conducted to quantify relationships between entrainment of surface layer gravels and displacement of benthic insect larvae. One series (B) utilized a sediment mixture with a median size 6.9 mm, maximum size 45 mm, and 10% < 2mm. Two other series examined the effects of locally coarsening the bed surface (Bc) and increasing the < 2mm fraction to 20% (S). Aquatic insect larvae were collected in the field and placed in an upstream segment of the flume bed. Flow rate, flume slope, and sediment transport rate were varied systematically among experiments. Displaced larvae were collected in a net at the end of the flume. The distribution of larvae remaining in the bed was obtained by sorting larvae from the sediment in 25 channel segments.

Flow rate and mean boundary shear stress varied among runs by factors of 1.2 and 2.4 respectively. Proportional entrainment of >1mm surface grains ranged from <0.05 to >0.90. Displacement of insect larvae increased in a regular and consistent manner with increasing flow strength and surface sediment entrainment. Significant displacement occurred for some types of larvae (Ephemeroptera mayflies) over a relatively low range of shear stress and bed surface entrainment. Other larvae (*Atherix* sp.) were displaced only at the highest levels of bed surface entrainment. Displacement was lower from coarsened bed surfaces in series Bc, and higher from sandier sediments in series S experiments. The differential effects of bed surface entrainment upon various types of larvae are consistent

with anatomical and behavioral differences that influence exposure to near-bed flow and bedload transport. These results suggest that spatial patterns of sediment mobilization are important for understanding patterns of dispersal and disturbance of streambed communities.

B21A-0701 0830h POSTER

Earthworm Activity and the Potential for Enhanced Leaching of Inorganic Elements in Soils

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The potential influence of earthworms on the mobility of soil inorganic constituents was experimentally investigated. Six 20 cm long and 15 cm i.d. columns were packed with soil (loamy material, Paris basin, France). Three earthworm specimens - *Lombicus terrestris* - were introduced into 3 of the 6 columns (earthworm treatment or ET), the remaining 3 being used to study changes in water composition and solute fluxes without earthworms (control treatment or CT). The 6 columns were operated for 8 weeks and were subjected to 100 ml addition of distilled water at 1, 8, 15, 22, 29, 36, 43 and 50 days. Effluents were collected weekly, filtered and analysed for their Dissolved Organic Carbon (DOC) as well as Si, Na, K, Mg, Ca, Fe, Mn, Al, Sr, Ba, Cu, Zn, Cr, Cd, REE and U concentrations. Replicates yielded extremely consistent results, with standard deviations generally lower than 10%. Effluent volumes were greatest during ET simulations (28% difference on a cumulative basis), which can be attributed to the construction by *Lombicus terrestris* of permanent vertical burrows into the soil columns. Different temporal chemical trends were observed depending on whether earthworms were present or not. During ET simulations, a washout phenomenon occurred for DOC, Ca, Mg, Fe, Ba, Sr, Cu and U during the startup outflow period (week 2). This washout was followed by a period of apparent equilibrium with concentrations in ET effluents remaining roughly constant for all solutes except REE, Zn and to a lesser extent Mn. No such washout nor equilibrium period was observed during CT simulations. Instead, concentrations in Ca, Mg, Fe, Ba, Sr, Cr and Cu decreased from week 2 to week 8, while those in other solutes increased from week 2 to week 5, then declining until week 8. For many elements (not all), final (equilibrium?) concentrations (8 weeks simulation) were highest in ET effluents (e.g. 17% higher for Ca and Na; 30% higher for Zn), despite the enhanced infiltration rate (and thus the likely shorter soil-water interaction time). Although preliminary, these results suggest that earthworm activities can potentially increase the leaching of a wide variety of inorganic elements in soils. This increase could occur through the ability of earthworms to change the biogeochemical conditions in the soil along their burrows (so-called drilosphere).

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Ecogeomorphic Modeling of Biodiversity and Disturbance

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Biodiversity is modulated by the local exogenous disturbance regime, and in turn is itself instrumental in determining regional physiography. Disturbances may take on many forms including fluvial erosion, whose nature depends upon physiography and climate. This leads to a complex feedback between the biotic and abiotic landscapes. Two issues are addressed here. One is the effect climate change has on biodiversity, as mediated by fluvial erosion. The second is the geomorphic response to changes in biodiversity. These themes are explored using a regional ecogeomorphic landscape evolution model. The results are relevant to the study of long term climate change as well as to the understanding of the impact of short term natural and man-made perturbations on the landscape.