ALGAE INTER-CALIBRATION STUDY: TARGETED-RIFFLE AND MULTI-HABITAT SAMPLING APPROACHES FOR ALGAE BIOASSESSMENT

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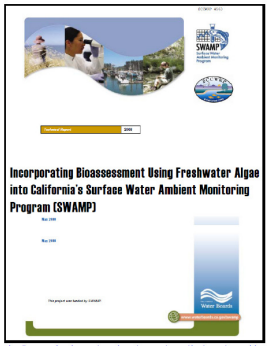
SWAMP Algae Plan: Recommendations



"…SWAMP [should] utilize the **multihabitat/ reachwide** approach for sample collection due to its versatility and anticipated applicability to a variety stream types… However, SWAMP should fund a **methods-calibration study** whereby targeted and reachwide methods are compared side-by-side in a set streams in the Lahontan Region…This will facilitate an assessment of whether, and how, datasets derived from samples collected in different ways can be integrated."

Objectives: Methods Comparability

1. Compare results of TR and MH field methods
   a. Algal biomass (AFDM, Chl a)
   b. Diatom assemblage
   c. Soft algae assemblage
   d. Metrics and IBI scores

2. Determine if datasets collected using different methods can be integrated

Sampling: Targeted vs. Multi-Habitat

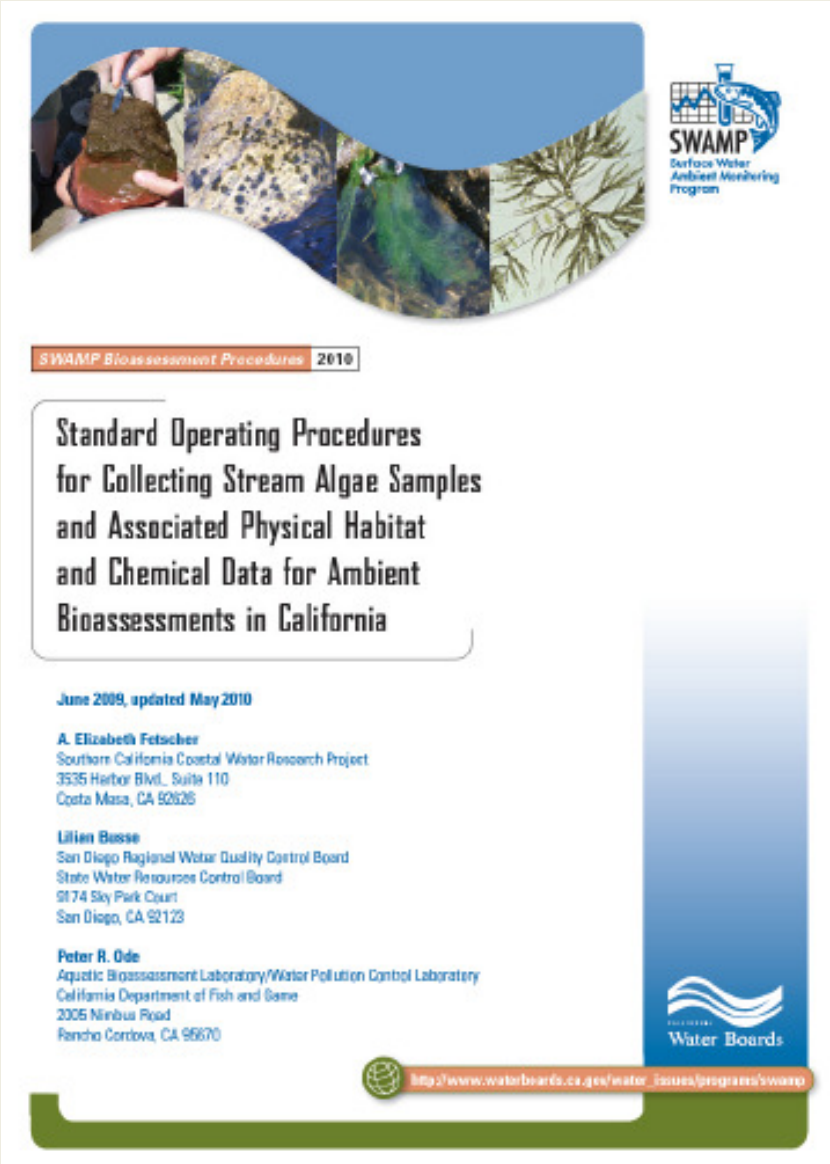
- Targeted: Requires specific substrate, usually cobble (USGS NAWQA)
- Multi-Habitat: Can be used in all systems (e.g., USEPA EMAP)
- Some evidence that metrics/IBIs are not necessarily dependent on sample method or substrate (e.g., Weilhoefer and Pan 2007 JNABS, Winter and Duthie 2000 Aquatic Ecology)

Targeted Riffle Method

- Developed by Sierra Nevada Aquatic Research Lab- used throughout Eastern Sierra for ~10 yrs
- Draft IBI developed (Herbst and Blinn 2008)
- Three cobbles from riffles are completely scrubbed

Algae Bioassessment

- 2008: California's "Algae Plan"- CA should develop a standardized protocol (Fetscher and McLaughlin 2008)
- 2010: CA adopted a Multi-Habitat sampling method for diatoms and soft algae (Fetscher et al.



Multi-Habitat Method

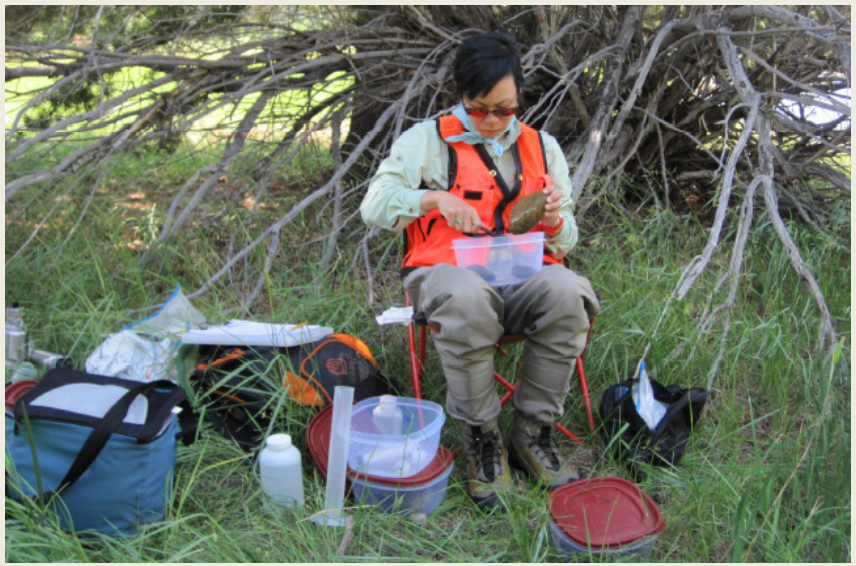
All substrates sampled

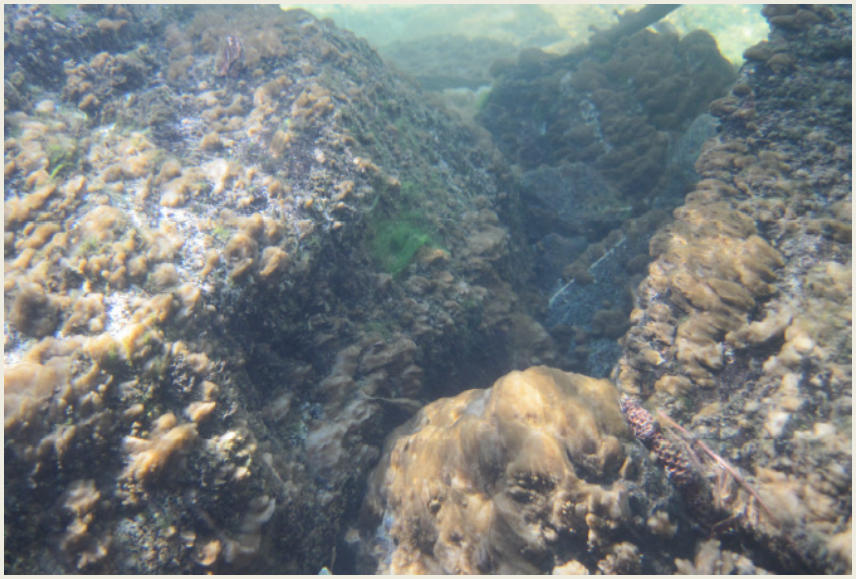
- **Rubber Delimiter + Brush**: cobble, large gravel
- **Coring device:** gravel, sand, silt, organic substrates…
- **Syringe scrubber**: immovable, submersed

Targeted Riffle	Multi-Habitat
3 Cobbles randomly selected from riffle habitat	One location (L, C, R) on each of 11 transects spaced 15 m apart
Sampling Area: 300 – 1000 cm^2	Sampling Area: 100-140 cm^2
One taxonomy sample (45 mL) preserved with 5 mL 37% formaldehyde	Diatoms: 40 mL sample + 10 mL formalin Soft algae: 45 mL sample + 5 mL

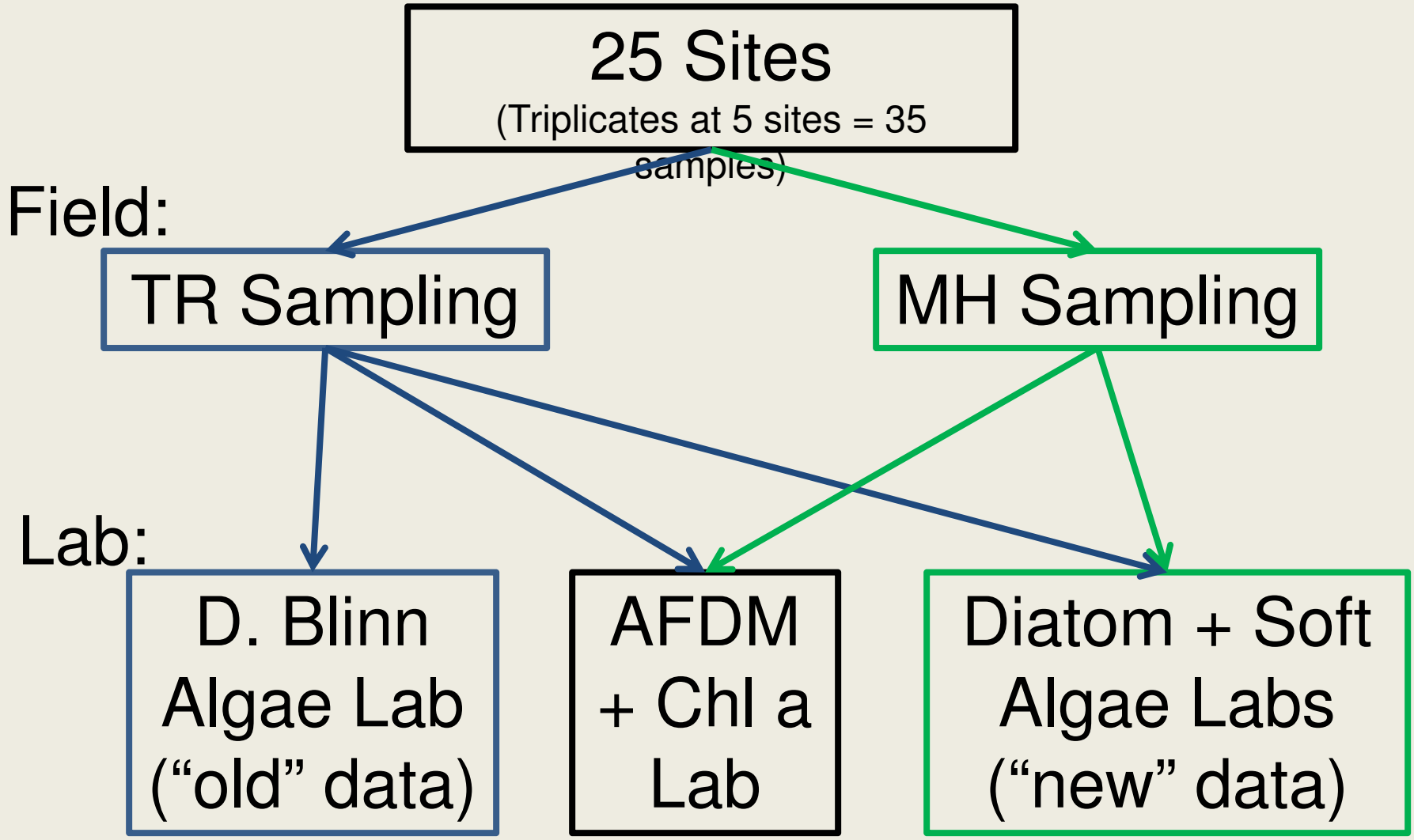
Hypotheses

The two methods will produce similar results (biomass, community comp.) in streams dominated by **cobble**; results will differ in streams with **variable substrate** (e.g., fines)

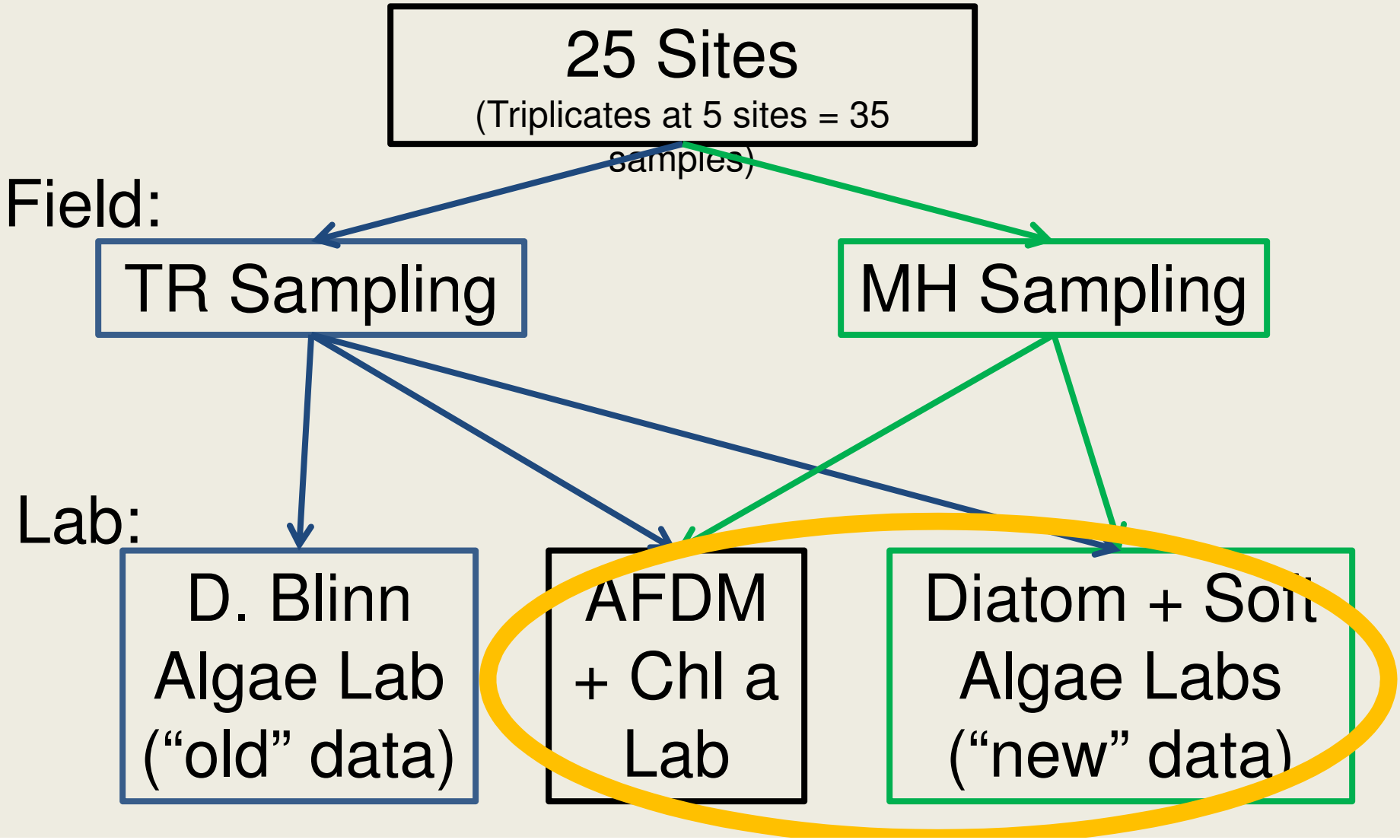




Sampling Design: Methods Comparability



Sampling Design: Methods Comparability



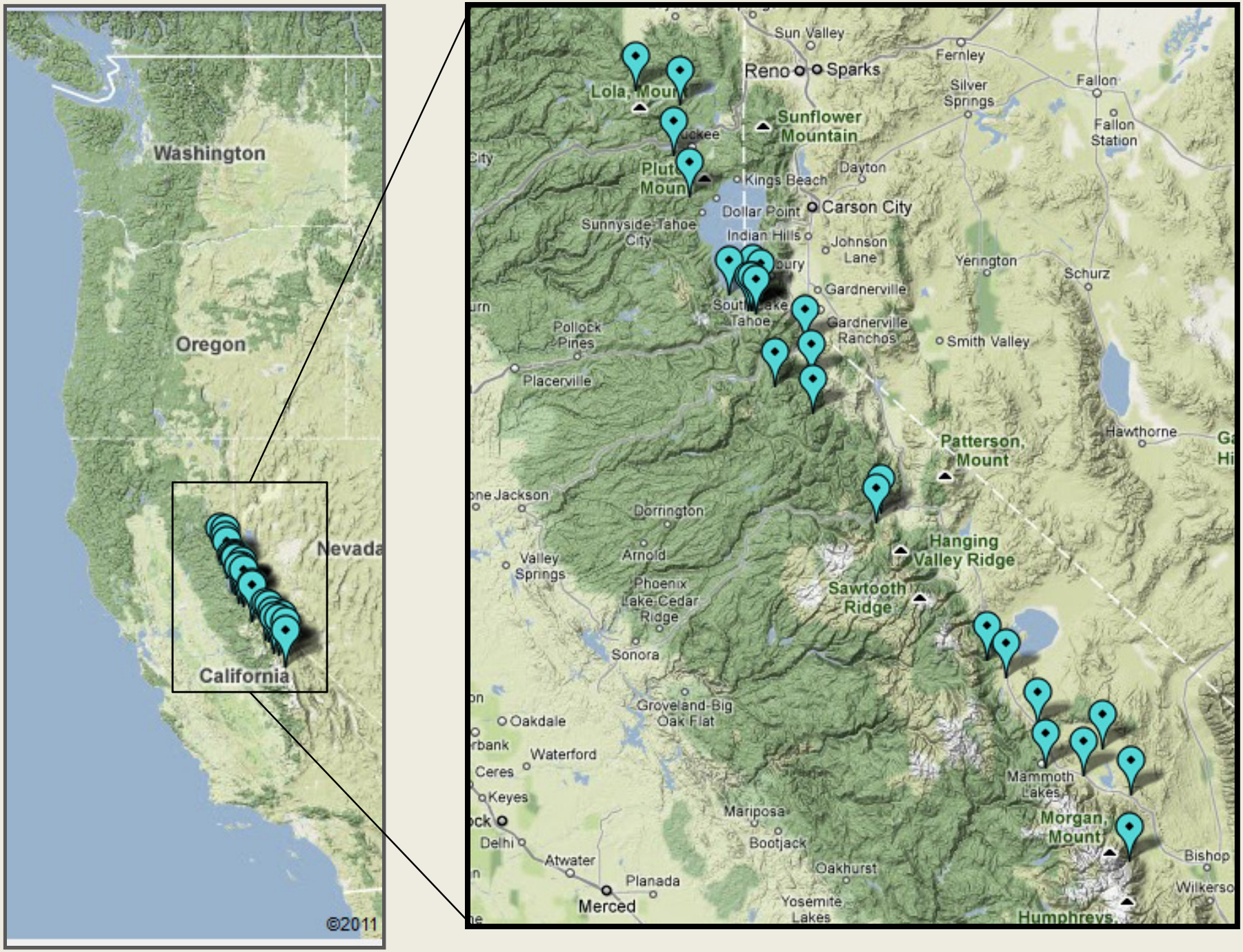
Study Timeline

January 2010: Project Planning

July - August 2010: Field Sampling

Sept. 2010 – June 2011: Lab Work

July 2011 – Dec. 2011: Data Analysis and Report Writing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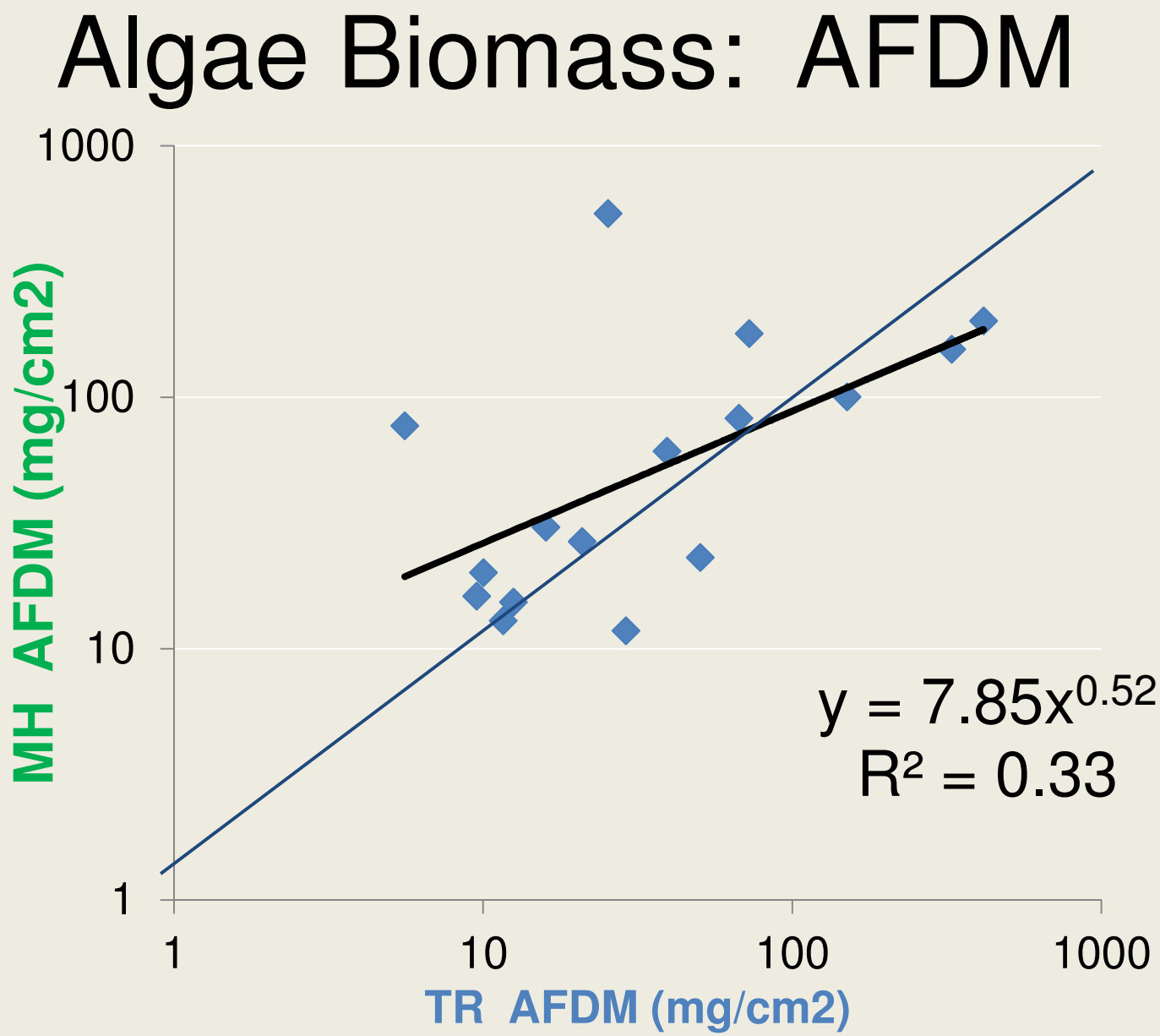
Bootjack
Delhi
Atwater
Planada
Merced
Oakhurst
Yosemite Lakes
Mammoth Lakes
Morgan, Mount
Bishop

Study Sites (25)

½ Reference

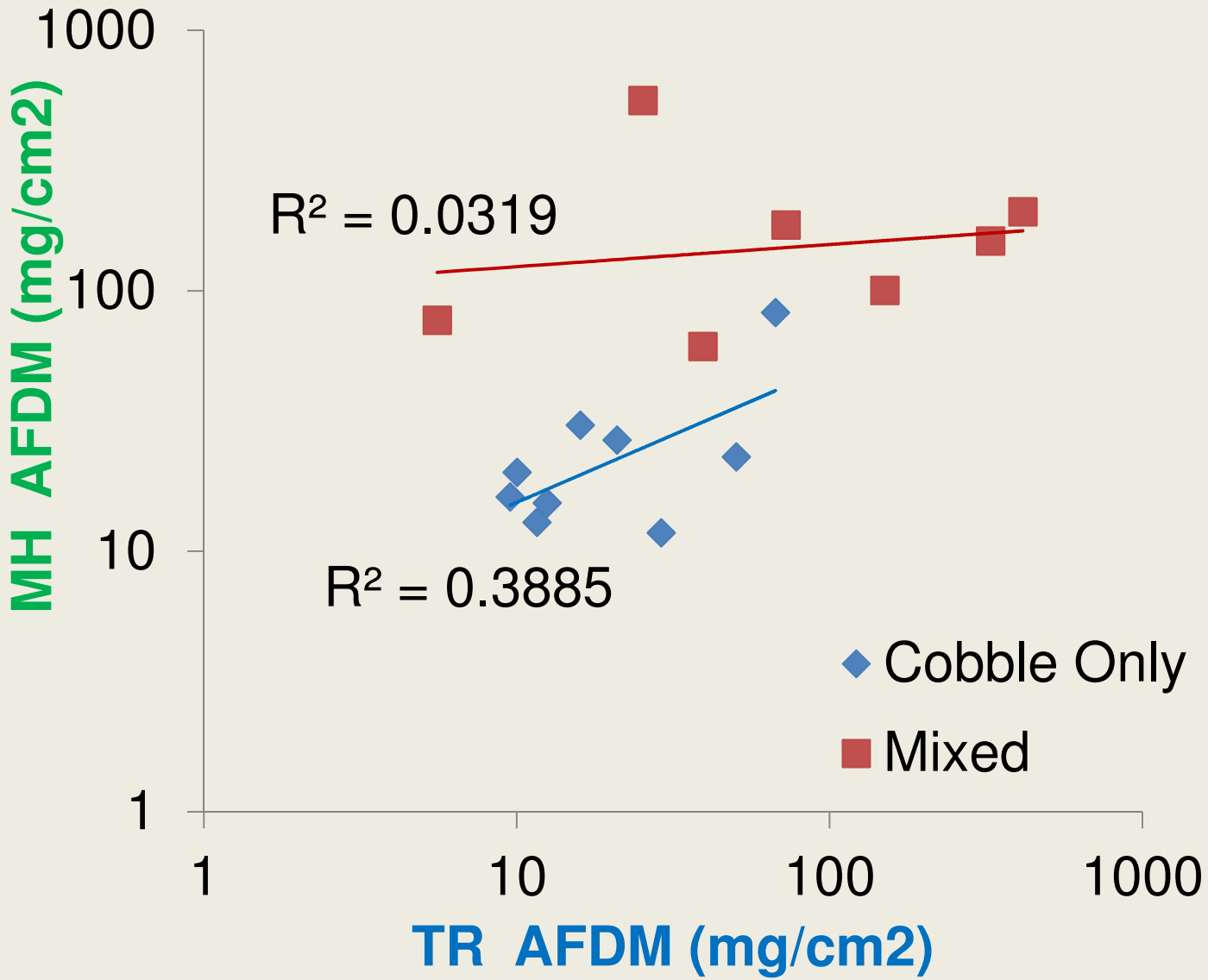
½ Low Gradient

Results


Algae Biomass: AFDM
1000
100
10
1
MH AFDM (mg/cm2)
1
10
100
1000
TR AFDM (mg/cm2)
y = 7.85x^0.52
R² = 0.33

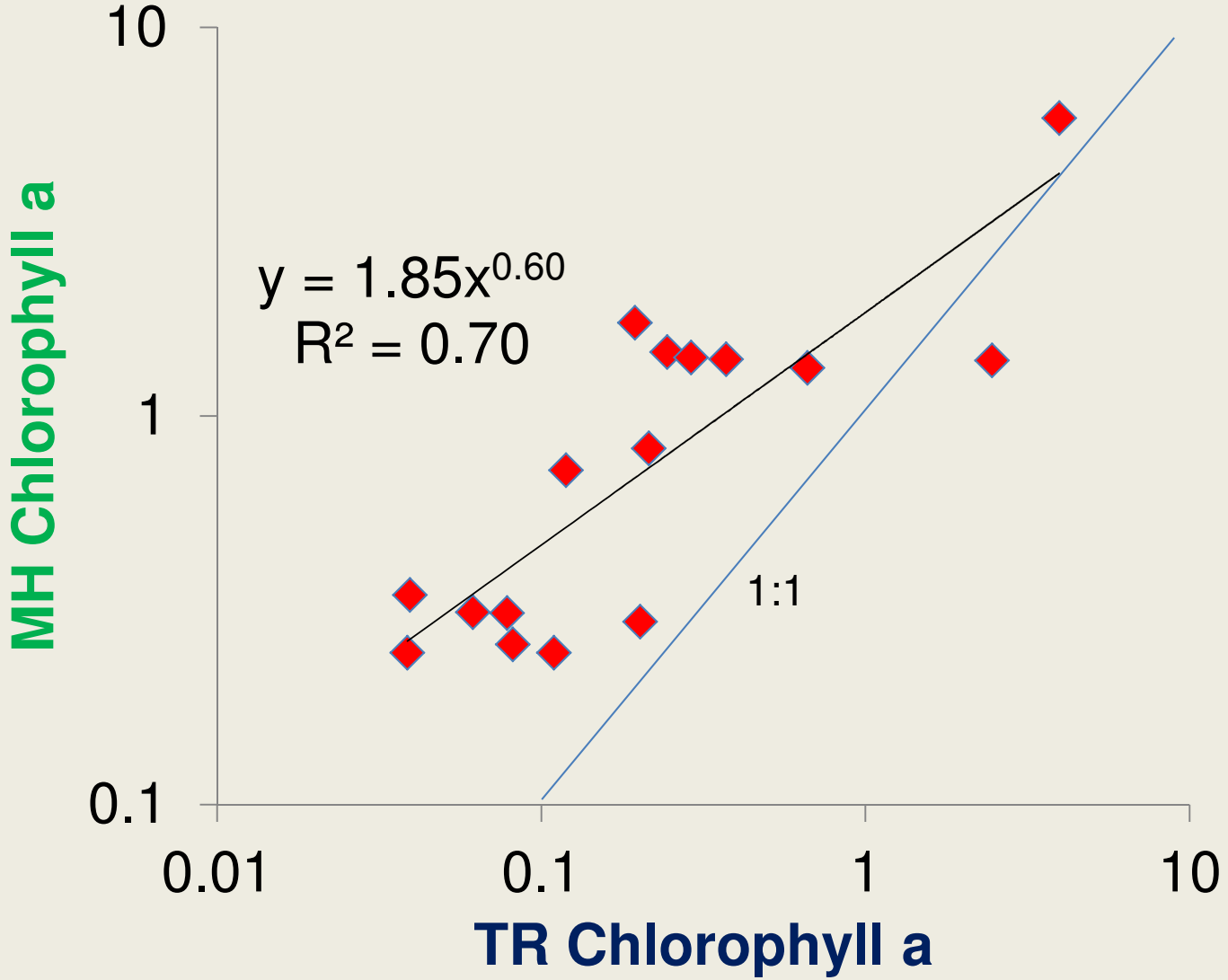
Results

Algae Biomass: AFDM



Results

Algae Biomass: Chlorophyll a



Results

Algae Biomass
MH: TR Ratios (Mean ± S.D.)

- AFDM
  - Cobbly sites: 1.3 ± 0.6 mg/cm^2
  - Mixed sites: 5.8 ± 8.3 mg/cm^2
  - t-test, p =0.12
- Chl a
  - All sites: 4.3 ± 2.5 ug/cm^2

Results

Diatoms

Insufficient number of organisms (<600)

- TR
  - **4** / 35 samples (11%)
  - **3** / 25 sites (12%)
- MH
  - **10** / 35 samples (29%)
  - **4** / 25 sites (16%)

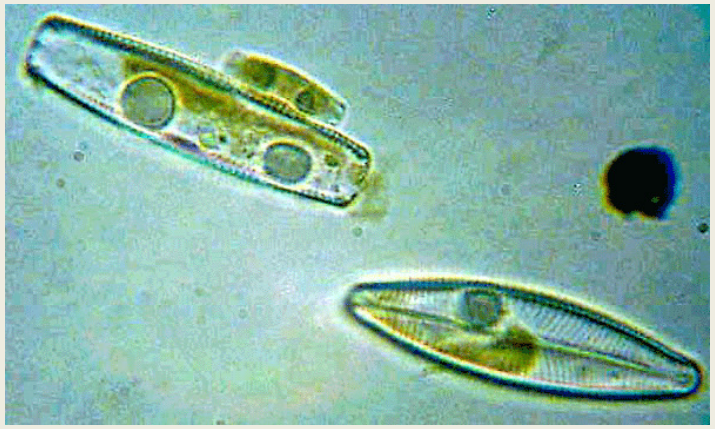
Results

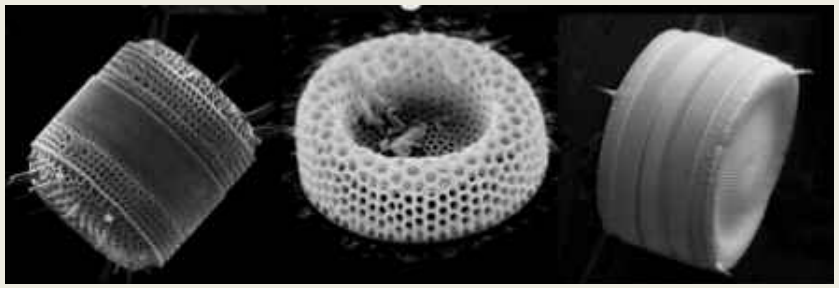
Diatoms

Taxonomic Richness (Mean ± SD)

- TR: 38.5 ± 10.8
- MH: 44.8 ± 17.3

Paired t-test (n = 27): p = 0.002





Results

Diatoms

Taxonomic Richness (Mean ± SD)

Cobble Sites:

- TR: 27.5 ± 7.4
- MH: 28.8 ± 7.0

Other Sites:

- TR: 41.3 ± 9.3
- MH: 49.0 ± 16.7

Paired t-test (n = 15): p = 0.003

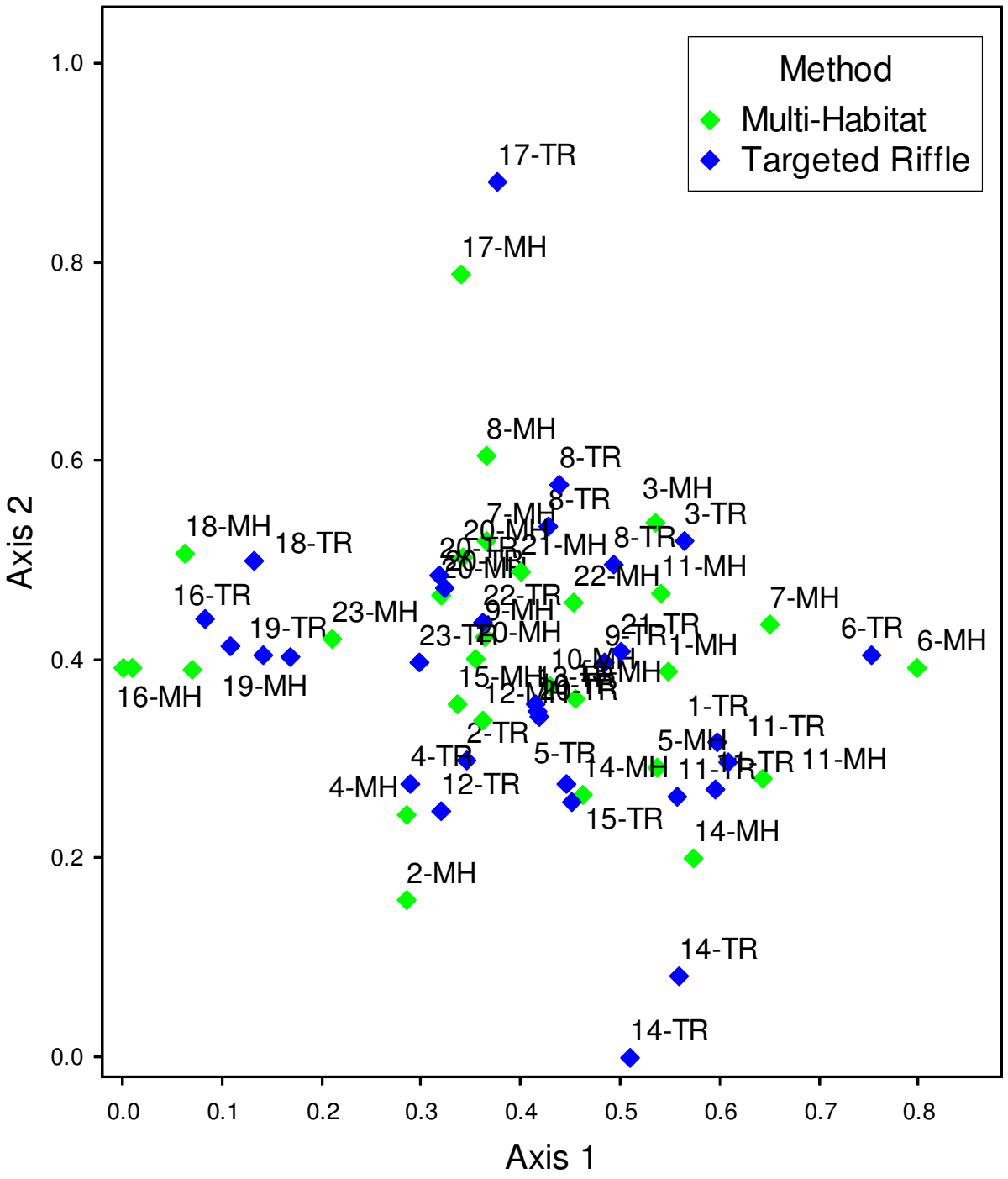
Results

NMS Ordination Diatom Abundance

3 Axis Solution
Variation explained ($R^{2)}$

- Axis 1: 0.158
- Axis 2: 0.173
- Axis 3: 0.168

Instability = 0.00001
Final stress = 14.4

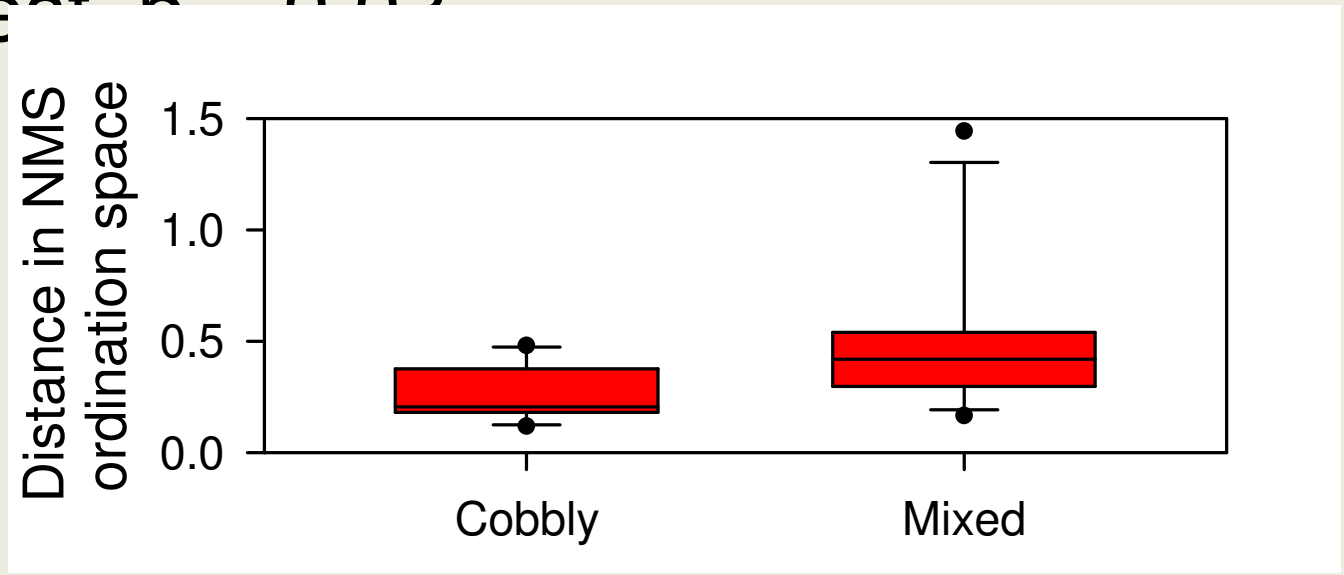


Results

Diatom Assemblages

Difference in 3D ordination space: |TR – MH|

- Cobbly streams (n = 10): 0.26 ± 0.12
- Mixed streams (n = 11): 0.50 ± 0.35
- t-test, p = 0.03



Conclusions:
TR and MH Comparability

Conclusions: TR and MH Comparability

- Biomass
  - AFDM comparable in cobbly streams; substantial variation in other substrates
  - Chl a significantly greater using MH method; correction factor possible?
- Diatoms
  - Community: variation among sites >> method differences
  - But: substantial method differences (richness, abundance, community comp.) in mixed substrate streams
- Next steps:
  - Do these differences affect bioassessment (metrics, IBI)?
  - Relative importance of variability in labs, taxonomy?