

Factors related to growth inhibition in juvenile mussels exposed to ambient stream conditions

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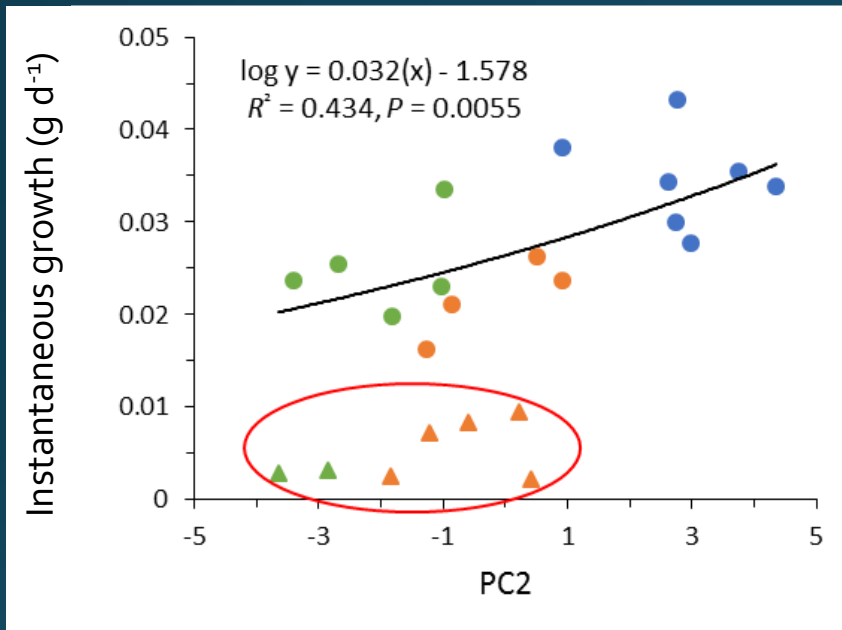
Kentucky State University

Background: 2015 study

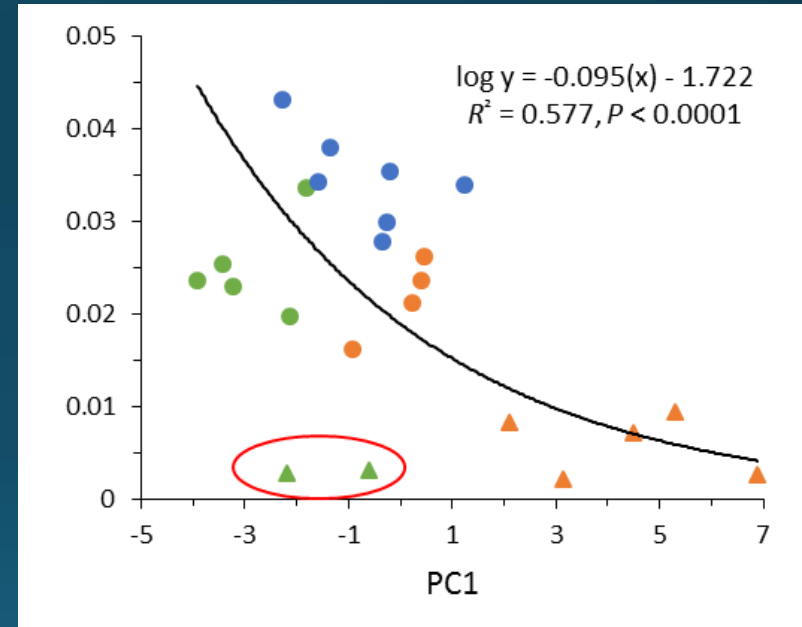
- High survival
- Very low growth in defaunated streams



Background: 2015 study



Nutrients, TOC, temperature



Pesticides, NO_3

2016 study goals

- Repeated 2015 study at subset of 10 sites from 2015
- Measured diatom and bacterial abundance and assemblage composition
- Measured C and N stable isotopes in mussels, periphyton, and seston
- Examined physiological status with metabolomics

Study design

- Exposed juvenile mussels in silos to ambient conditions in 10 streams; five low-growth and five 'normal' growth streams
- Pocketbook mussel, *Lampsilis cardium*: 4 months old, mean length = 5.0 mm, mass = 0.026 g.
- 3 silos/site; 25 mussels/silo
- 91-day exposure period (average; June-September)



Study streams

Low-growth sites

Drakes Creek

Horse Lick Creek*

Little River

Nolin River*

Red River

'Normal-growth' sites

Beech Fork

South Fork Licking River

South Fork Kentucky River

Rockcastle River

Russell Creek

Methods – mussel food resources

- Sampled diatom assemblages at each site:
 - Replicate, quantitative rock scrapings and sediment samples.
 - One sample/site, approx. mid-way through study.
 - Diatoms identified and counted (EnviroScience, Inc)
- Sampled bacterial assemblages
 - Collected one composite sediment sample/site
 - Microbes identified to major groupings with fatty acid methyl ester profiles (FAME).

Methods – isotopes

- Sampled periphyton and seston at each site
 - One sample/site, approx. mid-way through study
 - Periphyton: same methods as for diatoms
 - Seston: 9-500 ml samples filtered through 50 μm filter, composited, and 50 ml subsample pulled across 0.7 μm filter
 - Samples frozen
- Initial sample of mussels frozen prior to deployment
- Subsample of mussels frozen mid-way through study (July)
- Final sample frozen at end

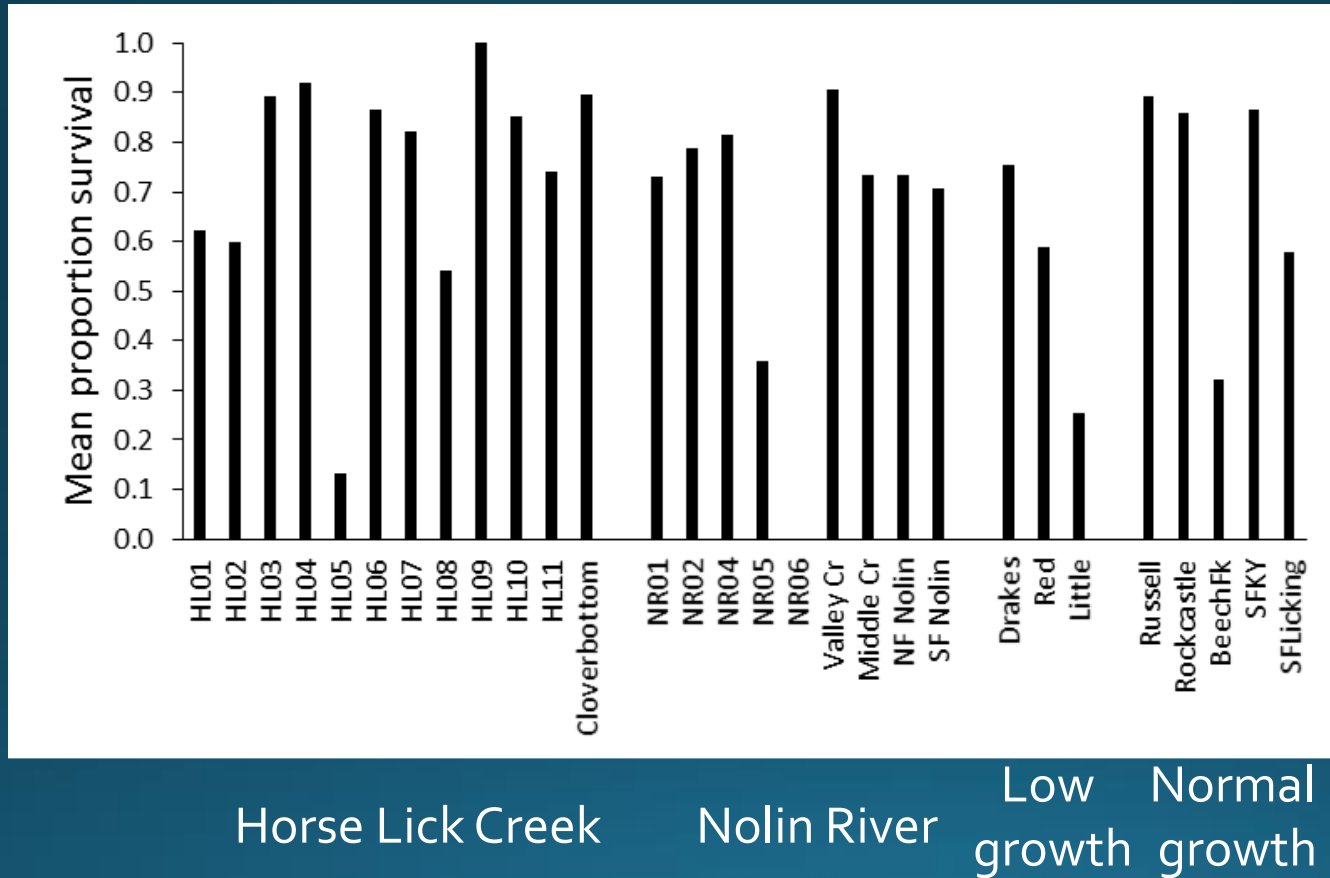
All samples analyzed at University of Georgia

Methods – metabolomics

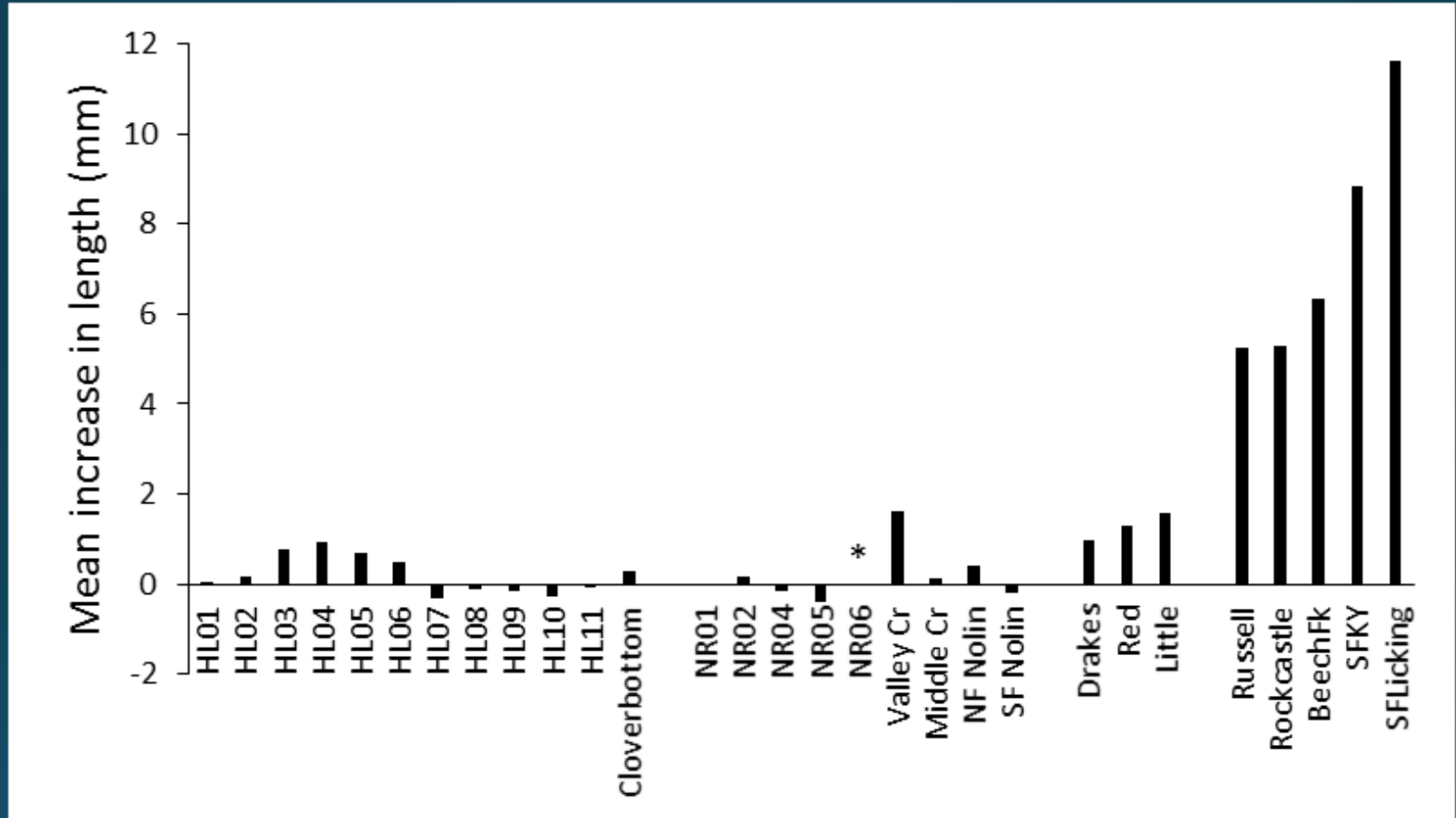
- Final sample flash-frozen at end of study
- Samples pooled from Little and Red rivers
- Samples analyzed by Metabolon, Inc., Durham, NC
- Measured 417 named biochemicals

Results

Silos: retrieval = 87%, range = 33-100%
median survival = 74%



Results



Horse Lick Creek

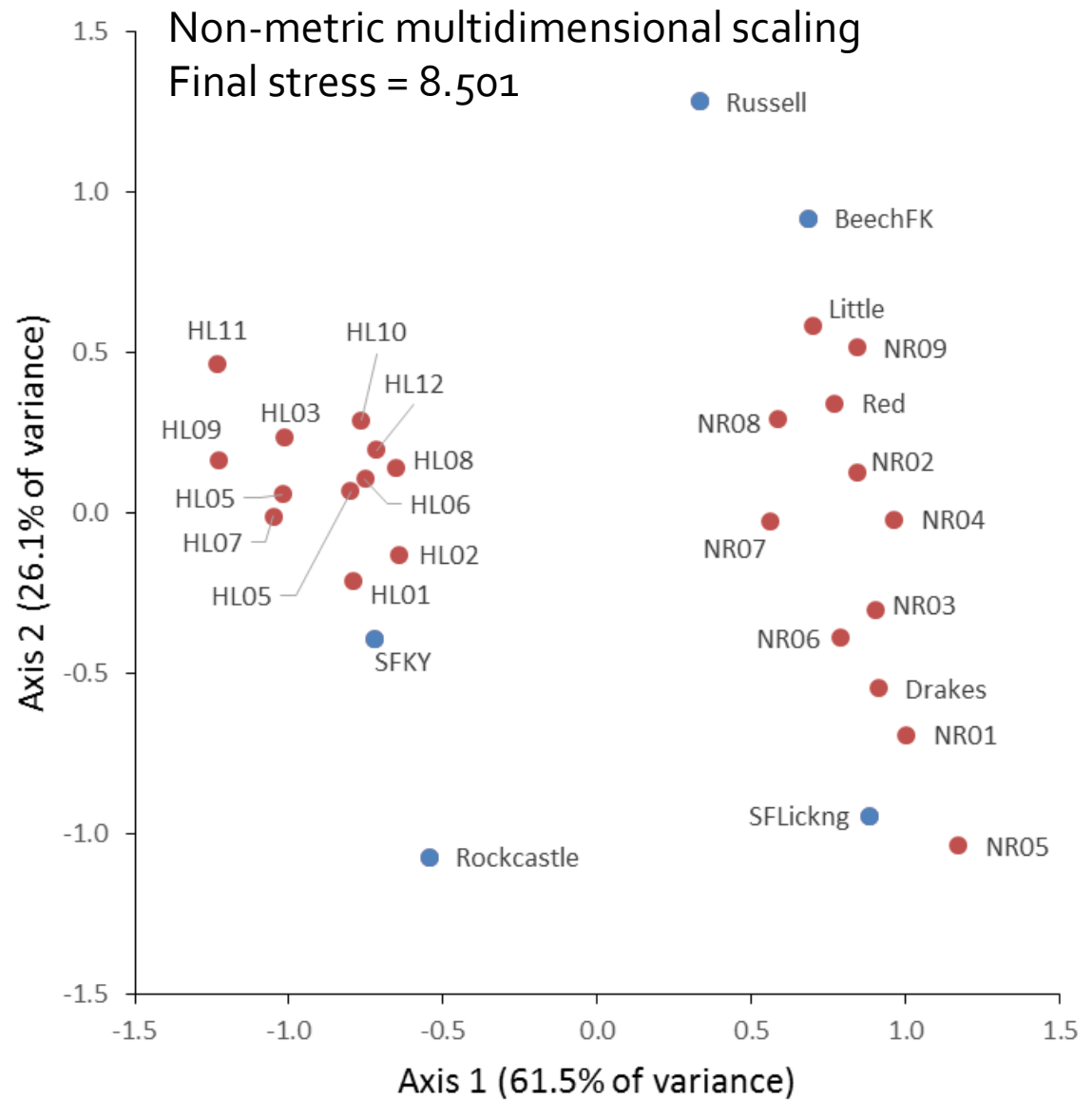
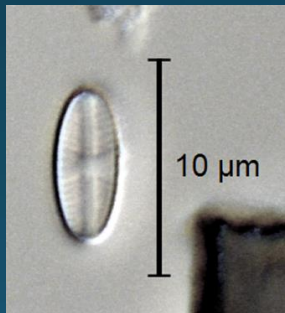
Nolin River

Low
growth

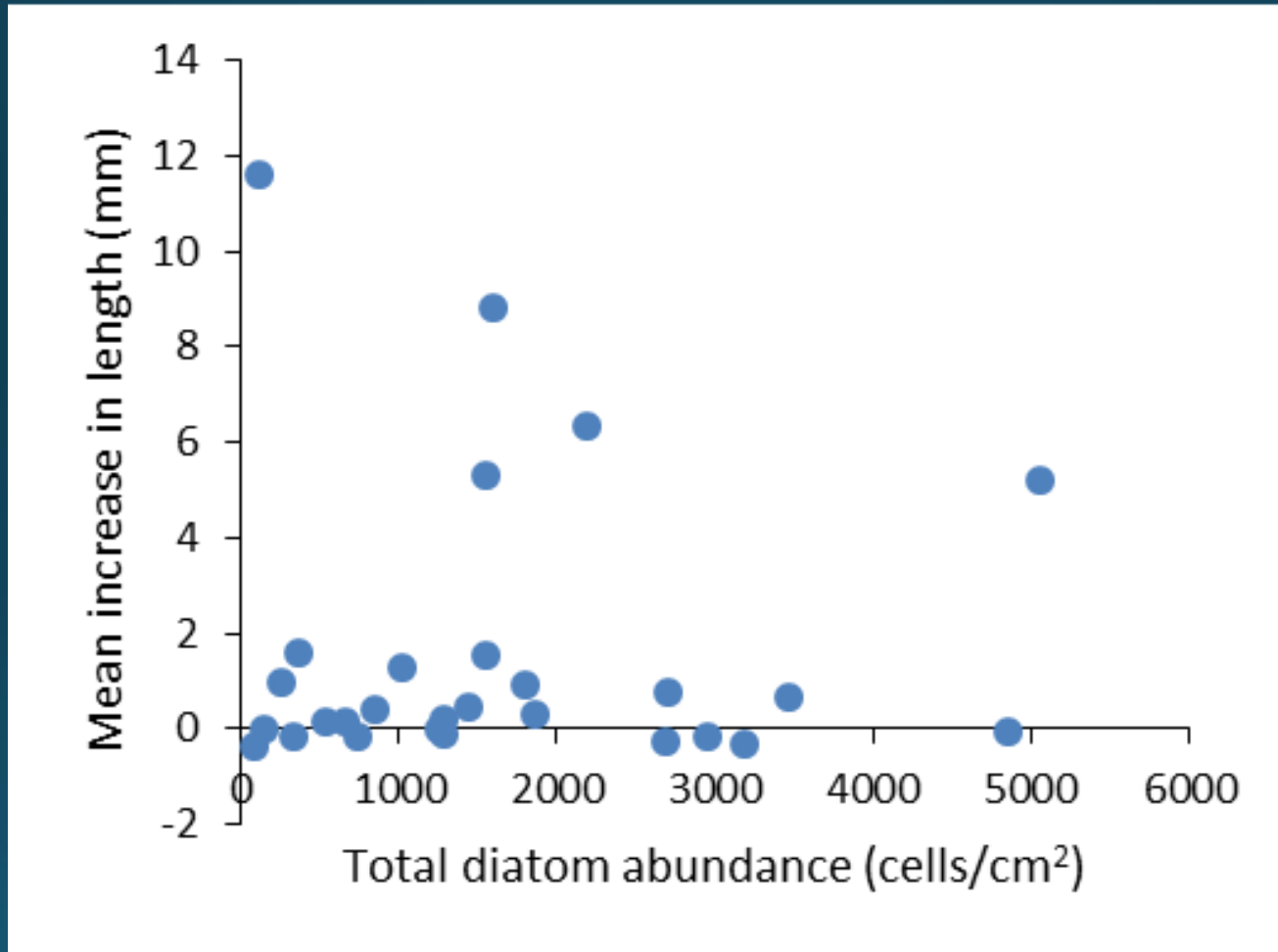
Normal
growth

Diatoms

- 227 species present
- Appalachian vs. other streams
- Little relationship to growth

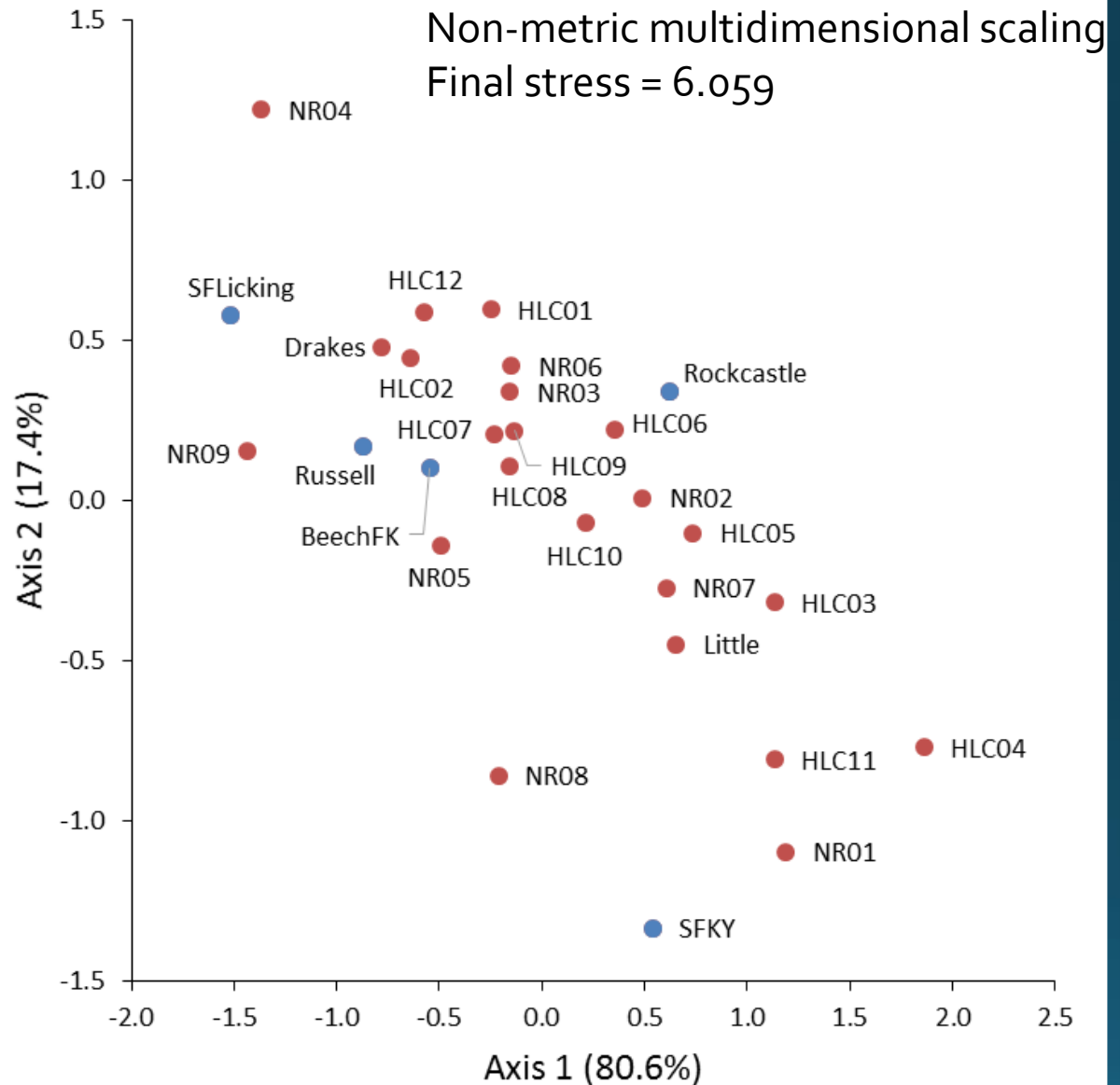


Diatoms

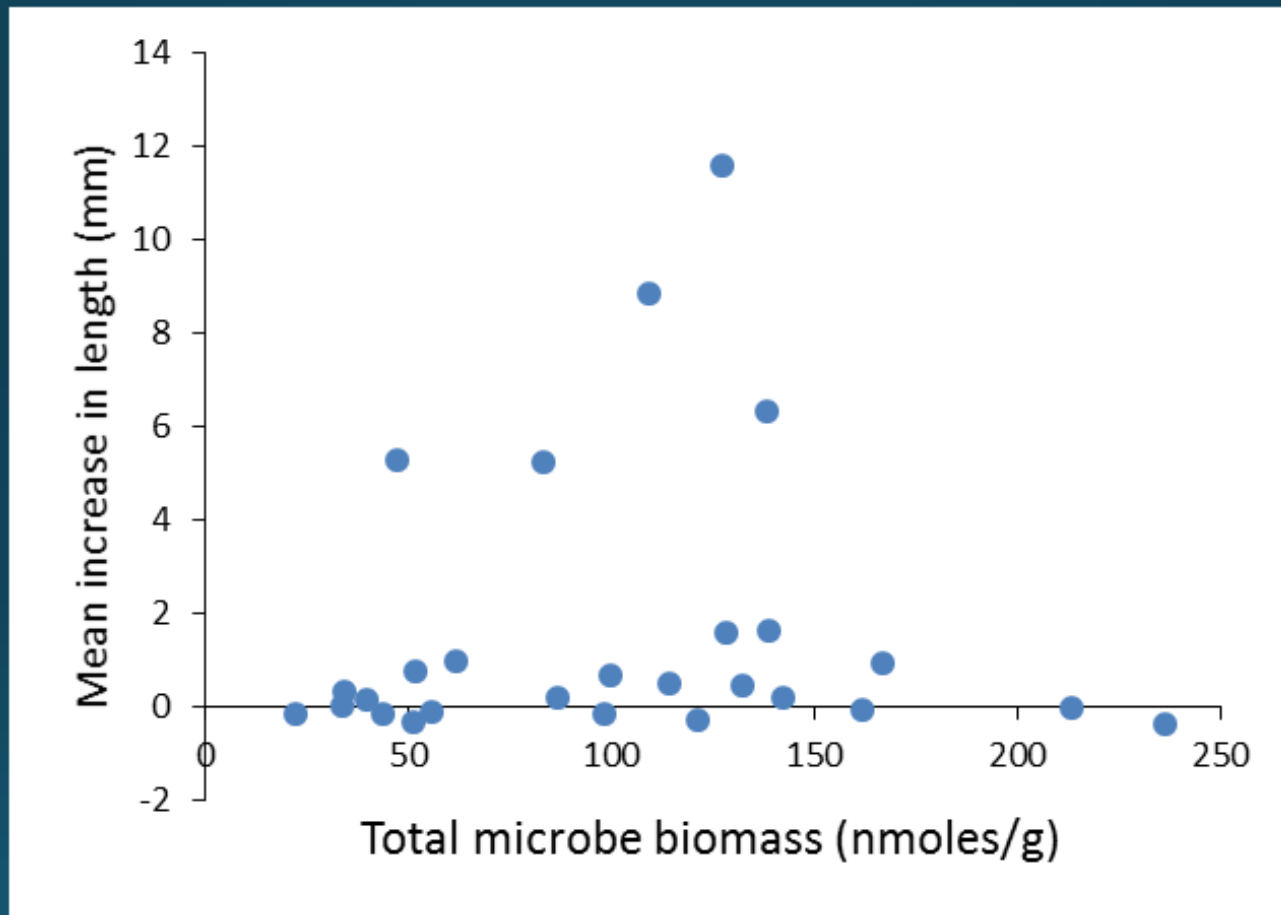


Bacteria

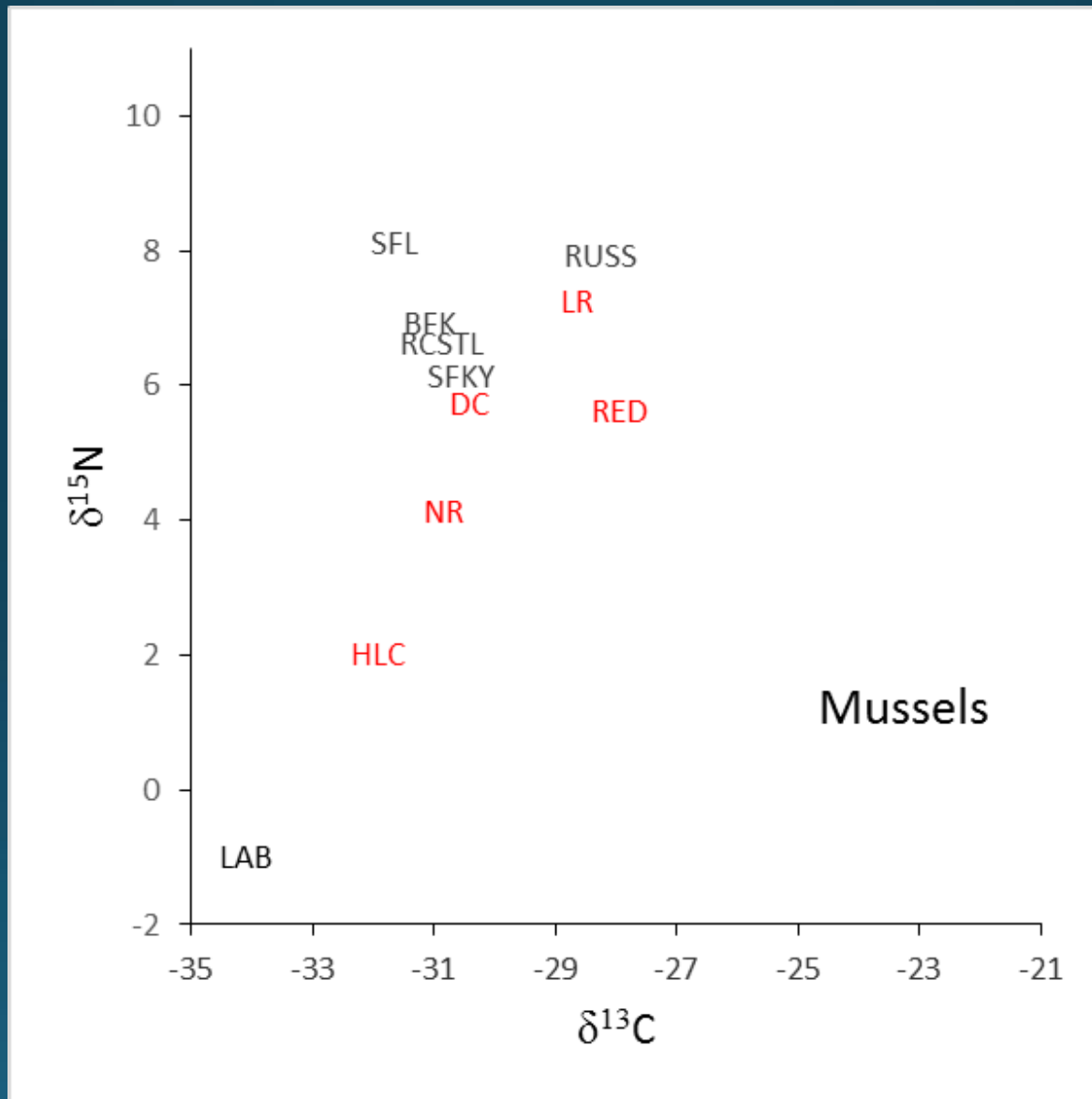
- Seven major groupings identified
- Little pattern with regard to physiography or growth



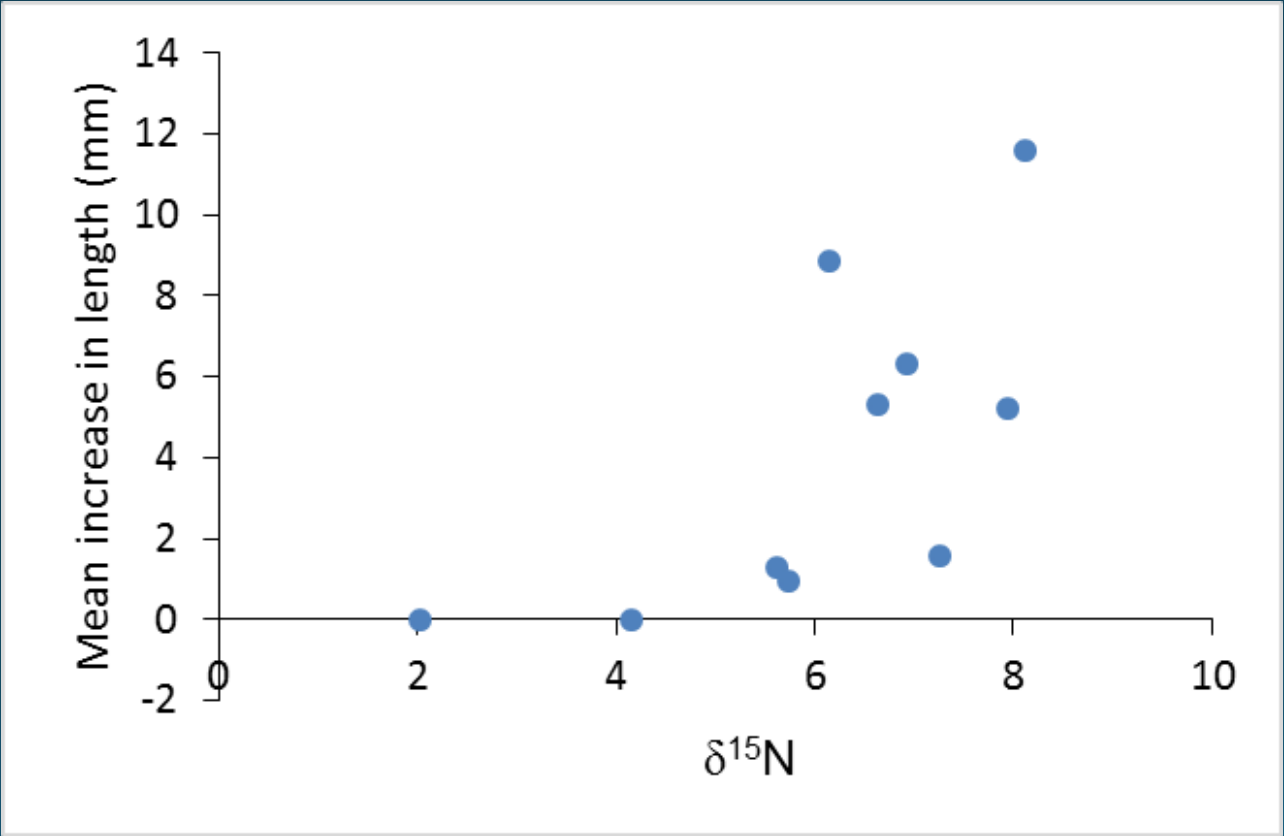
Bacteria



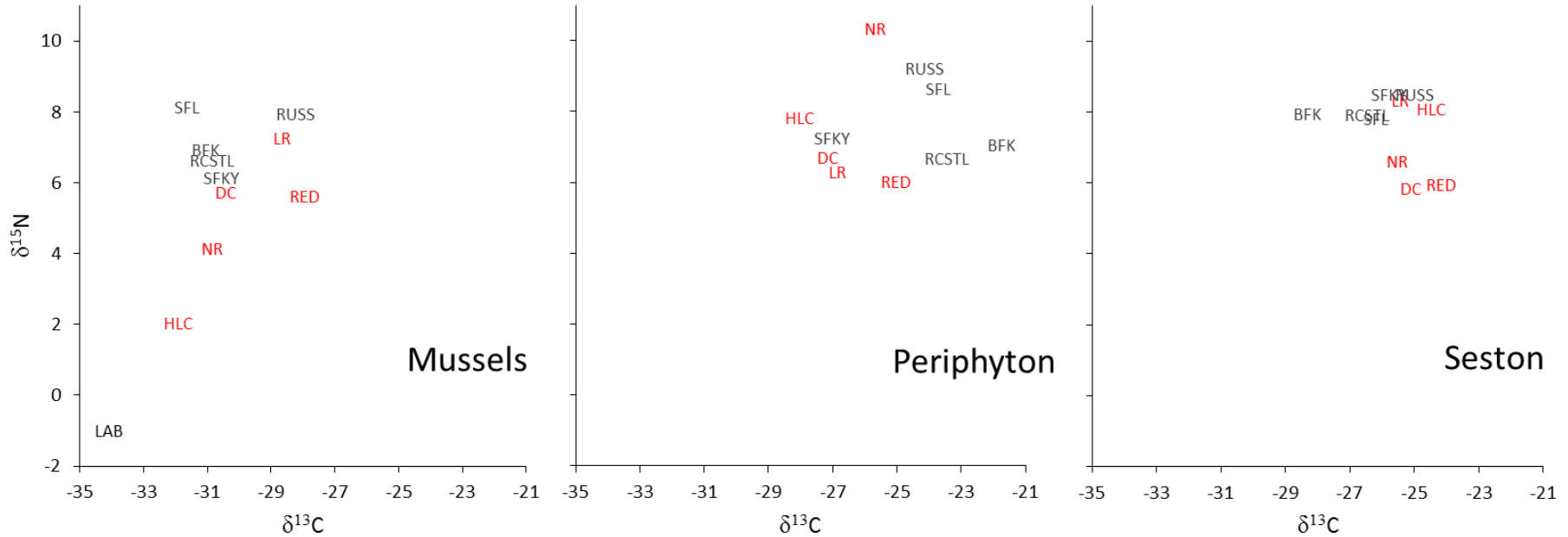
Stable isotopes



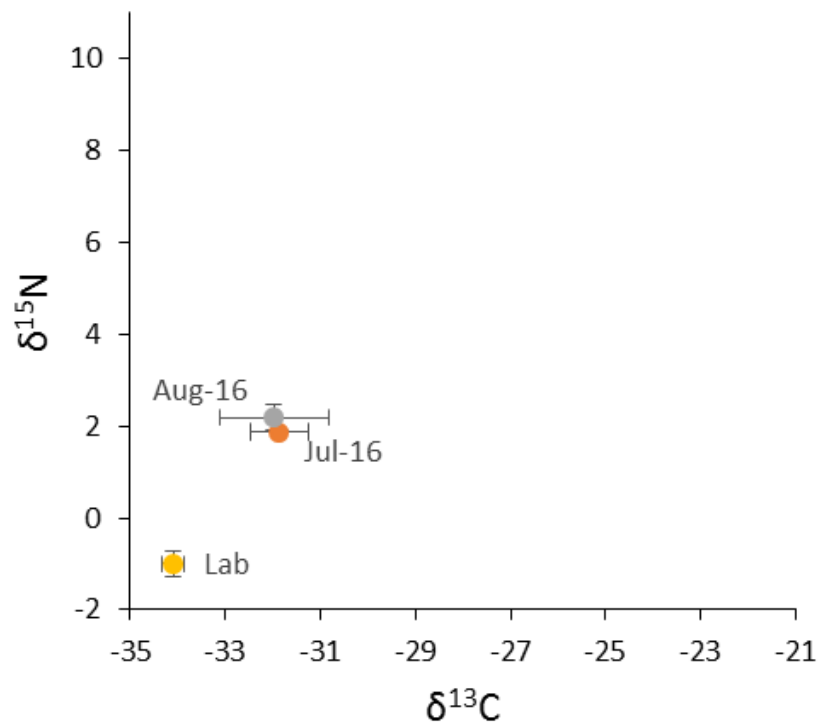
Stable isotopes



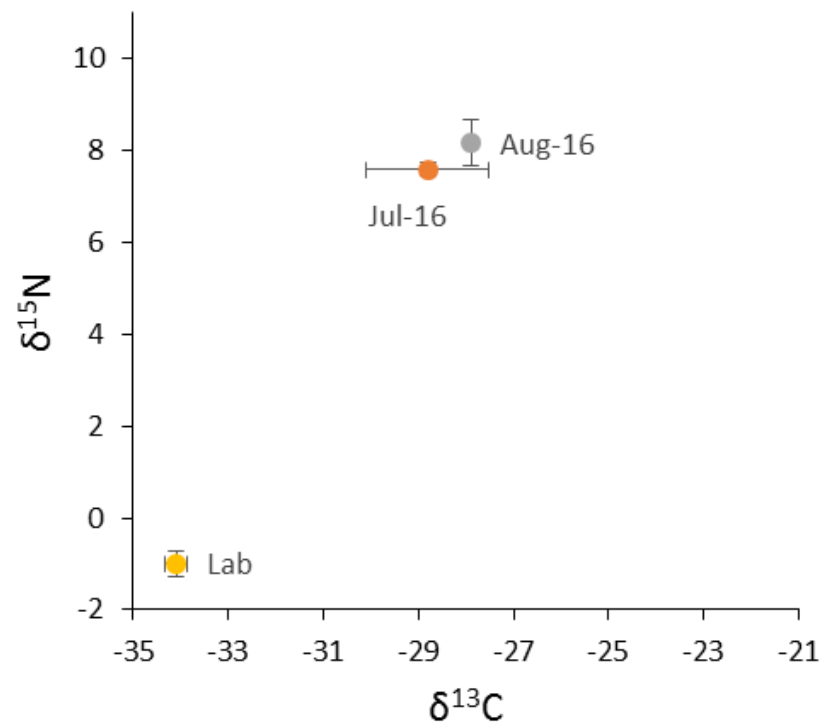
Stable isotopes



Horse Lick Creek

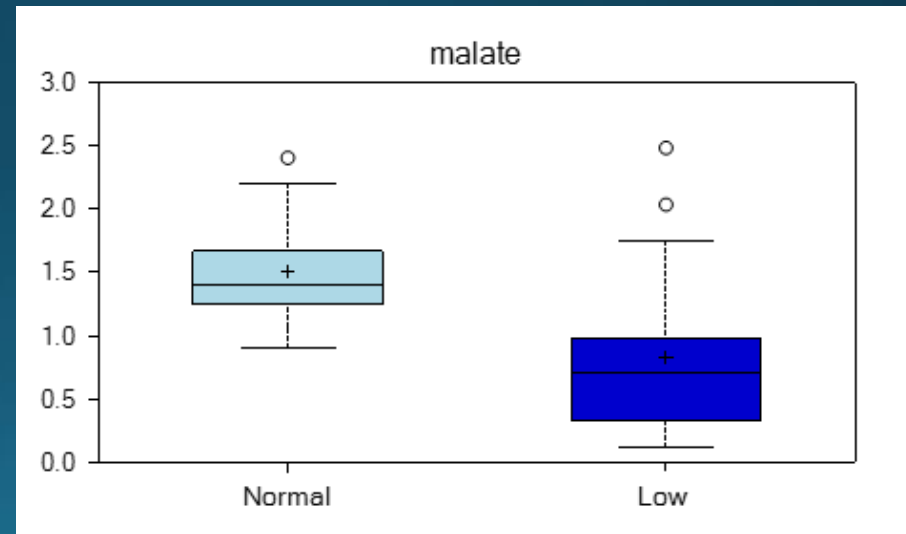
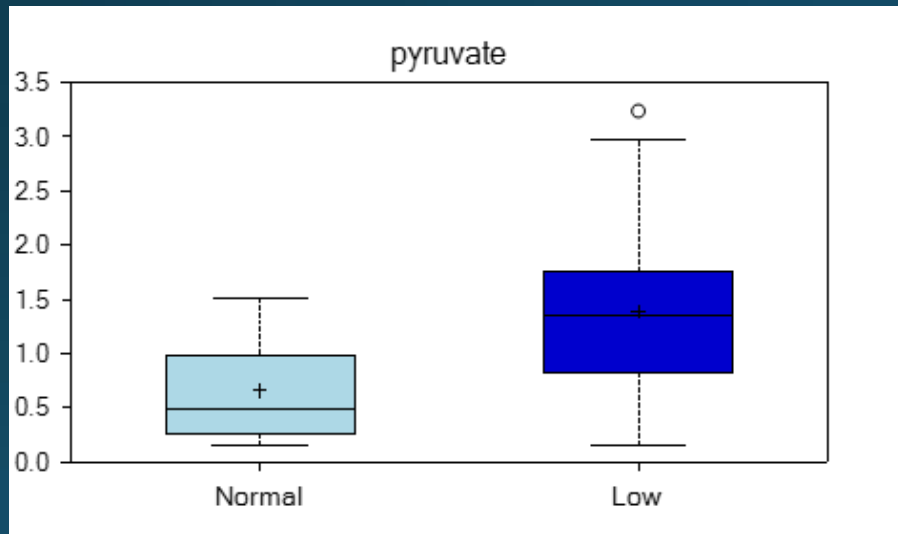


Russell Creek



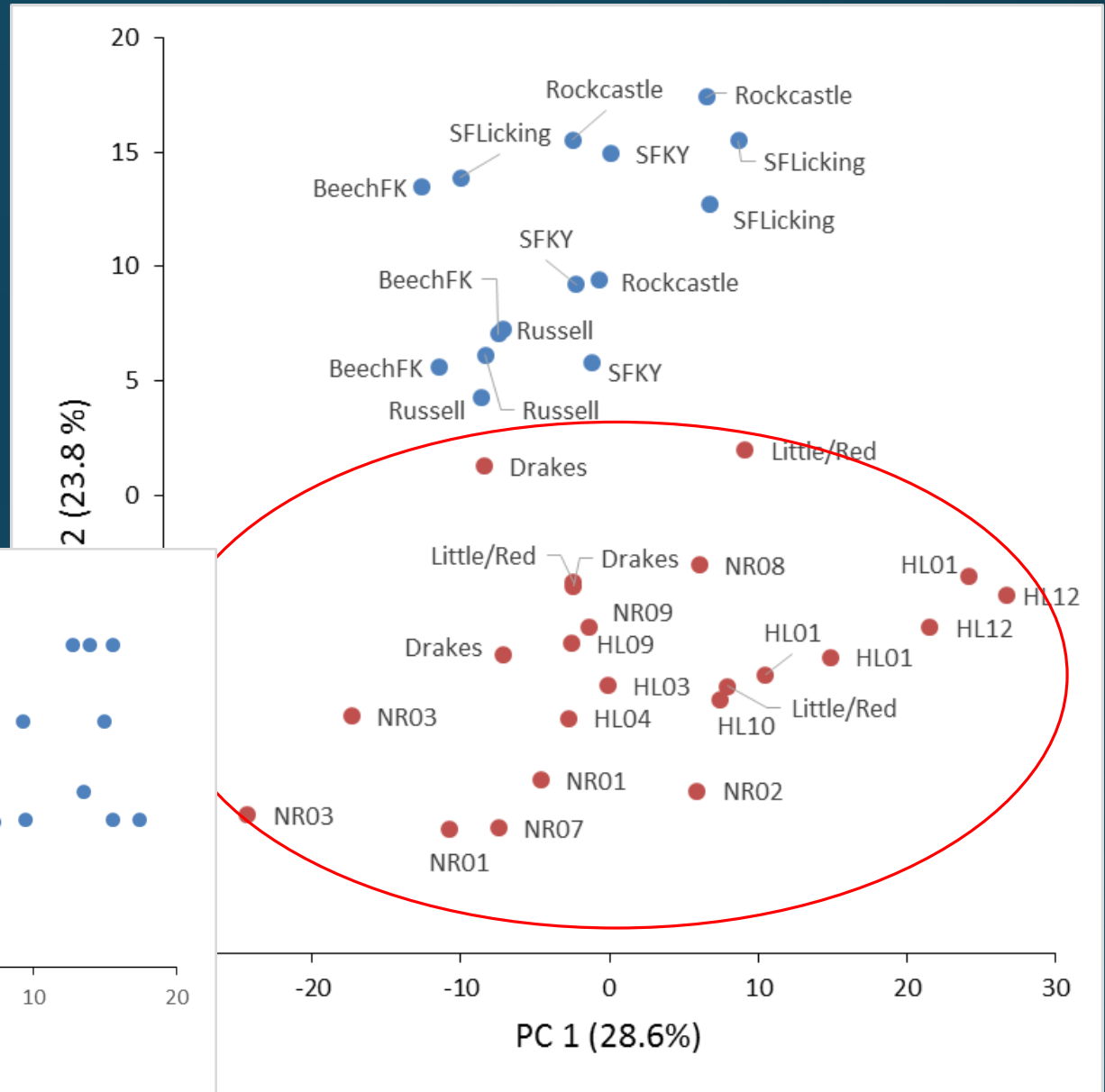
Metabolomics

- 417 biochemicals detected
- 247 significantly different between low and normal growth groups.



Metabolomics

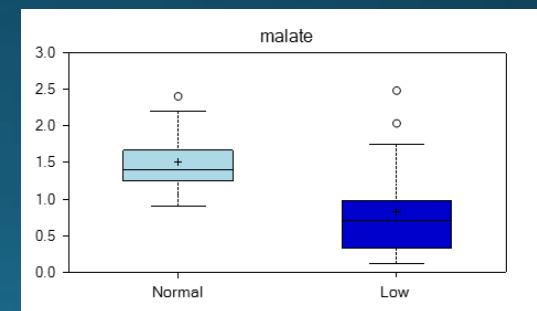
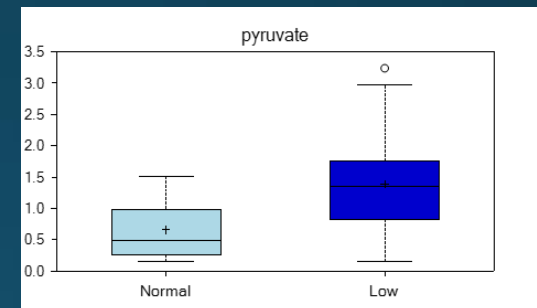
- Strong separation on PC 2
- PC 2 strongly related to growth



Metabolomics

- Biochemical patterns indicative of following characteristics of low-growth animals:
 - Decreased Krebs Cycle activity
 - Lower amino acid levels and metabolism
 - Increased fatty acid oxidation

= starvation?



Summary

- Not much evidence for major differences in food resources among streams; coarse data
- Stable isotopes: mussels in low growth streams either not obtaining or assimilating available food resources
- Starvation appears to be a consistent trait

Thanks!

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