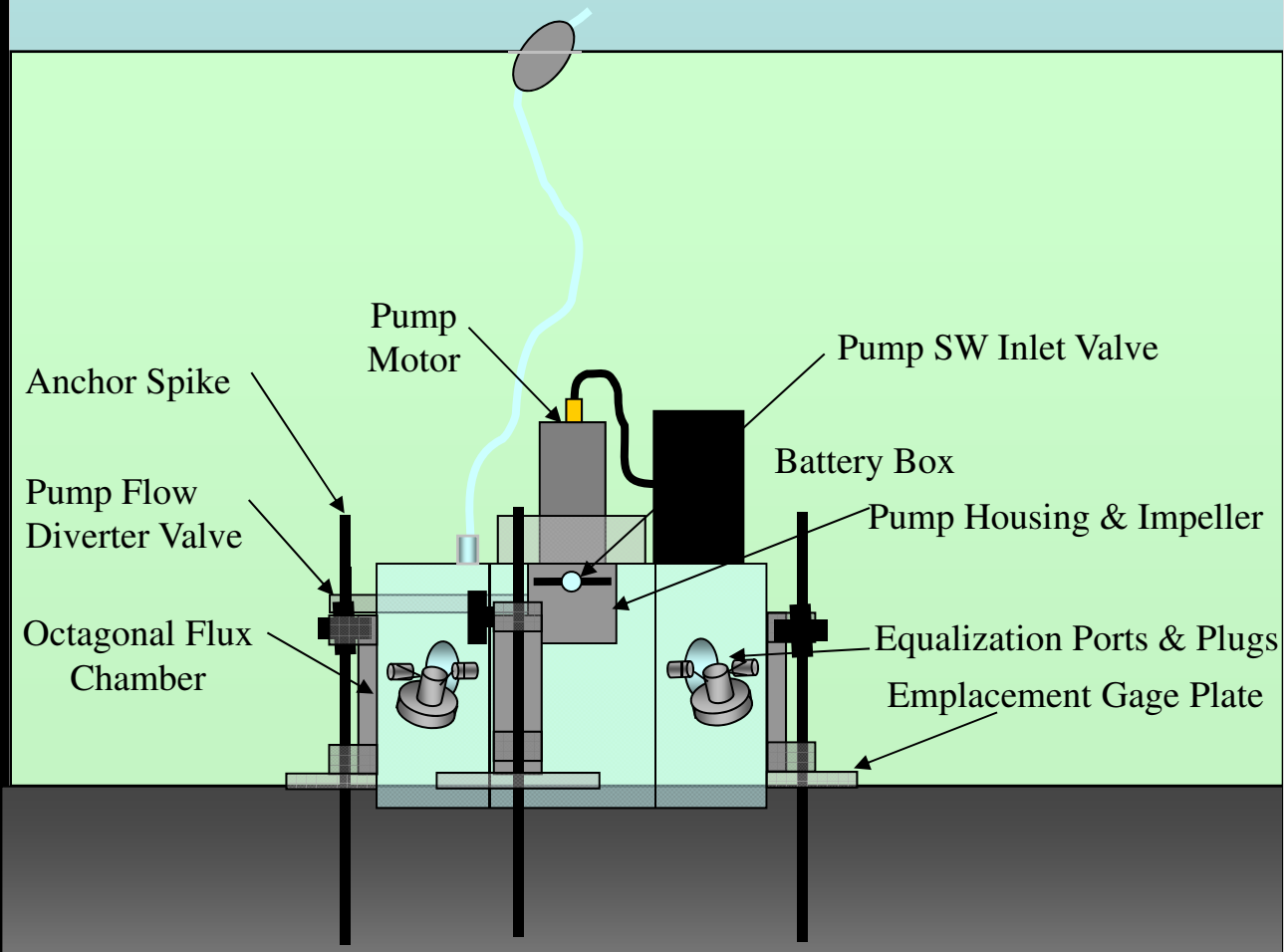
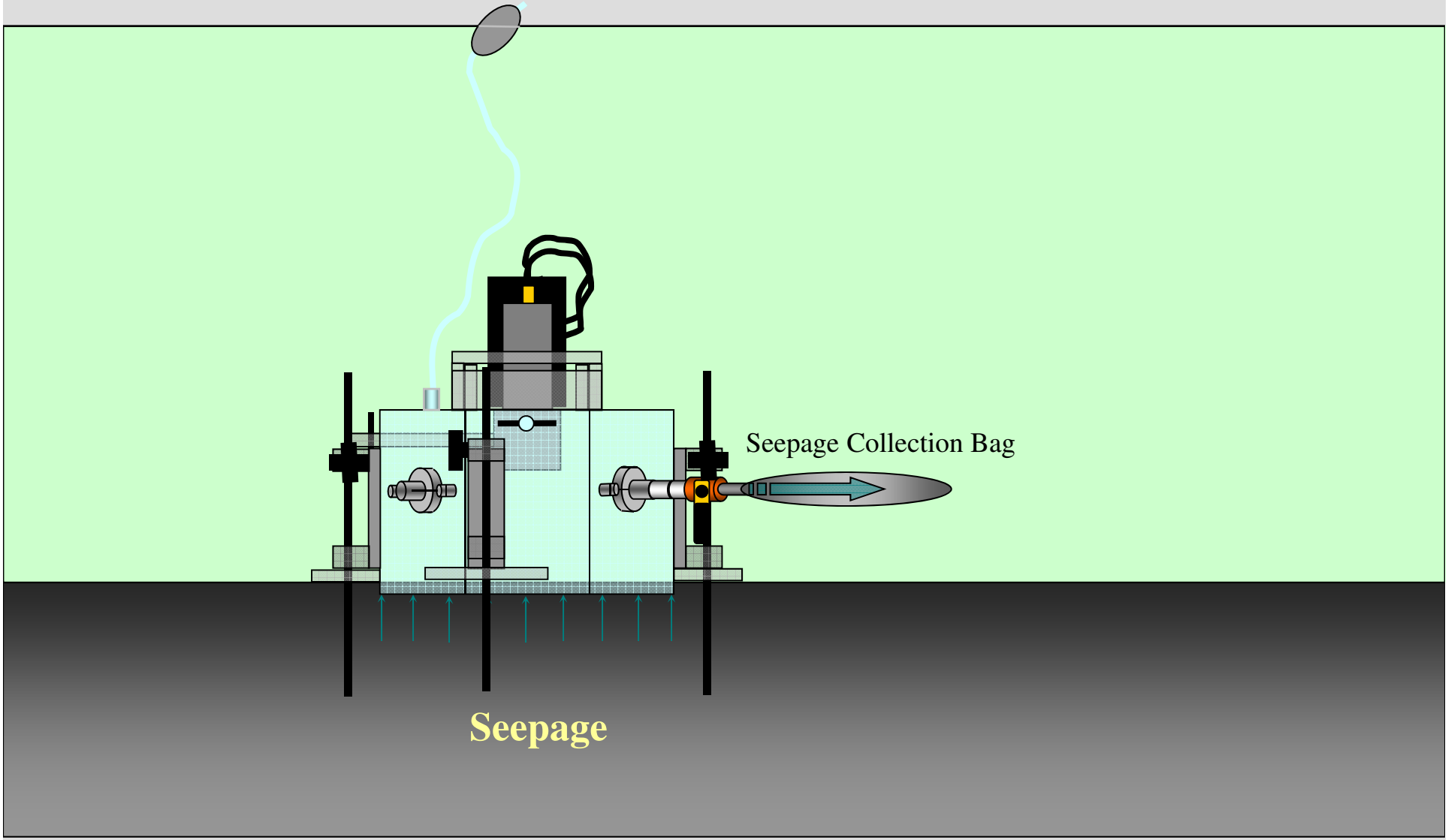
Flux Chamber Update



Rich Landis - DuPont

May 18, 2005

Tedlar Seepage Collection Bag



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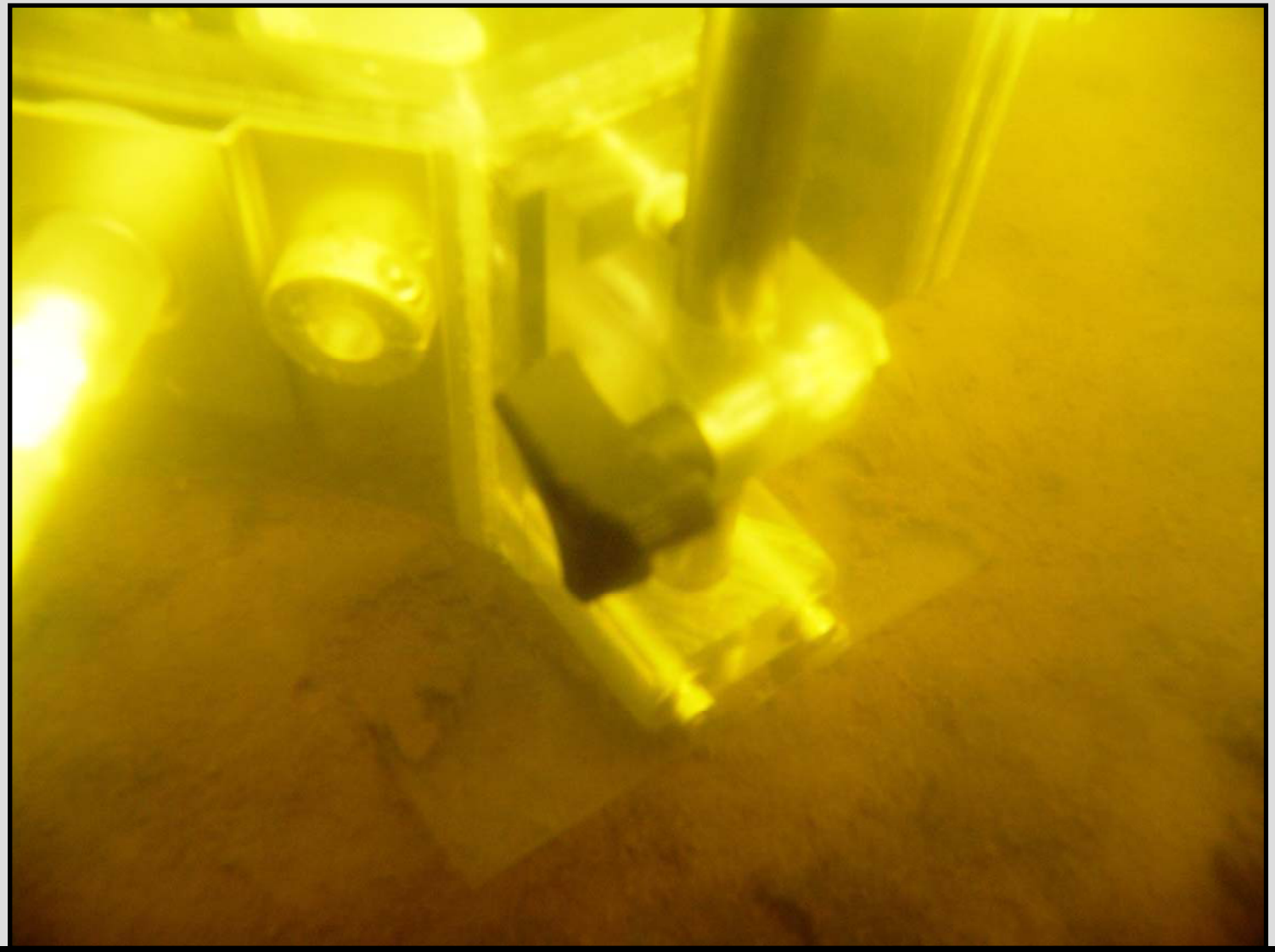
Gauge Plate



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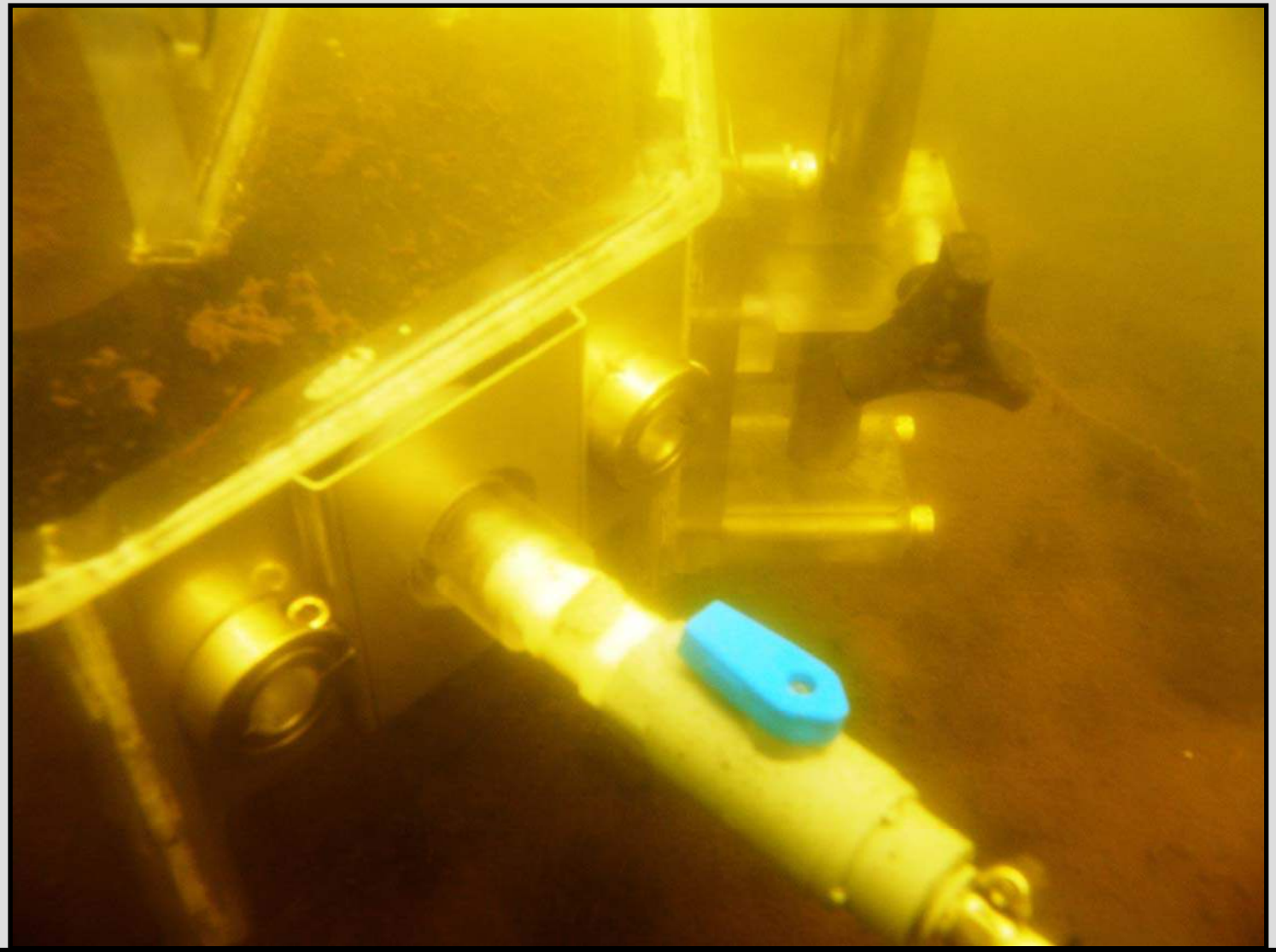
Seepage Bag Connection



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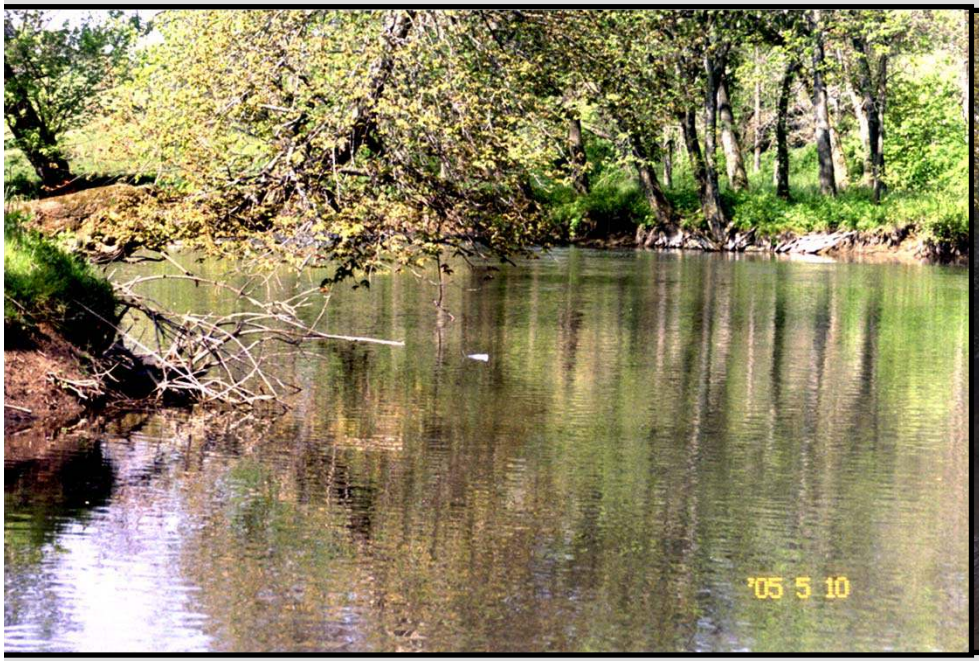
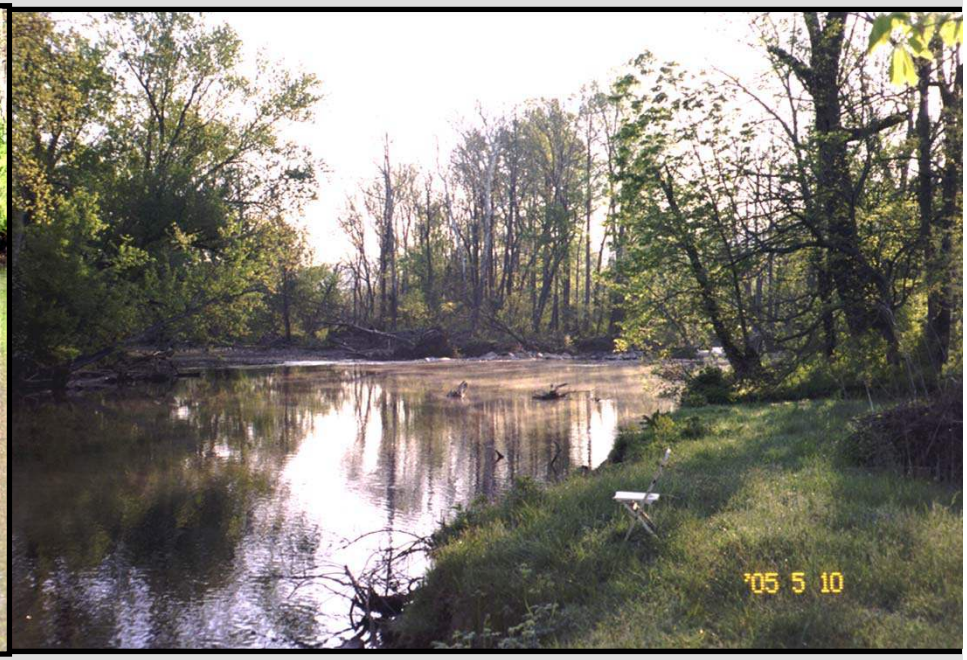
Benthic Flux Chamber Pilot Site
Dooms' Dam Area



Looking Upstream Towards Sawmill Run



Looking Downstream Towards Dam

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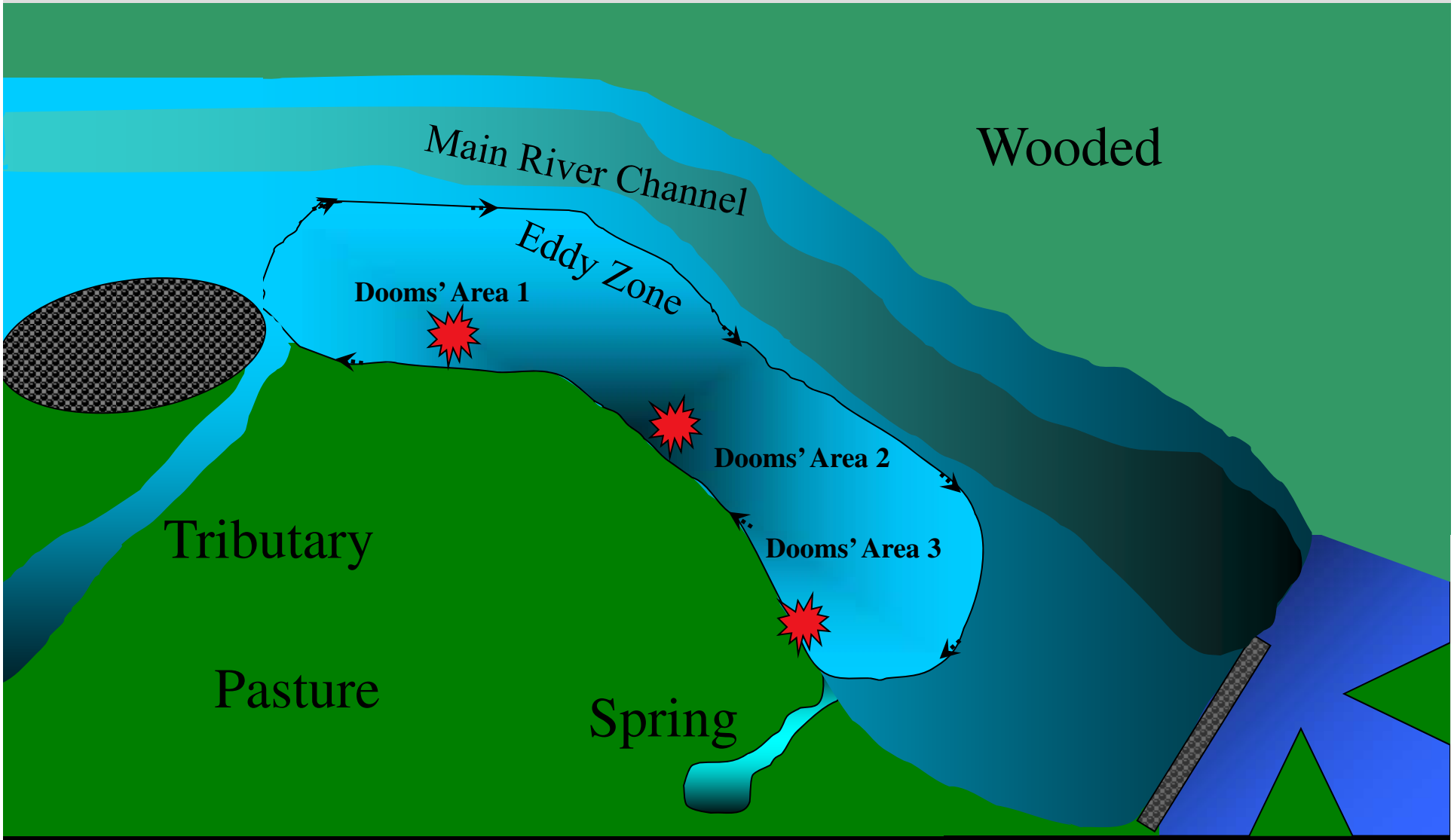
Dooms' Dam Pilot Test Areas



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Dooms' Dam Area 1

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Dooms' Dam Area 1

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Dooms' Dam Area 2

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Dooms' Dam Area 3

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Sampling

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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

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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

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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

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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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