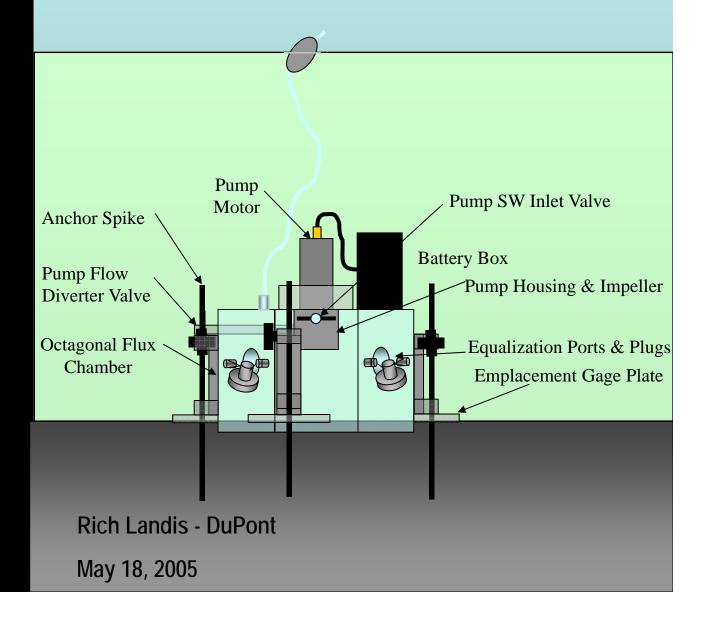
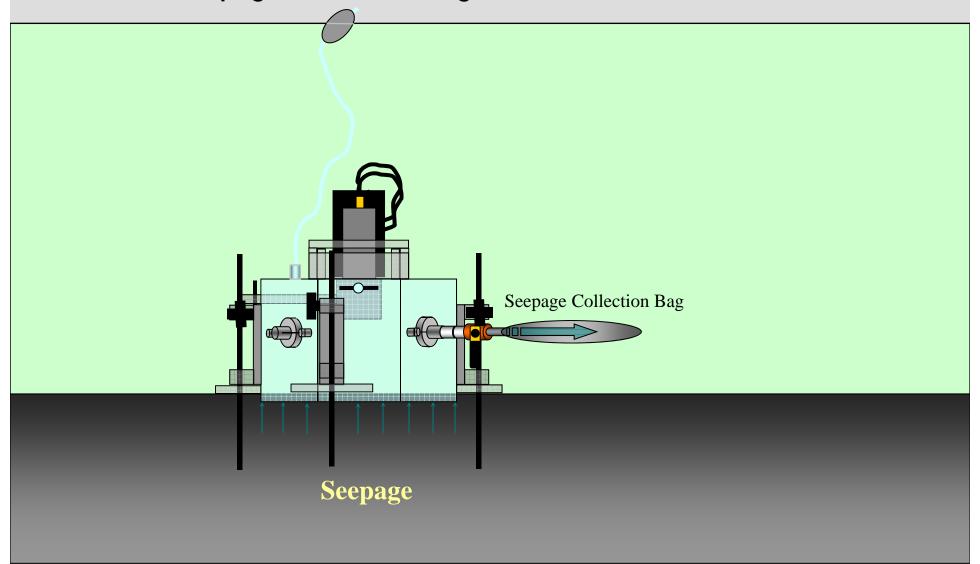


Flux Chamber Update



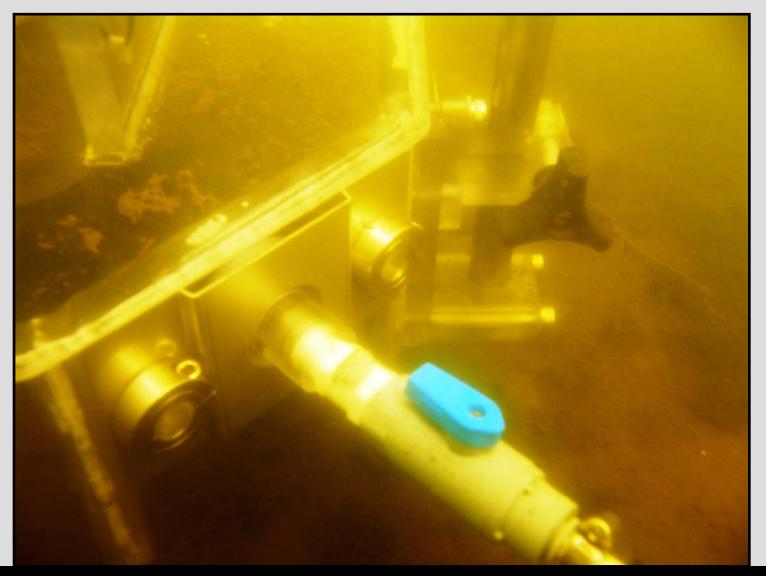
Tedlar Seepage Collection Bag



Gauge Plate



Seepage Bag Connection



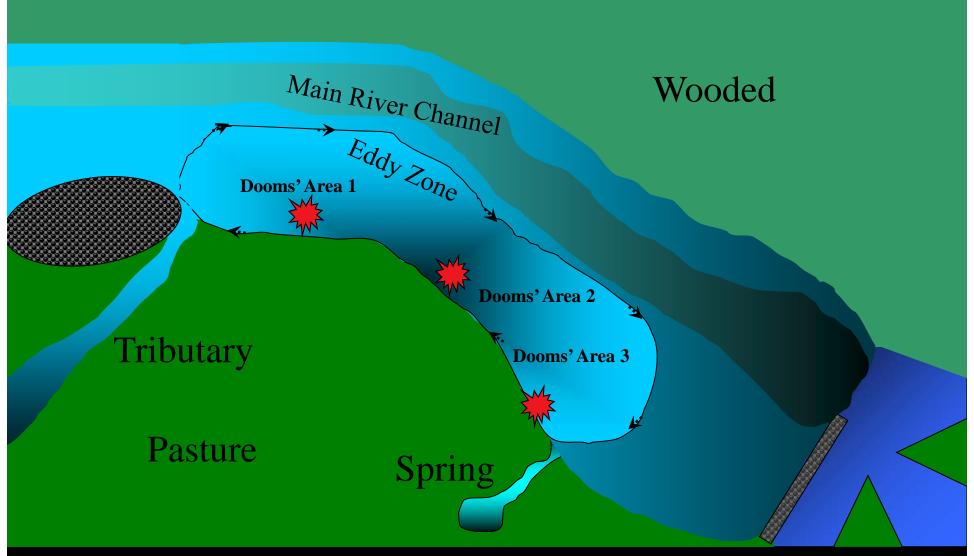
Benthic Flux Chamber Pilot Site Dooms' Dam Area



Looking Upstream Towards Sawmill Run

Looking Downstream Towards Dam

Dooms' Dam Pilot Test Areas



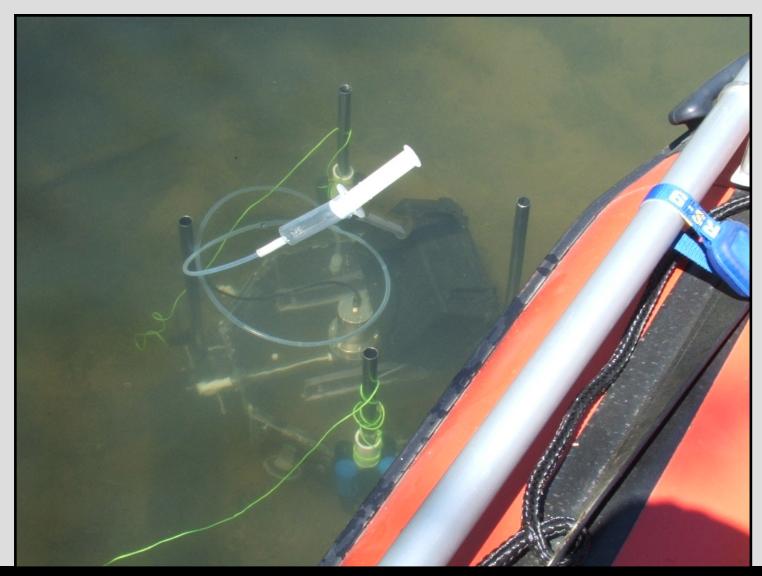








Sampling



Observations

- At least one chamber was not positively keyed into the sediment very well
- Ebullition from the sediments was observed at Dooms' Area 1 and 2 pilot sites
- Organic rich sediment was observed
- Pilot test sites 2 and 3 were hummocky
- Location was in an relatively large eddy current zone
- Limited data but interesting

Results

- Benthic flux chamber samples were analyzed by Nick Bloom's lab for dissolved total Hg and MMHg.
- Dooms' Area 1 chamber showed a trend of increased methylation over night
 - Sampled at 5:37pm, 7:37pm, and 8:10am (next day)
 - DO was decreasing during sampling event
- Dooms' Area 2 chamber appears to had been poorly keyed into the sediment (observed in the field as well)
- Doom's Area 3 chamber showed little to no MMHg flux
 - Sampled at 10:12am, 1:50pm, and 4:35pm
 - DO was increasing during sampling event

Results

- Benthic flux chamber in Dooms' Area 1:
 - MMHg flux rate of roughly 1.81 ng ft⁻² hr⁻¹ on average over 2 hours (5.01 Total Hg)
 - MMHg flux rate of roughly 5.96 ng ft⁻² hr⁻¹ on average over 12.5 hours (5.76 Total Hg)
 - MMHg flux rate of roughly 5.39 ng ft⁻² hr⁻¹ on average over 14.5 hours (5.66 Total Hg)
- Estimated average flux based upon two SW samples locate above and below Dooms' Dam:
 - MMHg flux rate of roughly 0.90 ng ft⁻² hr⁻¹ on average over a river section 1119 feet long and 112 feet wide (6.83 Total Hg)
 - Samples were taken around 10:25am and 10:52am and mid stream

Possible Path Forward

- Deploy benthic flux chambers in transects across the South River at key locations to look for trends in methylation (banks, sediment, flow channels, eddies, quiescent areas, etc.)
 - Collect SW samples and SW DO measurements during deployments
 - Sample the chambers during the day and night to determine relative methylation rates.
 - Sample the chambers every 1 to 2 hours until DO drops to 50% of initial value or 5 samples have been collected.



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