



Environment and Natural Resources Trust Fund (ENRTF) M.L. 2011 Work Plan

Date of Status Update:

Date of Next Status Update: 1/1/2012

Date of Work Plan Approval: 6/23/2011

Project Completion Date: 6/30/2014

Is this an amendment request? _____

Project Title: Mississippi River Water Quality Assessment

Project Manager: Michael Sadowsky

Affiliation: U of MN

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Location:

Counties Impacted: Statewide

Ecological Section Impacted: Lake Agassiz Aspen Parklands (223N), Minnesota and Northeast Iowa Morainal (222M), North Central Glaciated Plains (251B), Northern Minnesota and Ontario Peatlands (212M), Northern Minnesota Drift and lake Plains (212N), Northern Superior Uplands (212L), Paleozoic Plateau (222L), Red River Valley (251A), Southern Superior Uplands (212J), Western Superior Uplands (212K)

Total ENRTF Project Budget:

ENRTF Appropriation \$: 557,000

Amount Spent \$: 0

Balance \$: 557,000

Legal Citation: M.L. 2011, First Special Session, Chp. 2, Art.3, Sec. 2, Subd. 05c

Appropriation Language:

\$278,000 the first year and \$279,000 the second year are from the trust fund to the Board of Regents of the University of Minnesota to assess water quality in the Mississippi River using DNA sequencing approaches and chemical analyses. The assessments shall be incorporated into a Web-based educational tool for use in classrooms and public exhibits. This appropriation is available until June 30, 2014, by which time the project must be completed and final products delivered.

I. PROJECT TITLE: Mississippi River Water Quality Assessment

II. PROJECT SUMMARY:

The Mississippi River is one of the Earth's largest and most important waterways, yet we know little about the most common organisms populating this system, its microbiota. This project proposes to provide a more complete understanding of the impact of human activity on the Mississippi River, with the goal of improving water quality and improving public understanding of the importance of this River to the well being of the people and industries in the Mississippi watershed. In this project we will produce an extensive database cataloging the biodiversity and functions of microbial life in the Mississippi River in Minnesota using the new tool of metagenomic analyses. Metagenomics provides us a way to understand, for the first time, more about the microbiology of the River than we currently know through traditional microbiological analyses. The Mississippi River metagenome represents all of the microbial DNA in a water sample from the Mississippi River, regardless of its origin. Information about the diversity and function of microorganisms in the Mississippi, and the types of pathogens present, can be rapidly and directly obtained through the high throughput analysis of the DNA sequences and functional expression of microbial genes in each sample. We will also determine how the sequence and functional data relates to other indicators of water quality, such as hydrological dynamics, and the input of chemical pollutants, pharmaceuticals, and nutrients from run-off. This will allow us to better understand how human and environmental drivers influence this riverine ecosystem. The studies proposed here will put Minnesota at the forefront of this important area of environmental research, providing information on how to dynamically manage this important resource and provide insights into proper remediation efforts and future environmental needs of the Mississippi River. Water is an increasingly strained resource even here in Minnesota where it seems plentiful, and the public needs to know more about how to use this resource wisely. To accomplish this, we will engage the public through exhibits at the Science Museum of Minnesota, the Bell Museum, and the Itasca State Park Nature Center, and by teaching G7-12, undergraduate, and graduate students about metagenomics and analysis of metagenome sequence data. We will also engage the state's citizens in this novel exploration of the Mississippi River.

III. PROJECT STATUS UPDATES:

Project Status as of December 31, 2011:

Project Status as of June 30, 2012:

Project Status as of December 31, 2013:

Project Status as of June 30, 2013

Project Status as of December 31, 2013

IV. PROJECT ACTIVITIES AND OUTCOMES: More specific details of the project activities are provided in the attached addendum.

ACTIVITY 1: Analysis of Microorganisms and Metagenomics

Description:

This proposal will fund two and a half years of sampling and metagenome and chemical analysis of water samples from the Mississippi River at 11 critical junctures in Minnesota, from Lake Itasca to La Crescent, focusing on the headwaters and confluences with other major rivers. We are currently obtaining preliminary data from 10 of these 11 sites sampled this last summer, and are requesting funding here for in-depth studies of these 11 sites for two additional years. Surface water samples at each site will be analyzed twice per year and sediment samples at each site will be analyzed once per year. We also request funding for additional water sampling at one site to obtain information concerning the temporal and spatial variability of the microbial populations. At each sampling location we will also obtain information on other indicators of water quality, including industrial and agricultural chemicals and pharmaceuticals, inputs that impact bacterial diversity and at functionality.

The following information is abstracted from the attached addendum and the reader is directed there for more detailed information about each activity.

Metagenome Analysis

The Mississippi River will be sampled twice yearly at 11 sites from Lake Itasca to La Crescent during years 1 and 2 (see attached map), with sediment sampling done once yearly. We will also sample site #4 (Hidden Falls) 6 times per year (biweekly from May to August) at two sampling depths (0.3 and 1 meter below the surface). This will allow us to obtain information concerning the temporal and spatial variability of the microbial populations in the Minnesota River. The exact locations (latitude and longitude) of sampling sites at each location, when possible, will be the same as those used by MPCA and the Met Council to allow comparisons to existing data and those obtained in the future. At each site, two 1 L samples will be taken for water chemistry analysis (see below) and a 40L sample will be taken for metagenomic analyses. Total DNA will be extracted from cell pellets using Bio101 FP120 Fastprep instrument and MoBio Powersoil DNA extraction kits (Mo Bio Laboratories, Solana Beach, CA) as previously described (Ishii et al. 2006) and DNA corresponding to the V6 hypervariable region of the full-length 16S rDNA will be amplified by PCR using primers as described by Wang et al. 2007 and Lazarevic et al. 2009. The PCR primers will contain a unique sequence tag (Binladen et al. 2007) and the amplicons from each of the 11 samples will be pooled together and the multiplexed amplicons will be sequenced on a Illumina/Solexa Sequencer at the National Center for Genomic Research (NCGR) in Santa Fe, New Mexico. The 16S rDNA sequence data obtained in our studies will be compared to V6 reference databases as described by Dethlefsen et al. 2008 and Lazarevic et al., 2009. The taxonomic classification of 16S rDNA PCR products will be assigned using the GAST (Global Alignment for Sequence Taxonomy) taxonomic classification tool as described by Sogin et al. (2006), and by analyses done using reference database of V6 rDNA sequences (RefHVR_V6) from SILVA (Pruesse et al., 2007), the taxonomy from known cultured isolates, the Entrez Genome and the Ribosomal Database Project (Cole et al. 2009), Greengenes (DeSantis et al., 2006) and the software program ARB (Ludwig et al. 2004). The resulting phylogenetic relationships that are identified will be tested by maximum-likelihood bootstrap trees (with 1000 iterations) using distance-based subsampling and a minimum distance of 3% between sequences. Operational taxonomic units (OTUs) will be determined and compared by using the sortx subroutine of XplorSeq (Frank 2008). Comparisons of bacterial constituents of the river, between sites and sampling dates, will be determined by examining the numbers and types of phyla (or operational taxonomic units) at each sample site. We will also determine species diversity, species richness, and evenness using rarefaction analysis (Robertson et al. 2009).

In addition to phylogenetic information, our metagenomic analyses will also examine the functionality of the bacterial community of the Mississippi at each sampling site. To do this, we will send one half of the frozen cells from each site (as described above) to the Clemson University Genome Institute (<http://www.genome.clemson.edu/>) for the construction of functional gene libraries. This will be done only for the samples obtained once per year at each site. The libraries, consisting of randomly sheared metagenomic DNA, will be constructed in fosmid vector pEPIFOS-5 and transformed into *E. coli* DH10 as the host. Each fosmid will have an average insert size of ~39 kb (we have made libraries for year -1 already and have these data), enough to encode to about 20-40 bacterial genes. We will obtain ~10,000 clones (containing about 390,000 kb of DNA) from each sample. Library clones will be picked into 384 well microplates using a Qbot colony picking robot and screened, by students, for functionally active genes involved in resistance to antibiotics and heavy metals, and those that encode for degradation of recalcitrant organic compounds. Functionally active fosmid clones will be sequenced at the Biomedical Genomics Center at the University of Minnesota, and this sequence data will be assembled into contigs and analyzed by Blast and IMG-ACT software and websites (<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>).

Water Analysis

We will also obtain data on the presence and concentration of chemical compounds known to influence human health and water quality. At each site we will examine for the presence of the following compounds and chemicals: **pharmaceuticals** – acetaminophen and caffeine; **antibiotics** - tylosin, erythromycin, and trimethoprim; **pesticides** - atrazine, acetochlor, and metolachlor; **personal care products** - DEET, triclosan, and nonylphenol; and **endocrine disrupters** - trenbolone and estradiol. The data obtained from these analyses will be entered into the same relational database described above so that students and researchers can examine the possible relationship between the chemical constituents of the Mississippi River at each site and the presence and types of microbes recovered at each site. Water samples at each site and during each sampling event will also be analyzed for standard limnological parameters, including: water pH and temperature, turbidity, and nutrient (N, P, and C) concentrations, and inorganic trace elements via ICP analysis, and *E. coli* counts. All samples used for chemical analyses will be collected in glass bottles and will be analyzed by our collaborator Dr. William Koskinen at the USDA-ARS Soil and Water Management Unit at the University of Minnesota.

Depending on the compound under analysis, extracted chemicals will also be analyzed using a Waters Alliance high performance liquid chromatography/mass spectrometer with electrospray interface operating in positive-ion (LC/MS-ESI(+)) mode, or by using a Agilent 6890 gas chromatograph with capillary column coupled to a mass selective detector (GC/MS) operating in selected ion mode. Many of the chemicals to be analyzed in this study are also being examined in a current LCCMR-funded study of the Zumbro River led by Deborah L Swackhamer at the University of Minnesota. This will allow cross comparison of results obtained at different sites along this same waterway. Water chemical and physical data obtained from each site and sampling time will added to the relational database using to store metagenomic data, allowing for analysis of the potential correlative relationship between microbial community structure and the presence of chemical contaminants.

Summary Budget Information for Activity 1:

ENRTF Budget: \$ 407,291
Amount Spent: \$ 0
Balance: \$407,291

Activity Completion Date:

Outcome	Completion Date	Budget

1. Sampling of the Mississippi River and analysis of samples for microbial species diversity and functionality at each sampling location.	12/31/2013	\$397,736
2. Correlations of structural (sequence of diversity) and functional metagenome data to physical and chemical data at each location.	12/31/2013	\$3,822
3. Initial development of relational web database consisting of metagenomic and physical chemical data.	12/31/2011	\$1,911
4. Uploading of metagenomic data into IMG-ACT for searching and retrieval by researchers, students, river managers, regulatory agencies, and the public to better understand how human activity influences the microbiology of the Mississippi River.	12/31/2013	\$3,822

Activity Status as of December 31, 2011:

Activity Status as of June 30, 2012:

Activity Status as of December 31, 2013:

Activity Status as of June 30, 2013:

Final Report Summary: December 31, 2013

ACTIVITY 2: Professional Development of Grade 7-12 Teachers

Description: In this result we will develop a hands-on professional development program for G7-12 teachers, offered both in the Twin Cities and in Northwest Minnesota (Itasca) to provide greater access to this opportunity statewide. This professional development program will focus on preparing teachers to include Mississippi metagenomics studies in their science curriculum in a way that meets state standards for science inquiry.

The following information is abstracted from the attached addendum and the reader is directed there for more detailed information about each activity.

Learning science requires building a foundation of skills and knowledge. However, science itself is essentially an inquiry-based endeavor. This is recognized nationally in the National Science Education Standards (National Research Council 1996; <http://www.nap.edu/openbook.php?isbn=0309053269>) and in the state of Minnesota's science standards for K-12 students (http://www.education.state.mn.us/MDE/Academic_Excellence/Academic_Standards/Science/index.html). In addition, the fast pace of the biological sciences requires constant attention to bring advances in biology to teachers, students, and the public so they are able to understand new discoveries and their social implications. Our program provides opportunities for G7-12 teachers and students and for the general public to become engaged in the Minnesota Mississippi Metagenomics project. Our project goals for the following individuals are outlined below:

G7-12 teachers and students:

Good inquiry-based science in the G7-12 classrooms is often complicated for schools due to cost - school districts often have difficulty finding adequate funding, difficulties that teachers have in obtaining commitments for professional development programs by scientists in the field, and the necessary “hook” to keep students engaged. The use of the data from the Minnesota Mississippi Metagenome project (M3P) in the classroom addresses each of these issues. Firstly, the M3P provides a platform for students to work on this project whether in a wet-lab setting, or by doing online genome analyses requiring only a web browser. Thus, the costs can be scaled to the budget of the district. Secondly, our program will provide workshops for teachers that will allow them to interact with scientists and build a learning community with scientists and each other. Thirdly, the M3P provides a “hook” for engaging students by fostering the excitement of discovering something no human has known before. (How cool is that?). The other “hook” is that the Mississippi River is the largest and most historic river in the United States and, through this project, the students have an opportunity to contribute to knowledge about, and care of, this incredible environmental resource.

The professional development plan of this project is to engage 20 teachers per year, in 2012 and 2013, via workshops to bring Mississippi Metagenomics to their classrooms. Teachers participating in this project will receive graduate credit, books for their own reference, teaching materials for their classrooms, and continuing support. Each cohort will begin with a one week, full time workshop. The 2012 workshop will be held at the University of Minnesota -Twin Cities Campus and will recruit districts and teachers in the metro area. The 2013 workshop will be held at the University of Minnesota Itasca Biological Station and Laboratories (<http://www.cbs.umn.edu/itasca/>) which has laboratories, housing, and dining facilities, as well as the same instrumentation (e.g., high throughput genomic and robotic facilities) as are present on campus. This will allow teachers at both locations to experience the real science of metagenomics. In addition, both the campus and Itasca sites have access to the Mississippi River for sampling activities.

In this result we will also develop dedicated and jointly administered websites making the metagenome diversity and functional and chemical data accessible to middle and high school students, undergraduate and graduate students, researchers, and the public. As discussed above, students and teachers participating in this activity will also be involved in annotating the functionally active fosmid clones that will be sequenced at the Biomedical Genomics Center at the University of Minnesota. They will also analyze Mississippi River metagenome data that reflects microbial diversity issues, the presence of pathogens, and the relationship between microbial data and chemical constituents in the river. School participants in this project will chiefly use the IMG-ACT software and websites (<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>.) The IMG-ACT is a database of microbial genomes and metagenomic data that is maintained by the DOE. We will also utilize existing national web resources, such as Dolan DNA Learning Center (<http://www.dnalc.org/>) and Mothur databases (Schloss et al. 2009) to facilitate archiving, retrieval, and analysis of metagenome data. This will allow students to participate in the Mississippi Metagenome project, learn about bioinformatic and metagenomics, and help discover novel microbial genes that are related to growth and survival in the Mississippi River. It will also allow students throughout the state to gain an appreciation for how human activity influences the functioning of the river ecosystem. Since student access to the website and annotation of genes will be monitored by us, we will obtain near instantaneous metrics on how many students are participating in our educational and outreach programs.

The same inquiry-based activities that the teachers will be engaged in will be modified to be used in their classrooms. Teachers will be asked for their input on the development of curricular action plans for their students that will be worked on throughout the academic year. These curriculum plans will include

mechanisms to meet state science standards using metagenomics as the focus. Three required follow-up meetings in the academic year will provide teachers with a learning community for support, continued access to the scientists in the project, and support to gauge additional needs for the incorporation of metagenomics in their classrooms. These follow-up meetings will also provide teachers with the increased and continued intellectual support identified by Huffman, et al (2003) as instrumental for changing teaching practice. Throughout this project we will also develop educational materials, such as webinars and PowerPoint presentations that can be used by teachers for instructional purposes.

Summary Budget Information for Activity 2:

ENRTF Budget: \$79,909
Amount Spent: \$ 0
Balance: \$79,909

Activity Completion Date:

Outcome	Completion Date	Budget
1. Provision of professional development workshops, in the summer 2012 and 2013.	9/1/2013	\$78,495
2. Production of a web accessible, searchable database with downloadable datasets for use in the 7-12 and undergraduate classrooms, as well as by researchers in Minnesota and elsewhere. This will occur via a partnership of researchers with G7-12, undergraduate, and graduate students and educators, and citizens working on this database.	6/30/2012	\$1,414
3. Production of curriculum packets, webinars, books, materials, presentations, and approaches that can be incorporated into G7-12 classrooms.	9/1/2013	<i>This outcome will be accomplished by the course instructor whose salary is included in 1 above (in the \$78,495).</i>
4. Annotation of gene identity and function in IMG-JGI website by G7-12 students.	12/31/2013	<i>No cost to grant, data input is by students in classrooms .</i>
5. Development of trained teachers that incorporate this cutting edge science into their classrooms and pedagogical materials for other teachers to use throughout the state (and nation).	12/31/2013	<i>This outcome will be accomplished by the course instructor whose salary is included in 1 above (in the \$78,495).</i>

Activity Status as of December 31, 2011:

Activity Status as of June 30, 2012:

Activity Status as of December 31, 2013:

Activity Status as of June 30, 2013:

Final Report Summary: December 31, 2013

ACTIVITY 3: Project Data Dissemination

Description:

Project data, teacher information, and research concerning the Minnesota Mississippi Metagenomics project will be disseminated via five main routes. Dissemination activity is paramount to the success of this project since the Minnesota Mississippi Metagenomics project has the potential to engage the public in the excitement of state-of-the-art research, application of this research to real problems in our state, and discussions about the implications of policy decisions on our natural resources. We have chosen three venues through which to reach the general public: the Science Museum of Minnesota, the Bell Museum of Natural History on the University of Minnesota campus, and Itasca State Park. At the Science Museum, we will work with exhibit staff (via our collaborator Patrick Hamilton, Director, Environmental Sciences and Earth-System Science, Science Museum of Minnesota) to incorporate information and database access for this project both on their EarthBuzz website (<http://www.sciencebuzz.org/buzz-tags/earth-buzz>) and in kiosks in their exhibit about Minnesota and the environment. As part of the Minnesota Mississippi Metagenome Project, the SMM will build an Earth Buzz kiosk and install at public venue in the Twin Cities area and support the Earth Buzz project manager who will devote their time over the 2.5 year duration of the project. The SMM staff will coordinate the generation of stories and blogs about the Minnesota Mississippi Metagenomics project for the Museum's Earth Buzz network, mentor graduate students involved in the research project on how to write science blogs for general public audiences, and stay abreast of the research project in order to prepare relevant stories and blogs for Earth Buzz. At the Bell Museum, we will be working with the museum curators to add materials at existing aquatic dioramas to explain the use of metagenomics in measuring water quality. And finally, at Itasca State Park, we will work with the Park Naturalist to design and build two exhibits, one for the Nature Center at the East entrance to the Park, and one along the trail to the Mississippi headwaters, that will explain and engage the visitors in this research on the Mississippi. Together these venues have the ability to engage a large population of the public concerning metagenomics, the Mississippi River, the microbial constituents of the river, including pathogens, and how human activity influences the structure and function of this important waterway and ecosystem.

Results from this project will also be disseminated via reports made to the LCCMR, the generation of teaching materials, in periodic update reports made to cooperators, in seminars given throughout the state and nation, and in scientific publications in peer-reviewed scientific and teaching journals. Lastly, project data and approaches, including all teaching and learning activities will be disseminated via a dedicated web site that will be built specifically for the project.

Summary Budget Information for Activity 3:

ENRTF Budget: \$ 69,800

Amount Spent: \$ 0

Balance: \$69,800

Activity Completion Date:

Outcome	Completion Date	Budget
1. Development of Minnesota Mississippi Metagenome Website.	12/31/2011	<i>This outcome is also in activity #2 where it is budgeted.</i>
2. Production of public exhibits at SMM, Lake Itasca, and the Bell Museum.	6/30/2012	\$69,800
3. Production of curriculum packets, webinars, books, materials, and presentations for G7-12 students and teachers.	6/30/2013	<i>This outcome is also in activity #2 where it is budgeted.</i>
4. Dissemination of project data and results via webinars, seminars and workshops, and publications.	12/31/2013	<i>This outcome is also in activity #1 where it is budgeted. This will be accomplished by the postdoctoral student, the faculty PI, and others as a normal part of their scientific work.</i>

Activity Status as of December 31, 2011:

Activity Status as of June 30, 2012:

Activity Status as of December 31, 2013:

Activity Status as of June 30, 2013:

Final Report Summary: December 31, 2013

V. DISSEMINATION:

Description: NOTE THAT DISSEMINATION IS PART OF ACTIVITY 3 AND HAS BEEN FULLY DESCRIBED ABOVE.

Activity Status as of December 31, 2011:

Activity Status as of June 30, 2012:

Activity Status as of December 31, 2013:

Activity Status as of June 30, 2013:

Final Report Summary: December 31, 2013

VI. PROJECT BUDGET SUMMARY:

A. ENRTF Budget:

Budget Category	\$ Amount	Explanation
Personnel:	\$ 213,681	Postdoctoral student and lab technician to gather and process samples, website staff to assist with initial website setup for data uploads, instructor for teacher professional development program, and graduate student for assessment of the teacher professional development program
Professional/Technical Contracts:	\$270,930	Two Teacher Co-leaders of workshop, \$12,000; exhibit staff at the Science Museum of Minnesota, \$54,800; Genome sequence analysis at NCGR, Chemical Analyses at USDA-ARS, and preparation of functional gene libraries at Clemson University. Genome preparation and all genomic, physical, and chemical analyses are done most cost effectively in specialty labs that charge by the sample, \$204,130.
Service Contracts	\$0	
Equipment/Tools/Supplies:	\$45,097	Text books (\$190 - 3-4 books per teacher) and information materials that cover DNA technology, metagenomics theory, and microbiology for the 40 teachers while in class, \$7,600; lab materials such as filters, PCR materials, DNA sequencing, agar plates, tubes, etc. for 40 teachers in workshop, \$15,400; filtering materials for samples, \$7763; exhibit materials such as casework for dissemination activities, \$15,000.
Travel Expenses in MN:	\$15,452	Travel for taking river water samples, travel and room and board for teachers and instructors in teacher professional development program
Other:	\$11,840	Administrative and student fees for teachers in professional development program; physical analysis of river water samples. This will be moved out to activity 1 and into contracts [\$60,000 in stipends was in the original budget and was disallowed on 5/20/2011. These funds have now been used for more extensive sampling and sequence analysis].
TOTAL ENRTF BUDGET: \$557,000		

Explanation of Use of Classified Staff: One technician (Lab Services Coordinator) hired specifically for this project will be paid on this funding to assist in river sampling and genomic analysis of the samples, as well as providing lab support to the teacher professional development programs and dissemination activities. The staff member identified has been working on this project for two years already and is highly skilled in the specific requirements of the job.

Explanation of Capital Expenditures Greater Than \$3,500: NA

Number of Full-time Equivalent (FTE) funded with this ENRTF appropriation: 2.35 in year 1; 2.65 in year 2.

B. Other Funds:

Source of Funds	\$ Amount	\$ Amount	Use of Other Funds
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	Proposed	Spent	
Non-state			
American Recovery and Reinvestment Act of 2009 (a.k.a. Federal Stimulus) funds	\$16,670	\$	<i>ARRA Federal Stimulus funds paying the undergraduate course instructor and laboratory support personnel, for July and August, 2011.</i>
State			
University of Minnesota O&M funds	\$4,533	\$	<i>Portion of Jane Phillips salary for management of teacher professional development programs; College match.</i>
TOTAL OTHER FUNDS:	\$21,203	\$	

VII. PROJECT STRATEGY:

A. Project Partners: The project will be carried out under the direction of Drs. Michael Sadowsky (PI) and co-PI James Cotner. Funded project partners will include Pat Hamilton of the Science Museum of Minnesota, Itasca State Park, and the Bell Museum, Dr. William Koskinen (USDA-ARS) who will be involved in sample analysis for chemicals and the NCGR who will do DNA sequence analysis on a fee basis. We will also collaborate with the National Park Service at the SMM, Adam Birr at the Minnesota Department of Agriculture, and Barb Peichel at MPCA for dissemination activities.

B. Project Impact and Long-term Strategy: This request seeks funding for the first 2.5 years of this program. This will provide the basis for a long-term, continuing study of the health of the Mississippi River that will include all the states bordering the Mississippi and eventually all the states in the Mississippi watershed. Since the River starts in Minnesota at Itasca, this new in depth study and broad impact program begins in Minnesota. Additional funding for more long term and more extensive analyses (of the upper and lower Mississippi River) will be obtained from the National Science Foundation, other states, and other foundations. This National project will be organized similar to the MN project, but involve researchers, students, and the public all the way to New Orleans.

C. Spending History:

Funding Source	FY 2011
Federal Stimulus Funds (9/1/2009 – 6/20/2011)	\$383,300

VIII. ACQUISITION/RESTORATION LIST: NA

IX. MAP: see attached

X. RESEARCH ADDENDUM: see attached

XI. REPORTING REQUIREMENTS:

Periodic work plan status update reports will be submitted not later than January 2012, July 2012, January 2013, and July 2013. A final report and associated products will be submitted between December 31, 2013 and February 1, 2014.

Attachment A: Budget Detail for M.L. 2011 (FY 2012-13) Environment and Natural Resources Trust Fund Projects

ENVIRONMENT AND NATURAL RESOURCES TRUST FUND BUDGET											
BUDGET ITEM	Activity 1 Budget	Amount Spent	Balance	Activity 2 Budget	Amount Spent	Balance	Activity 3 Budget	Amount Spent	Balance	TOTAL BUDGET	TOTAL BALANCE
Project Title: <i>Mississippi River Water Quality Assessment</i>											
Legal Citation: <i>Fill in your project's legal citation from the appropriation language</i>											
Project Manager: <i>Michael Sadowsky</i>											
M.L. 2011 (FY 2012-13) ENRTF Appropriation: \$557,000											
Project Length and Completion Date: <i>2.5 years; expected completion December 31, 2013</i>											
Date of Update: <i>Fill in the date of report submission</i>											
BUDGET ITEM											
<i>Fill in your activity title here.</i>											
Personnel (Wages and Benefits) <i>(List who is getting paid to do what and what is the % of full-time employment for each position. List out by position or position type—one row per position/position type. For each, provide details in this column on the inputs: i.e. % dollars toward salary, % dollars toward benefits, time period for position/position type, and number of people in the position/position type. Add rows as needed.)</i>										213,681	213,681
To be hired, one Postdoctoral student, \$95,200 (84% salary, 16% benefits) 100% time, 2 years	95,200	0	95,200								
Trevor Gould, Technician, \$95,900 (73% salary, 27% benefits) 100% time, 2 years	95,900	0	95,900								
To be determined, Website staff, \$1,414 (73% salary, 27% benefits), 2% time				1,414	0	1,414					
To be determined, one Instructor, \$12,000 (76% salary, 24% fringe), 5% time, 2 years.				12,000	0	12,000					
To be determined, one Advanced Graduate Student from CEHD, \$9,167 (77% salary, 23% benefits), 1 year				9,167	0	9,167					
Professional/Technical Contracts <i>(List out proposed contracts. Be clear about whom the contract is to be made with and what services will be provided. If a specific contractor is not yet determined, specify the type of contractor sought. List out by contract types/categories—one row per type/category. Add rows as needed)</i>										66,800	66,800
To be hired, Two Teacher Co-leaders of workshop, \$12,000 (2 teachers per year X \$3000/teacher X 2 years)				12,000	0	12,000					
One Exhibit staff member at the Science Museum of Minnesota, \$54,800 (73% salary, 27% benefits), 2 years							54,800	0	54,800		
Service contracts <i>(List out proposed contracts. Be clear about whom the contract is to be made with and what services will be provided. If a specific contractor is not yet determined, specify the type of contractor sought. List out by contract types/categories—one row per type/category. Add rows as needed)</i>										0	0
Equipment/Tools/Supplies <i>(List out general descriptions of item(s) or item type(s) and their purpose—one row per item/item type. Add rows as needed)</i>										45,763	45,763
Text and reference books, information materials for classrooms \$7,600 (\$190/teacher X 20 teachers/year X 2				7,600	0	7,600					
Laboratory supplies for teachers, \$15,400 (\$385 per teacher X 20 teachers/year X 2 years)				15,400	0	15,400					
Laboratory supplies for filtering, cultures, genome preps of river samples, \$1,111	7,763	0	7,763								
Exhibit materials (metal/wood stands, glass frames, photographs), \$15,000 (3 sites X \$5000/site)							15,000	0	15,000		
Capital equipment over \$3,500 <i>(List specific items. Add rows as needed.)</i>										0	0
Fee Title Acquisition										0	0
Easement Acquisition										0	0
Professional Services for Acquisition										0	0
Printing											
Travel expenses in Minnesota <i>(Specify types of travel expenses, e.g., mileage, lodging, meals. Per diems are not allowed.)</i>										15,452	15,452
In-State Travel for 10 samplings per year X 2 years @1800 mi *\$0.50/mi	900	0	900								
Room & board for 4 people X 3 days/year X 2 years for sampling: \$1664 for lodging; \$1120 for food	2,784	0	2,784								
Participant travel (30 mi/day X 5 day*20 teachers/yr *2year * 0.50/mi)				3,000	0	3,000					
Participant room and board for Itasca workshop held 2012 (2011 workshop held in the Twin Cities for Metro area teachers so no room and board needed): (\$362.50 each X 20 teachers)				7,250	0	7,250					
Instructor/co-leader travel to Itasca in 2012 (2 cars: 430 miles round trip * \$0.50/mile)				430	0	430					
Room and board for instructor and co-teachers during teacher professional development program in 2012 (2011 workshop held in Twin Cities so no room and board needed): 1 week at Itasca (\$362.50 per person) for instructor and 2 co-teachers				1,088	0	1,088					
Other (Describe the activity and cost - be specific)										215,304	215,304
Fees for participants for graduate credit: Tuition is waived for the project, but there will be an administrative fee of \$100 per registrant + \$157 fees (total \$282) X 20 teachers X 2 years				11,280	0	11,280					
Stipend (\$1500 per teacher for 1 week workshop/followup work X 20 teachers X 2 years)				60,000	0	60,000					
Sample analysis: 22 samples for each analysis: (genome preparation @\$5000/sample = \$110,000, genome analysis @\$4562/mixed sample X 7 mixed samples = \$31,934, physical analysis @ \$20/sample X44 samples = \$880, chemical and elemental analysis @\$75/sample X 44 samples = \$3300). Genome preparation and all genomic, physical, and chemical analyses are done most cost effectively in specialty labs that charge by the sample.	144,024	0	144,024								
COLUMN TOTAL	346,571	\$0	\$346,571	\$140,629	\$0	\$140,629	\$69,800	\$0	\$69,800	\$557,000	\$557,000