B31B-0020: Genome-to-Watershed Predictive Understanding of Terrestrial Environments

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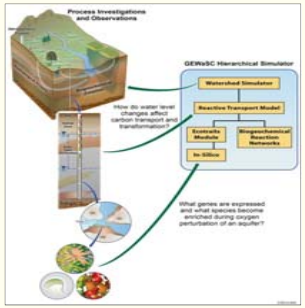
INTRODUCTION

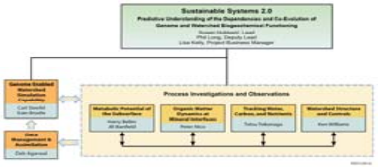
Launched in the Fall of 2013, the LBNL Sustainable Systems Scientific Focus Area "SFA 2.0" is a new team-based project that focuses on advancing approaches for quantifying and simulating genome-through-watershed scale interactions that govern biogeochemical cycling in complex terrestrial environments.

Scientific Question: How will climate induced changes in hydrology and vegetation affect subsurface carbon inputs, flowpaths, biogeochemical cycling and metabolic potential; how will these processes evolve over time, and what effect will interactions have on **watershed biogeochemical functioning?**

Deliverable: Development of a **genome-enabled biogeochemical watershed simulation capability (GEWaSC)** that can simulate how subsurface microbiome affects biogeochemical watershed functioning; how watershed-scale processes affect microbial functioning, and how these interactions co-evolve



* SFA team and guests at the 1 year project Retreat in Bodega Bay, October 2014



*The SFA team is comprised of ~60 scientists from 6 institutions.

The SFA is organized around four process components, GEWaSC, and a Data Management Component.

RIFLE & EAST RIVER COLORADO STUDY SITES

•We are using two sites in the Colorado River Basin for development of new approaches and insights about genome-through-watershed scale interactions

•The important Colorado River Basin is already threatened by global change (drought, diminished snowpack, wildfires, and pest outbreaks) that have largely unexplored impacts on the functioning of the river corridor and floodplain.

At the Rifle Site - we are conducting the first coordinated attempt to quantify the metabolic potential of an entire **subsurface ecosystem**, which requires an understanding of the underlying genetic, biochemical, and physiological basis of microbial activity in the context of **floodplain**-wide fluxes and biogeochemical processes that occur within a heterogeneous aquifer.

Photo by Roy Kaltschmidt, LBNL

Photo by Roy Kaltschmidt, LBNL

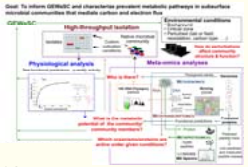
Joseph Guardiola

At **the East River Site**, we are extending our study to consider **watershed**-wide fluxes and **bedrock-though-canopy** biogeochemical processes

RECENT HIGHLIGHTS

The **Metabolic Potential** component is quantifying prevalent metabolic pathways in subsurface microbial communities that mediate biogeochemical cycles. Recently, we have:

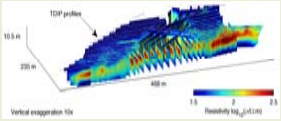
- Acquired around 2.5 Tbp of DNA sequence information, as well as some linked transcriptomic and proteomic datasets. Reconstructed >1,000 mostly novel genome, many involved in N, S, H, C cycling
- Used metatranscriptomics to quantify metabolic potential of the Rifle aquifer microbiome during NO_3^- perturbation, including inordinate importance of S- and Fe(II)-oxidizing chemolithoautotrophy



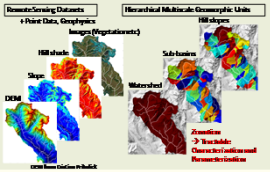
Analysis is providing the first insight into the metabolic roles of these organisms in biogeochemical cycles.

The Watershed Controls component is developing an integrated understanding of the primary factors controlling hydrobiogeochemical processes and nutrient cycling in terrestrial environments

Documented importance of hot spots and hot moments important to floodplain biogeochemistry at the Rifle Site



Developing approaches to identify functional zones at the East River watershed

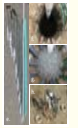


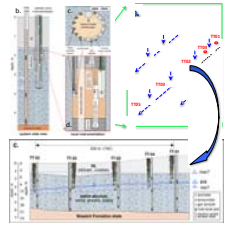
The Tracking component focuses on quantifying inventories and fluxes of C, N, and water in and across key subsurface compartments.

•Unique instrumentation suites have been installed for quantifying inventories and fluxes across soil-vadose zone-groundwater compartments. Key findings associated with role of subsurface in carbon cycling:

–Rifle vadose zone is relatively rich in DOC, DIC, and salts, and locally elevated in NO_3^-.

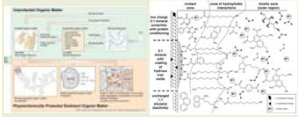
–Vadose zone CO_2 profiles reflect seasonal variations in microbial activity (T, water potential)





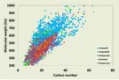
The Organic Matter Dynamics at Mineral Interfaces component is determining mechanisms by which organic-mineral associations affect subsurface C and electron fluxes.

Verifying, Modifying and Improving conceptual model



Recent advances include:

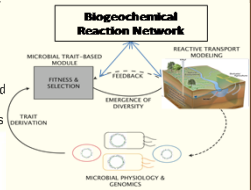
- Investigating chemical structure information of organic matter associated with sediment in the saturated zone using a variety of state-of-the-art methods.
- Fourier transform infrared (FTIR) spectroscopy suggests that dissolved and extracted OM exists as complex secondary structures of 'small' molecules

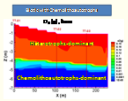


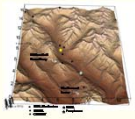
The Genome Enabled Watershed Simulation Capability (GEWaSC) is a framework for exploring interactions and feedbacks between microbial metabolic potential/activity, hydrology and watershed biogeochemistry.

We have developed trait-based and multi-scale models to represent the diversity of microbial functional processes within a larger scale reactive transport framework.

- Rifle Site: first study to document requirement of genome-informed reaction networks for accurate simulation of terrestrial environment behavior (chemolithoautotrophy)
- East River: Developing a framework to simulate carbon, nutrient, and metal cycling influenced by the short-term (seasonal) and long-term (climate) hydrologic forcings - from the genome to watershed scales and from the bedrock to canopy.



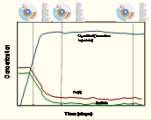


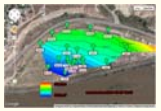


The Data Management and Assimilation component is an agile data ecosystem to enable investigations and simulations of genome through watershed scale processes.

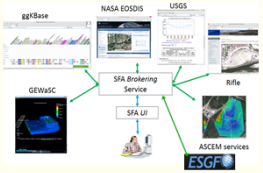
We have recently:

•Created the prototype data broker and SFA user interface
•Provide ability to quickly view, cross plot, and assess diverse data products needed by science teams
•Curate diverse Rifle data





DMA Architecture



EXPECTED OUTCOMES

The **SFA 2.0 is developing:**
A transformational and transferable APPROACH for gaining a predictive understanding of complex, biologically-based system interactions from the genome to the watershed scale.

Many rich **SCIENTIFIC ADVANCES**: First **coordinated attempt to gain a predictive understanding of metabolic potential of an entire subsurface ecosystem**, requiring understanding of the genetic, biochemical, and physiological basis of microbial activity in the context of floodplain-wide fluxes and biogeochemical processes in a heterogeneous aquifer (well suited for a national lab-based project).

Advanced COMMUNITY RESOURCES:

- Open source, modular, multi-scale simulation framework
- Community' biogeochemical field study sites
- Data Ecosystem

MORE – SFA 2.0 Genomes to Watersheds @ AGU

GENOMES TO WATERSHEDS

Scan QR codes for more information about the SFA

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Meet with SFA Scientists at Earth Sciences Division AGU Booth #2309, Moscone South

View other SFA and SFA Collaborator Presentations:

First Author	Title	Day
Roelof J Versteeg	H13H-1210: Predictive assimilation framework to support contaminated site understanding and remediation	Mon
Talia N. M. Jewell	B13H-0153: Metatranscriptomic Analysis of Groundwater Reveals an Active Anammox Bacterial Population	Mon
Stephen Farrington	H13C-1131: Development of a Sensor for Measuring In Situ Soil Moisture in Continuous Spatial Profile	Mon
Harry R. Beller	B22D-08: Metatranscriptomic Evidence of Chemolithoautotrophy in the Rifle [CO] Subsurface Relevant to C, S, N, and Fe Cycling	Tue
Markus Bill	B23B-0203: Seasonal variations and cycling of nitrous oxide using nitrogen isotopes and concentrations from an unsaturated zone of a floodplain	Tue
Donald Pan	B21B-0039: Redox Fluctuation Influences Viral Abundance in the Reduced Zone of a Shallow Alluvial Aquifer in Rifle, CO	Tue
John Bargar	B21B-0040: Importance of Organic Matter-Uranium Biogeochemistry to Uranium Plume Persistence in the Upper Colorado River Basin	Tue
W.Crawford Elliott	B21B-0043: Clay Mineralogy of Soils and Sediments from an Alluvial Aquifer, Rifle, Colorado	Tue
Mark E. Conrad	B31B-0016: Using Concentrations and Isotopic Compositions of CO_2 to Distinguish Microbial Production of CO_2in Unsaturated Zone Sediments in Hydrogeochemical Models	Wed
Susan S. Hubbard	B31B-0020: Genome-to-Watershed Predictive Understanding of Terrestrial Environments	Wed
Jiamin Wan	B33B-0164: Subsurface Carbon Cycling Below the Root Zone	Wed
Jinsong Chen	B31B-0022: Estimating groundwater dynamics at a Colorado floodplain site using historical hydrological data and climate information	Wed
Eric King	B31B-0021: Modeling Microbial Biogeochemistry from Terrestrial to Aquatic Ecosystems Using Trait-Based Approaches	Wed
Kenneth Hurst Williams	B33B-0163: Novel Approaches for Delineating and Studying "Hotspots" and "Hot Moments" in Fluvial Environments	Wed
Bhavna Arora	B31B-0019: Modeling the Biogeochemical Response of a Flood Plain Aquifer Impacted By Seasonal Temperature and Water Table Variations	Wed
Wenming Dong	B33B-0165: Ultraviolet-Visible and Fluorescence Analyses Reveal the Spatial and Seasonal Variability of Dissolved Organic Matter through the Vadose Zone to Groundwater at the Rifle, Colorado River Floodplain Site	Wed
Amy Marietta Kenwell	B33B-0168: Using Geochemical Indicators to Distinguish High Biogeochemical Activity in Sediments	Wed
Christina Pribulick	H31H-0720: A High Resolution, Integrated Approach to Modeling Climate Change Impacts to a Mountain Headwaters Catchment using PagFlow	Wed
Tetsu K Tokunaga	B44B-07: Water and Carbon Fluxes in a Semi-Arid Region Floodplain: Multiple Approaches to Constrain Estimates of Seasonal- and Depth Dependent Fluxes at Rifle, Colorado	Thu
John Neil Christensen	H43N-1174: Uranium and Strontium Isotopic Study of the Hydrology of the Alluvial Aquifer at the Rifle Former U Mine Tailings Site, Colorado	Thu
Eoin Brodie	B42B-05: Beyond The Blueprint: Development Of Genome-Informed Trait-Based Models For Prediction Of Microbial Dynamics And Biogeochemical Rates	Thu
Jenny L. Druhan	B42B-02: Evidence of a dynamic microbial community structure and predation through combined microbiological and stable isotope characterization	Thu
Anh Phuong Tran	H54B-06: Monitoring Soil Hydraulic and Thermal Properties using Coupled Inversion of Time-lapse Temperature and Electrical Resistance Data	Fri
Sergi Molins	H53A-0838: A Highly Resolved Direct Numerical Simulation Model of Reactive Transport at the Pore Scale	Fri

COLLABORATORS & RESOURCES

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