Update on Rutgers Program: Potentials for Methylation and Demethylation and Microbial Community Structure

South River Expert Panel Meeting October 7, 2009

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Project Scope:

- Title: Factors controlling methylmercury production in the South River, VA: Substrate bioavailabilty and potentials for methylation and demethylation
- Pilot Program to testing:
 - Application of bioreporter to probe bioavailability of Hg in S. River
 - Determination of potential rates of mercury methylation and methylmercury demethylation in South River sediment samples.
 - Determination of microbial community structure

Methods Used

Mercury Methylation Potential (MP) =
 % added ²⁰³Hg²⁺ → Me²⁰³Hg
 Carried out May and August 2008 on 9 sites

Potential Rate ≠
Rate in Nature

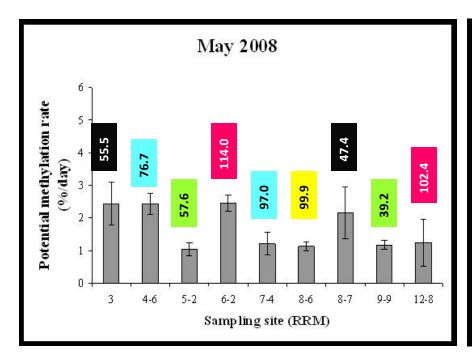
- Methylmercury Demethylation Potential (DP) = % added 14 CH $_3$ Hg+ \rightarrow 14 CO $_2$ or 14 CH $_4$ Carried out May and August 2008 on 9 sites
- Microbial Community = Determined by extracting and sequencing 16S Ribosomal RNA from samples.
 - Carried out on 4 samples with elevated MP
 - Ribosomal RNA is represents active community
 - 16S rRNA sequences identify groups of bacteria

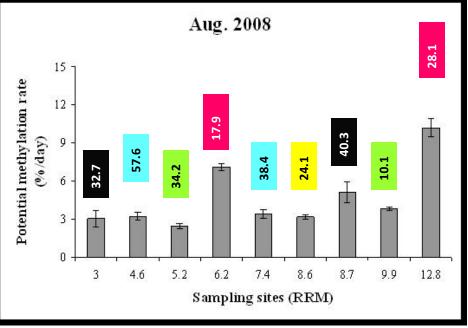
Thanks to JR Flanders and URS team in selecting and collecting samples

Mercury Methylation Potentials (MP)

Table 1: Habitat types and samples that were included in the study

Habitat type	Sampling sites
 Baseline monitoring stations in toe of river pool 	RRM 3.0 and RRM 8.7
River pools	RRM 4.6 and RRM 7.4
 Fine grained sediment deposit along river pool edge 	RRM 6.4 and RRM 12.7
Island or mill race side channel pool	RRM 5.2 and RRM 9.9
Floodplain wetland	RRM 1.6 and RRM 8.6



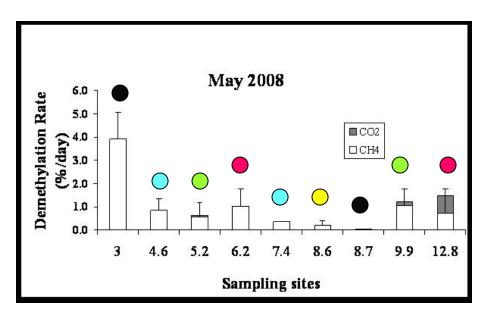


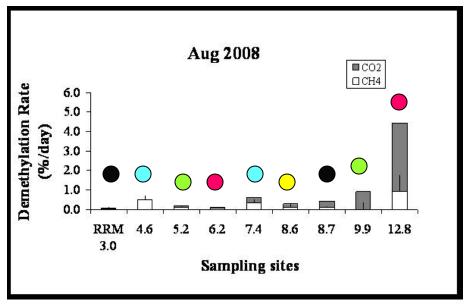
- MP's Highest in August
- In August, the fine grained sediment deposits had elevated methylation potentials

Methylmercury Demethylation Potentials (DP)

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Fine grained sediment deposit along river pool edge	RRM 6.4 and RRM 12.7
 Island or mill race side channel pool 	RRM 5.2 and RRM 9.9
Floodplain wetland	RRM 1.6 and RRM 8.6



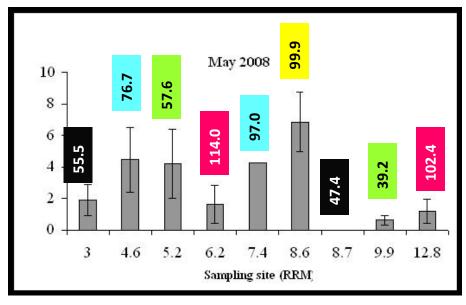


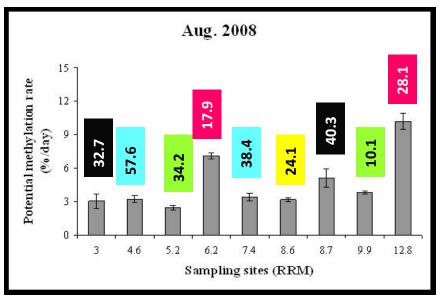
- Highest DP was observed at RRM 12.8 in August
- The dominant pathway of MDP appears to differ between May and August

Methylation / Demethylation Ratios

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 Baseline monitoring stations in toe of river pool 	RRM 3.0 and RRM 8.7			
O River pools	RRM 4.6 and RRM 7.4			
• Fine grained sediment deposit along river pool	RRM 6.4 and RRM 12.7			
edge				
Island or mill race side channel pool	RRM 5.2 and RRM 9.9			
Floodplain wetland	RRM 1.6 and RRM 8.6			

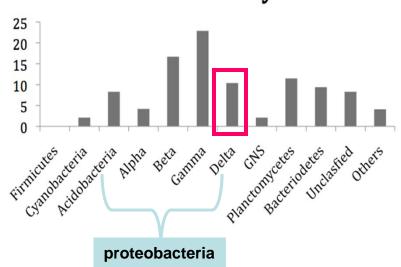




- All M/D ratios in August > 1
- Methylation / Demethylation ratios had a similar profile to River MeHg in May

RRM 6.2 May & Aug 30 25 20 15 10 RRM 6.2 May 5 RRM6.2 Aug Cyanobacteria Planctomycetes Bacteriodetes Acidobacteria Gamma Delta Unclasted Alpha Beta proteobacteria

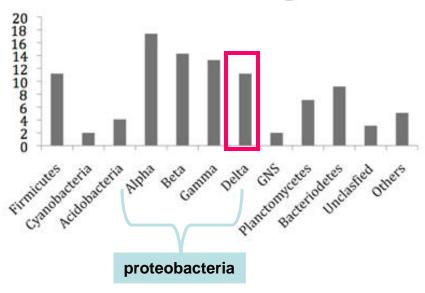
RRM 8.7 May



Microbial Community Structure

- Active populations dominated by proteobacteria
- Δ Proteobacteria include strains known to methylate mercury - - Iron reducing bacteria and Sulfate reducing bacteria
- In RRM 6.2 Δ Proteobacteria increased in August (correlates w/increased MP for this time)

RRM 12.8 Aug



Preliminary Results

- South River sediments methylate and demethylate mercury
- MP's and DP's change with site and season
- Measured MP's are not consistent with observations of MeHg in the river (i.e. highst MP measured in August)
- South River MP's comparable to those reported in the literature for other sites
- South River DP's lower than those reported in the literature and dominant mechanism of degradation may change with season
 - As a result, South River M/P ratios are relatively high
- Fine grain channel margin sediments may have elevated methylation potential relative to other sediments (August)
- Microbial community contains strains similar to known mercury methylating strains (iron reducers and sulfate reducers)

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Table 3: Physical and chemical characteristics of sediment samples collected in May 2008 (Mean \pm STD)

Study	Description	Moisture	LOI (%)	AVS	Total Solids	Inorganic	MeHg	Fe(II):Fe(III)
site		(%)		(µmol/g)	(%)	Hg (μg/g)	(ng/g)	
(RRM)								
1.6	Floodplain wetland	63.50±2.1 2	13.98±0.32	<1.8	36.86±1.24	4.0 ±0.2	5.3±0.4	1.30±0.01
3.0	Toe of pool (Bed sediment)	65.75±0.9 2	10.33±0	<1.9	34.74±0.01	20.4±0.05	55.5±2.8	1.00±0.02
4.6	Embedded pool	69.25±0.9 2	9.86±2.29	<2.1	36.84±4.36	21.0±2.6	76.7±11.0	2.40±0.08
5.2	Mill race	44.50±2.8 3	6.46±1.58	<1.2	43.90±13.93	45.2±11.5	57.6±5.0	2.00±0.03
6.2	FGCM deposit	75.90±1.2 7	15.29±0.11	<2.6	23.23±1.95	18.9±2.2	114.0±9.0	3.00±0.36
7.4	Embedded pool	71.50±1.1 3	12.14±0.24	<2.3	30.91±1.23	22.0±2.2	97.0±0.9	1.30±0.04
8.6	Floodplain wetland	74.50±1.1 3	11.23±0.58	<2.5	31.04±0.42	17.8±1.9	99.9±3.2	1.70±0.10
8.7	Toe of pool (Bed sediment)	75.00±0.7 1	11.91±0.74	<2.5	27.80±2.73	21.1±0.1	47.4±0.0	0.40±0.00
9.9	Mill race	79.20±2.2 6	36.73±25.7 5	6.1 (1.5)	28.94±8.53	6.3±2.0	39.2±9.9	7.70±0.07
12.8	FGCM deposit	76.50±0.4 2	6.60±8.97	3.7 (0.8)	25.23±9.81	22.6±6.0	102.4±21.7	4.30±0.26

Back up slide

Table 4: Physical and chemical characteristics of sediment samples collected in August 2008 (Mean \pm STD)

Study	Description	Moisture	AVS	Total Solids	Total volatile	Inorganic Hg	MeHg (ng/g)
site (RRM)		(%)	(μmol/g)	(%)	solids (%)	(µg/g)	
1.6	Flood plain wetland	64.0±0.6	1.8±0.1	48.2±0.6	12.4±0.3	4.2±1.0	5.7±0.0
3.0	Toe of pool (Bed sediment)	75.6±2.1	2.6±0.2	37.1±3.8	12.6±1.2	26.2±0.5	32.7±0.1
4.6	Embedded pool	68.2±3.0	2.0±0.1	31.4±3.5	21.0±3.6	23.4±5.9	57.6±1.3
5.2	Mill race	45.9±2.1	1.2 ± 0.1	61.0±1.1	7.2±0.3	32.7±1.8	34.2±15.1
6.2	FGCM deposit	52.7±8.1	4.3±2.5	62.8±1.0	4.6±0.1	6.8±0.1	17.9±0.0
7.4	Embedded pool	75.0±0.7	2.6±0.1	33.4±2.3	12.9±0.1	23.7±0.4	38.4±1.6
8.6	Floodplain wetland	70.3±2.8	4.3±0.9	47.9±2.3	10.9±0.1	14.4±0.3	24.1±0.6
8.7	Toe of pool (Bed sediment)	77.4±0.8	2.8±0.1	36.9±5.3	12.2±0.5	21.0±0.3	40.3±3.9
9.9	Mill race	80.9±1.9	12.5±1.6	36.5±4.2	15.4±1.0	8.7±0.3	10.1±2.7
12.8	FGCM deposit	53.8±0.6	1.4±0.1	46.3±2.5	11.2±2.5	15.2±6.6	28.1±5.6