Comparing eDNA metabarcoding and standardized electroshocking to assess fish assemblages in Texas rivers and streams

Kylie Perkins[12], Jenny Oakley[13], Erik Pilgrim[4] , Mandi Gordon[1]

[1] University of Houston – Clear Lake, Environmental Institute of Houston, Houston, TX
[2] University of Houston – Clear Lake, College of Science and Engineering, Houston, TX
[3]Houston-Galveston Area Council , Houston, TX
[4] Environmental Protection Agency, Office of Research and Development, Cincinnati, OH

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INTRODUCTION

- The Why?
  - Climate change and anthropogenic influences threaten vital freshwater resources and are causing rapid changes to these habitats.
  - Tracking widespread species assemblages regularly and easily could play an important role in future management decisions.
  - eDNA could help in those processes.

INTRODUCTION – eDNA

Mucus membrane

Blood/Injury

Scales

Predation

Excretions

Spawning

INTRODUCTION – eDNA

What?

- eDNA studies target one or a few species of interest
- eDNA metabarcoding studies take all the DNA in a sample to look at communities

Why?

- Non- invasive
- No major field equipment needed
- Detection of rare, cryptic, invasive, or endangered species

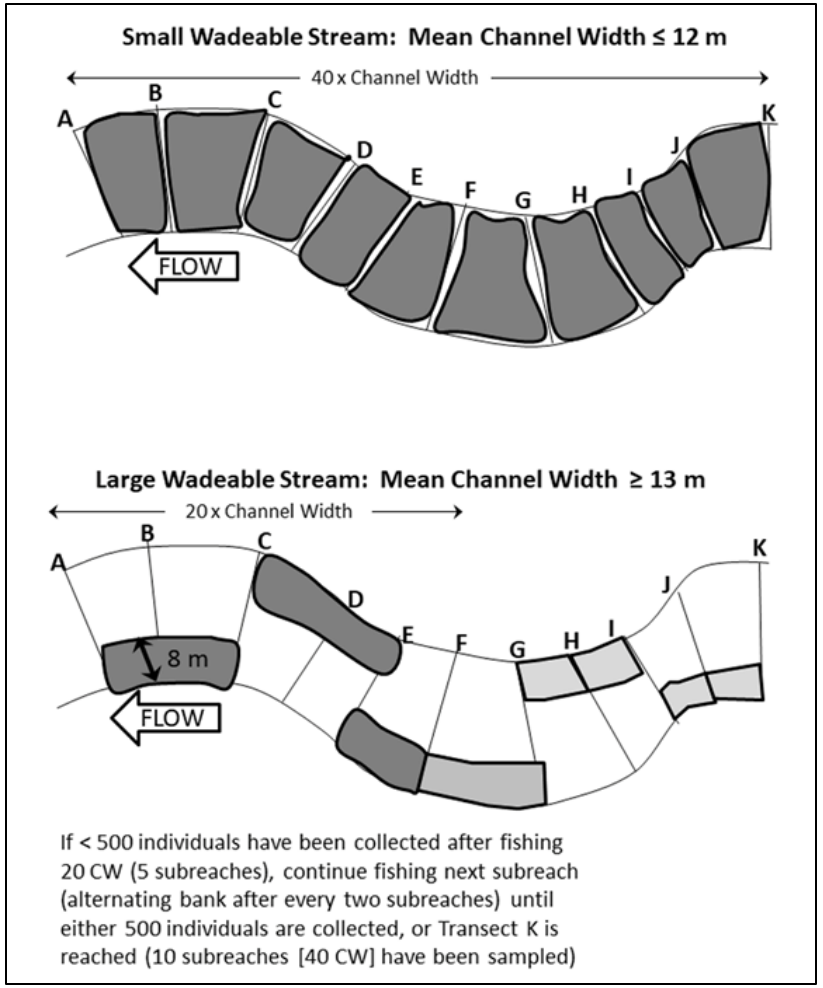
The Cons?

- The need for a genetic library (metabarcoding)
- Fish not necessarily alive and in area
- No information as to size, age, growth, population

INTRODUCTION – objectives

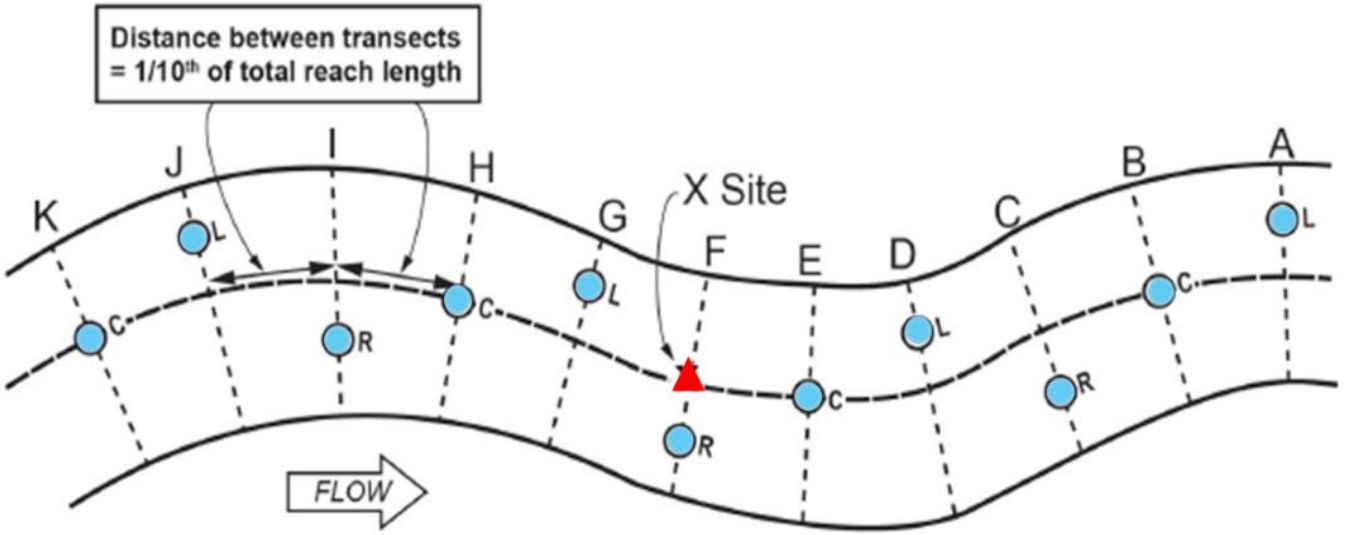
1. Describe the fish assemblages in rivers and streams of Texas
2. Compare fish assemblage results from electrofishing and eDNA metabarcoding
3. Compare the fish detections from the 12S and 16S primers
4. Compare methodology in eDNA collection

METHODS – electroshocking (wadeable)



METHODS – eDNA

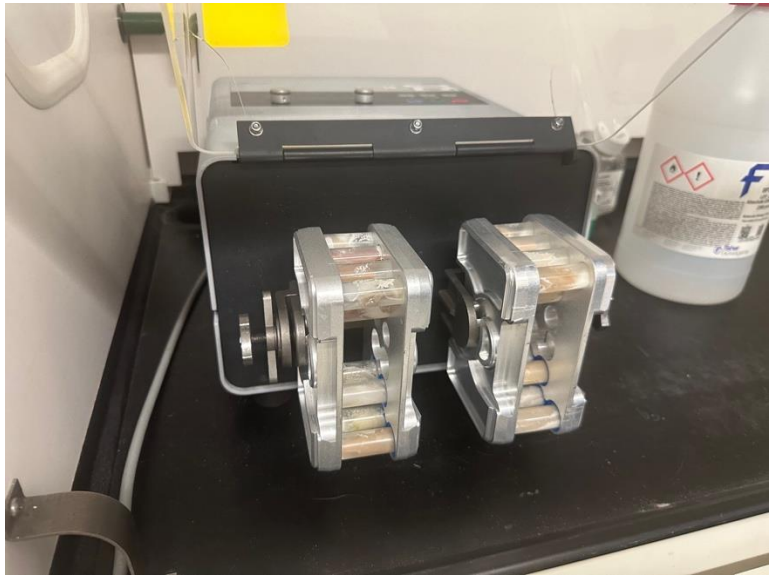
1. Collection
   - FIL – One Liter grab (red)
   - COM – Composite sample (blue)

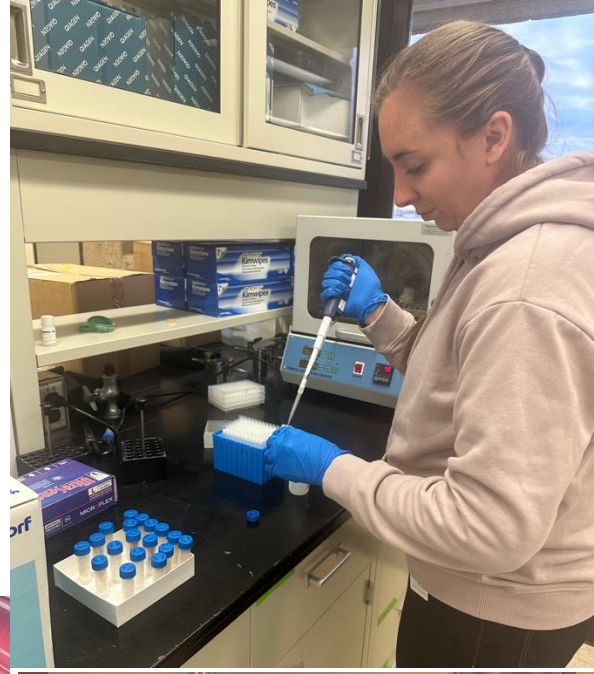


2. Filtering
   - up to 1000 mL
   - ASAP after sampling

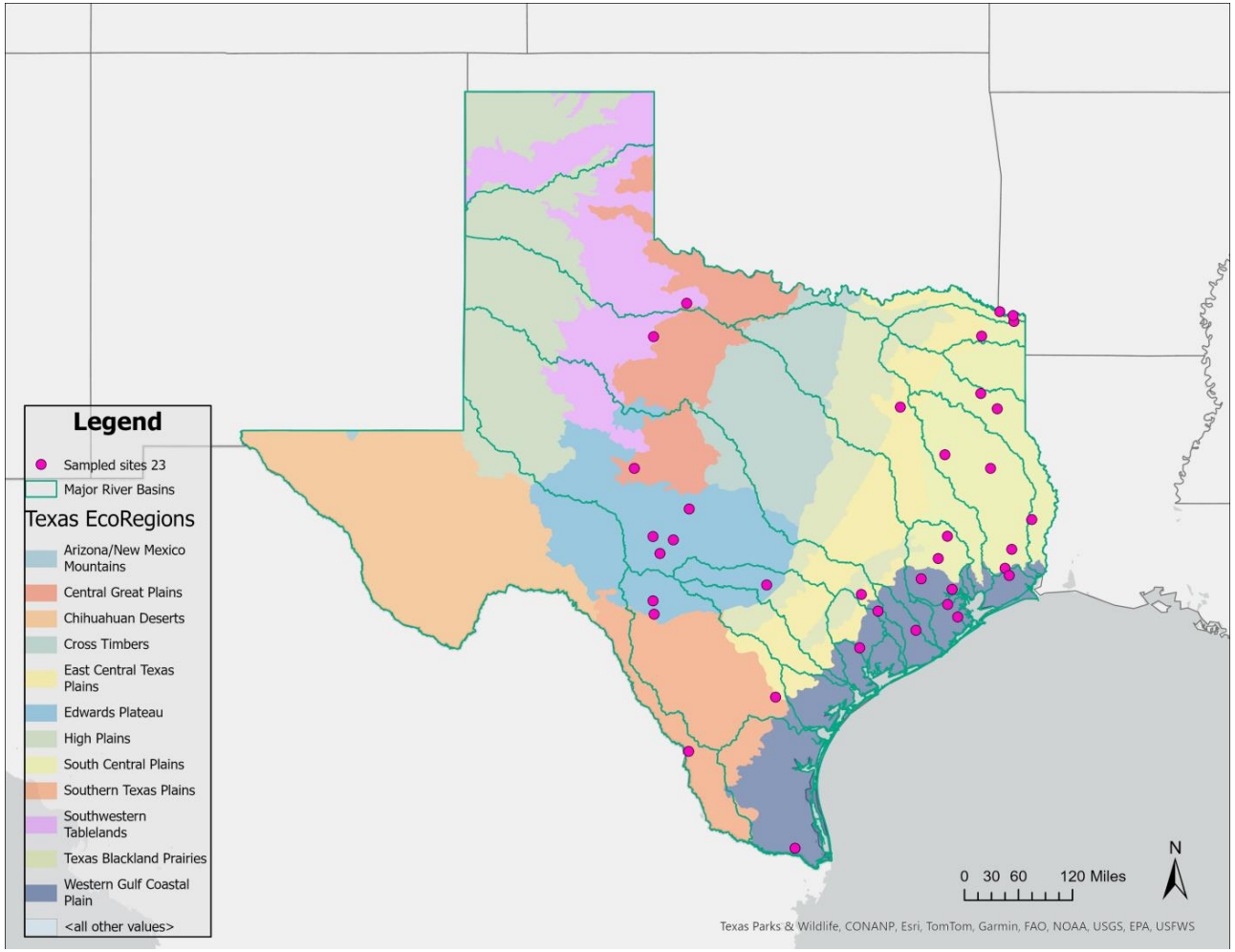
METHODS – eDNA

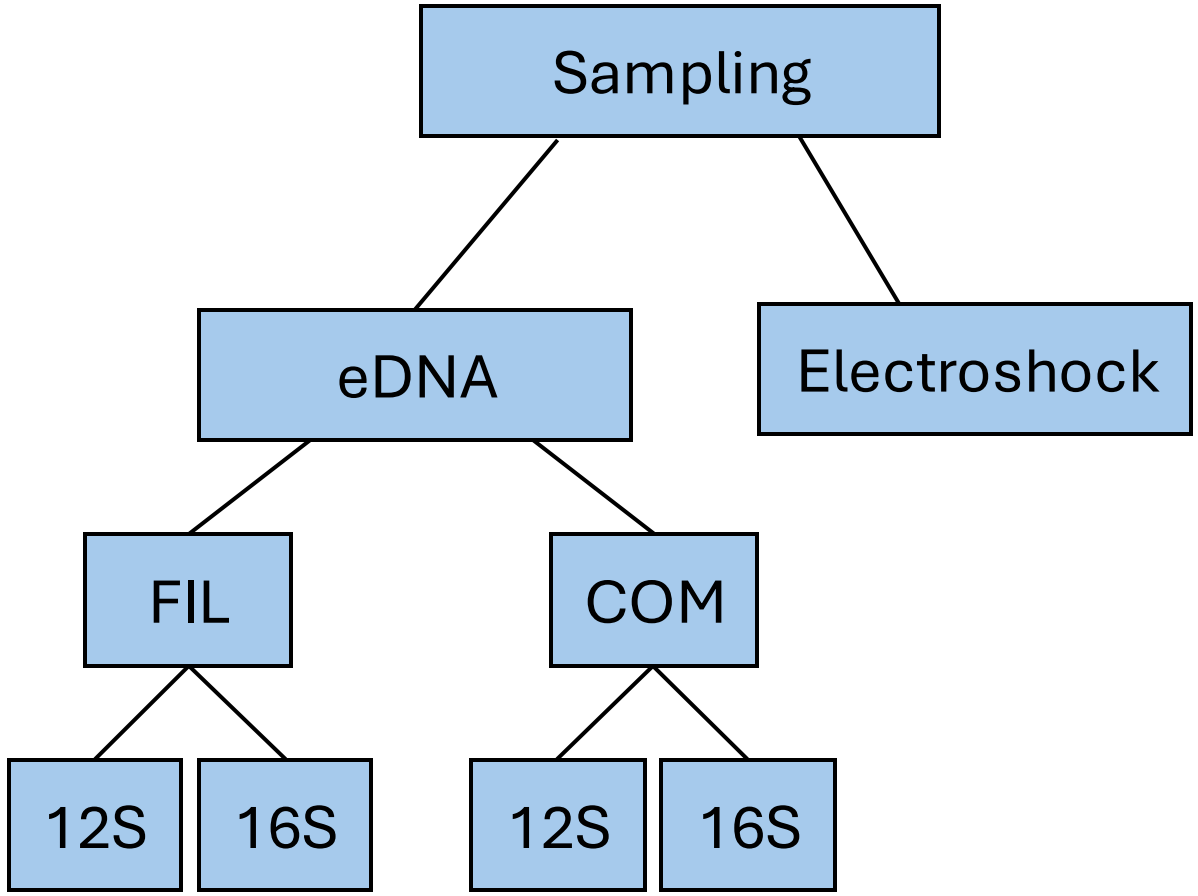
1. Collection
2. Filtering
3. Processing
   - Extraction
   - Amplification
   - Gel Electrophoresis
   - Sequencing





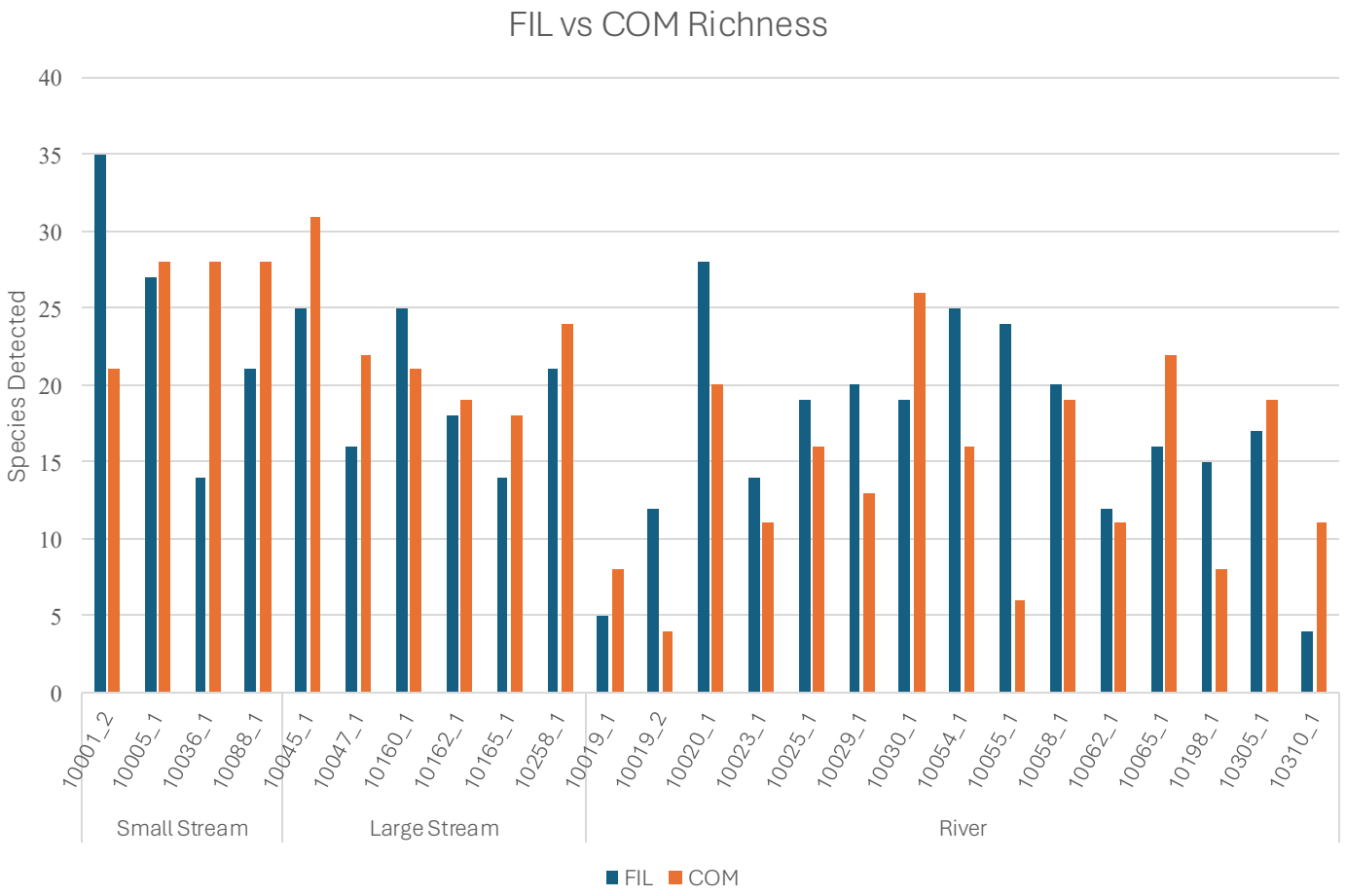
METHODS

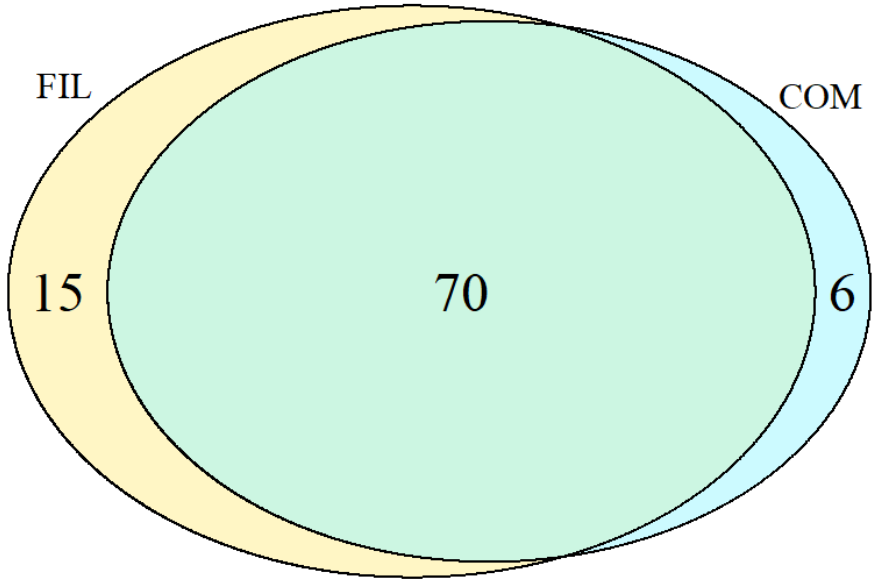




38 sampling events; 3 no eDNA results, 10 partial eDNA results, 25 all samples successful

RESULTS – FIL vs COM



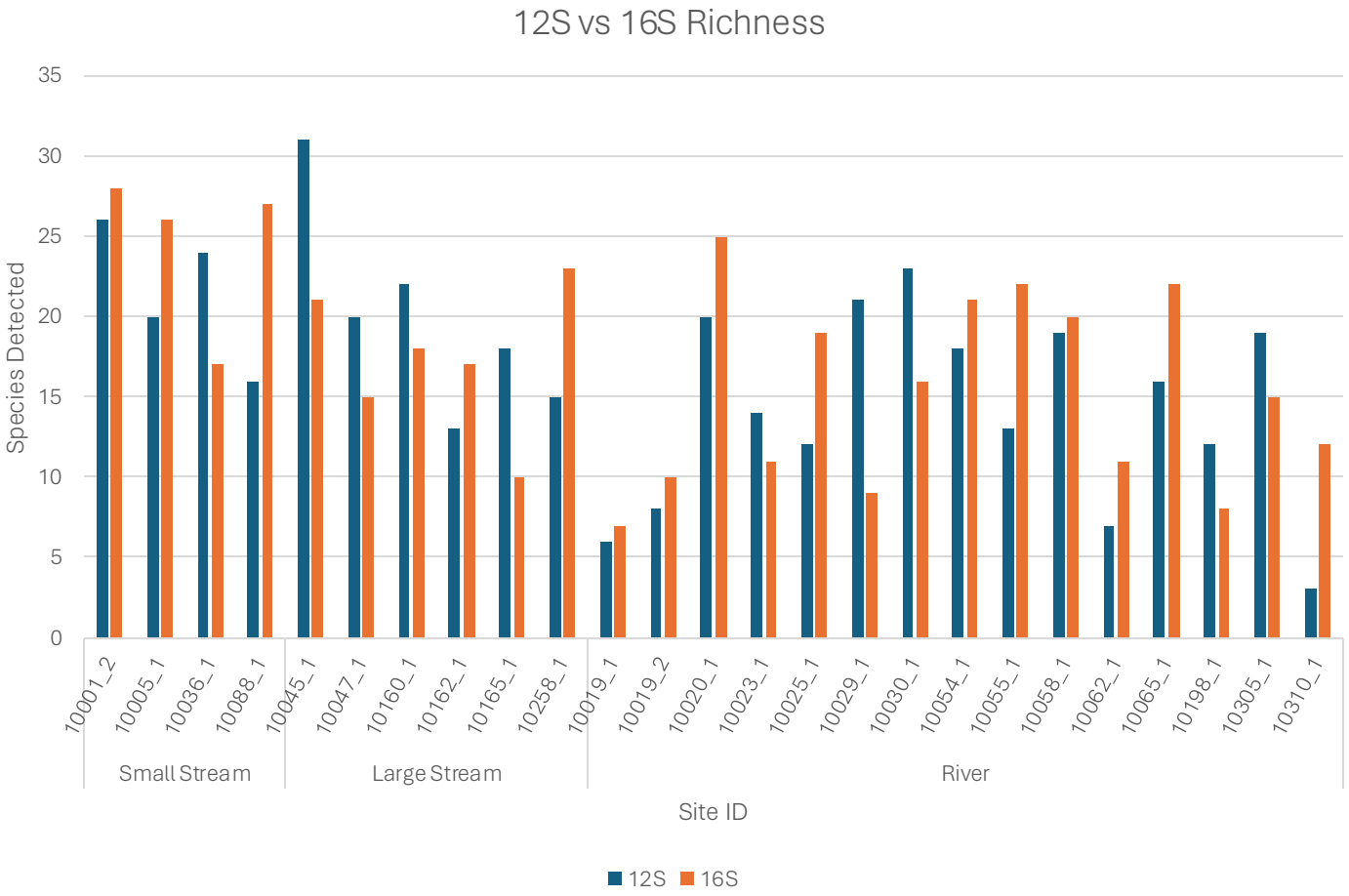


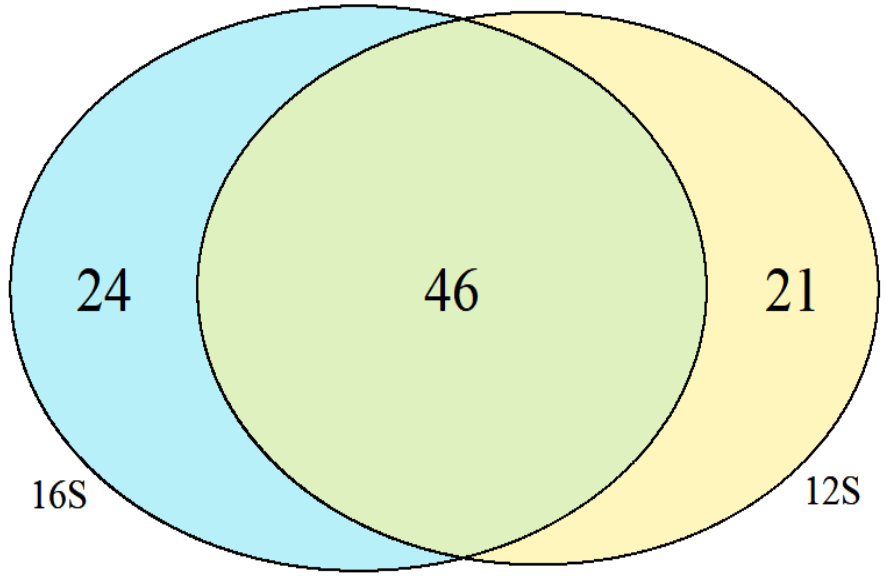
FIL = 85 species, COM = 76 species
91 Species total

COM = 13 sites higher richness, FIL = 12 sites higher richness
Paired t-test p-value = 0.6727

One-way ANOSIM p-value = 0.964

RESULTS – 12S vs 16S

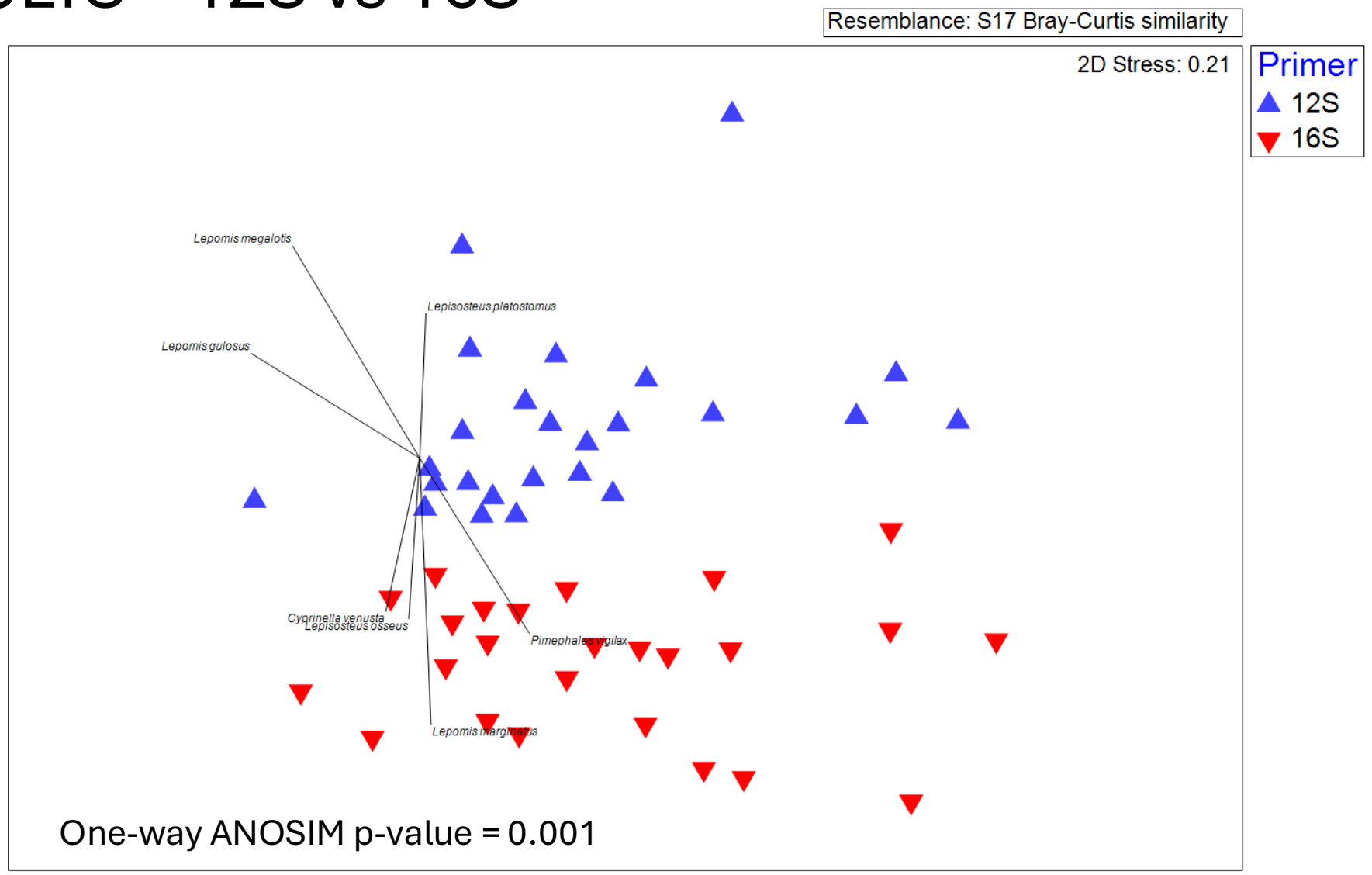




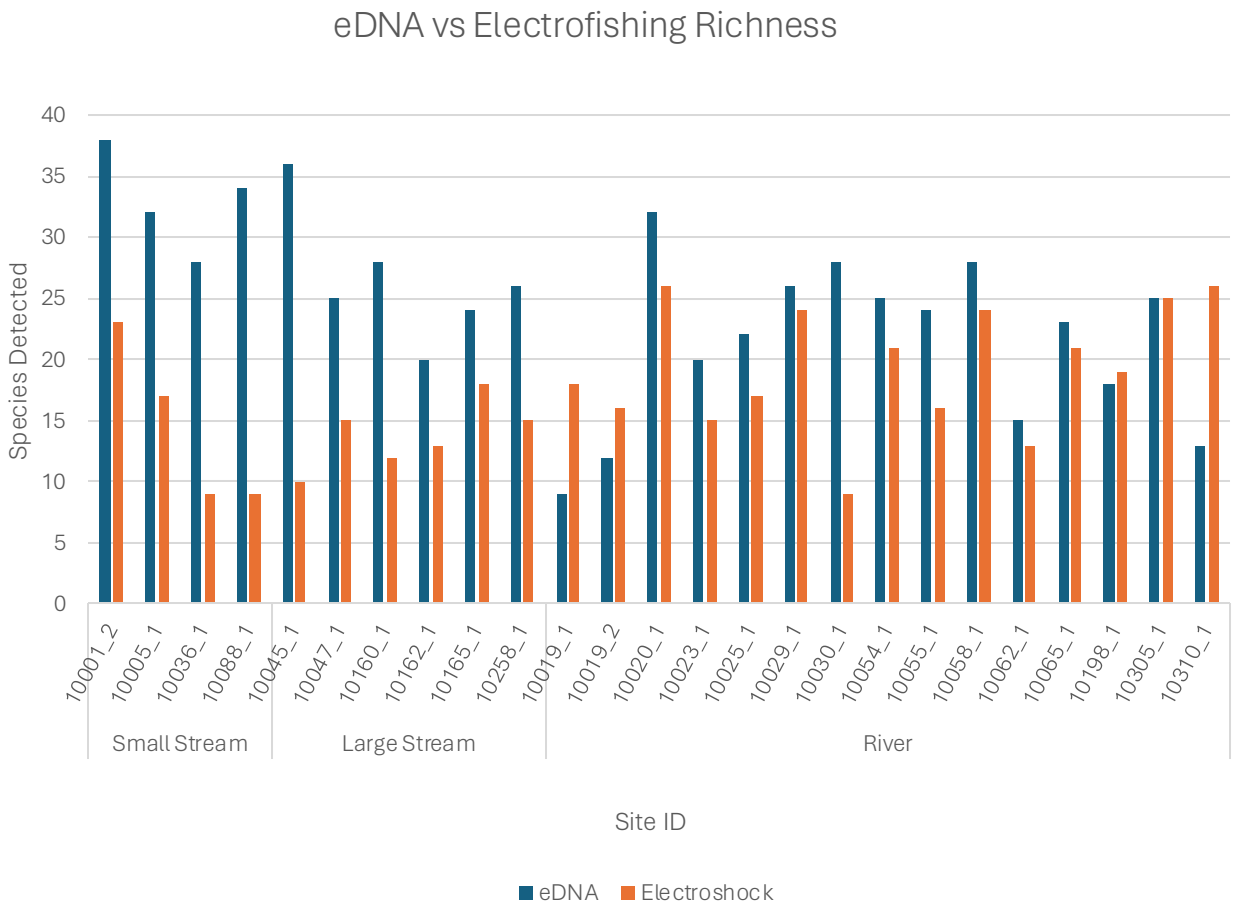
16S = 70 species, 12S = 67 species
91 Species total

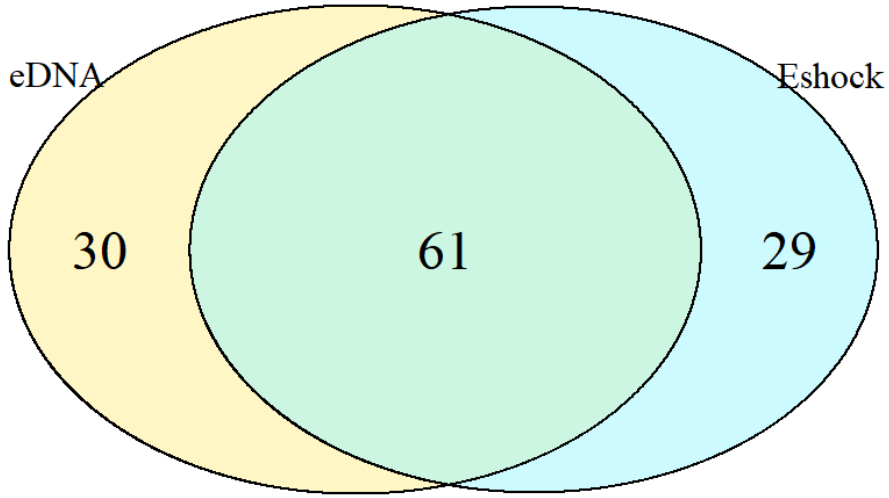
Paired t-test p-value = 0.672

RESULTS – 12S vs 16S *Non-metric MDS*



RESULTS – eDNA vs electroshocking

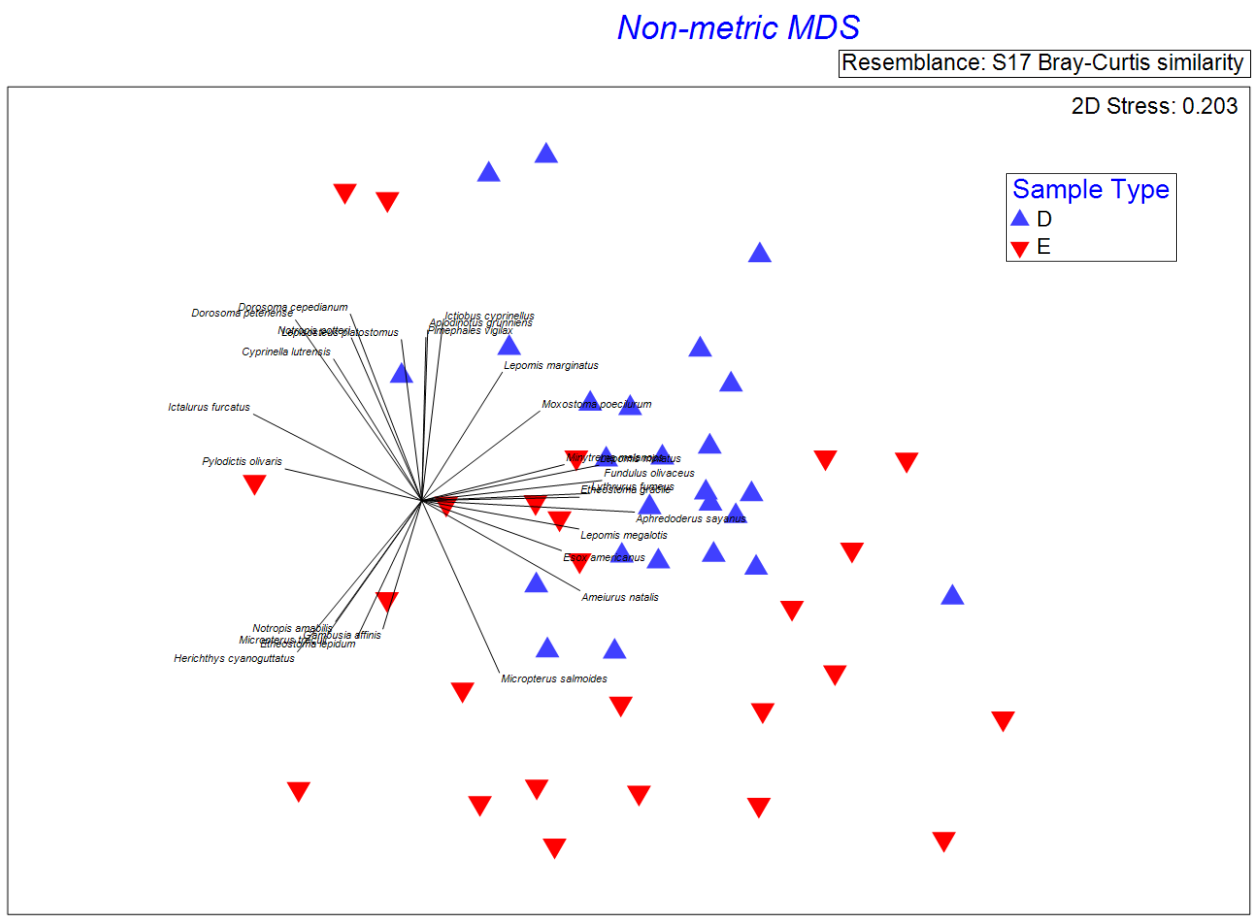


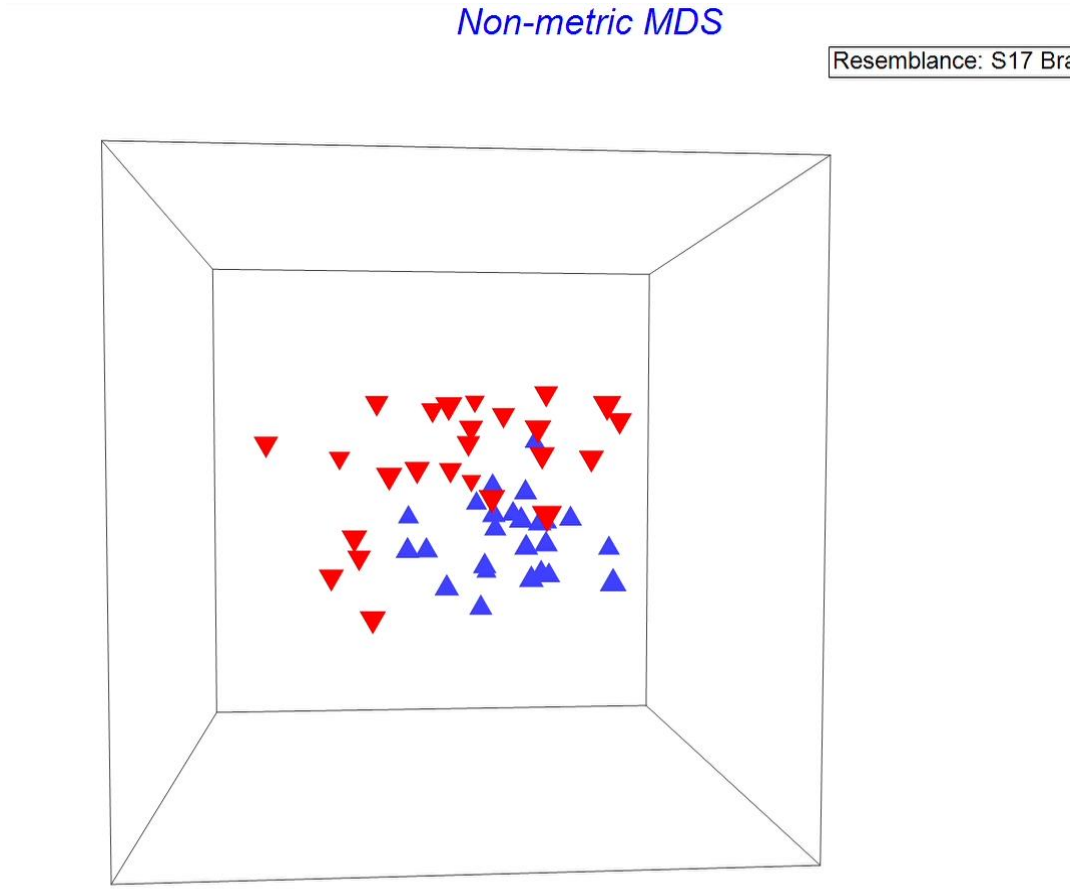


eDNA= 91 species, eShock = 90 species
120 species total

Paired t-test p-value = 0.00096

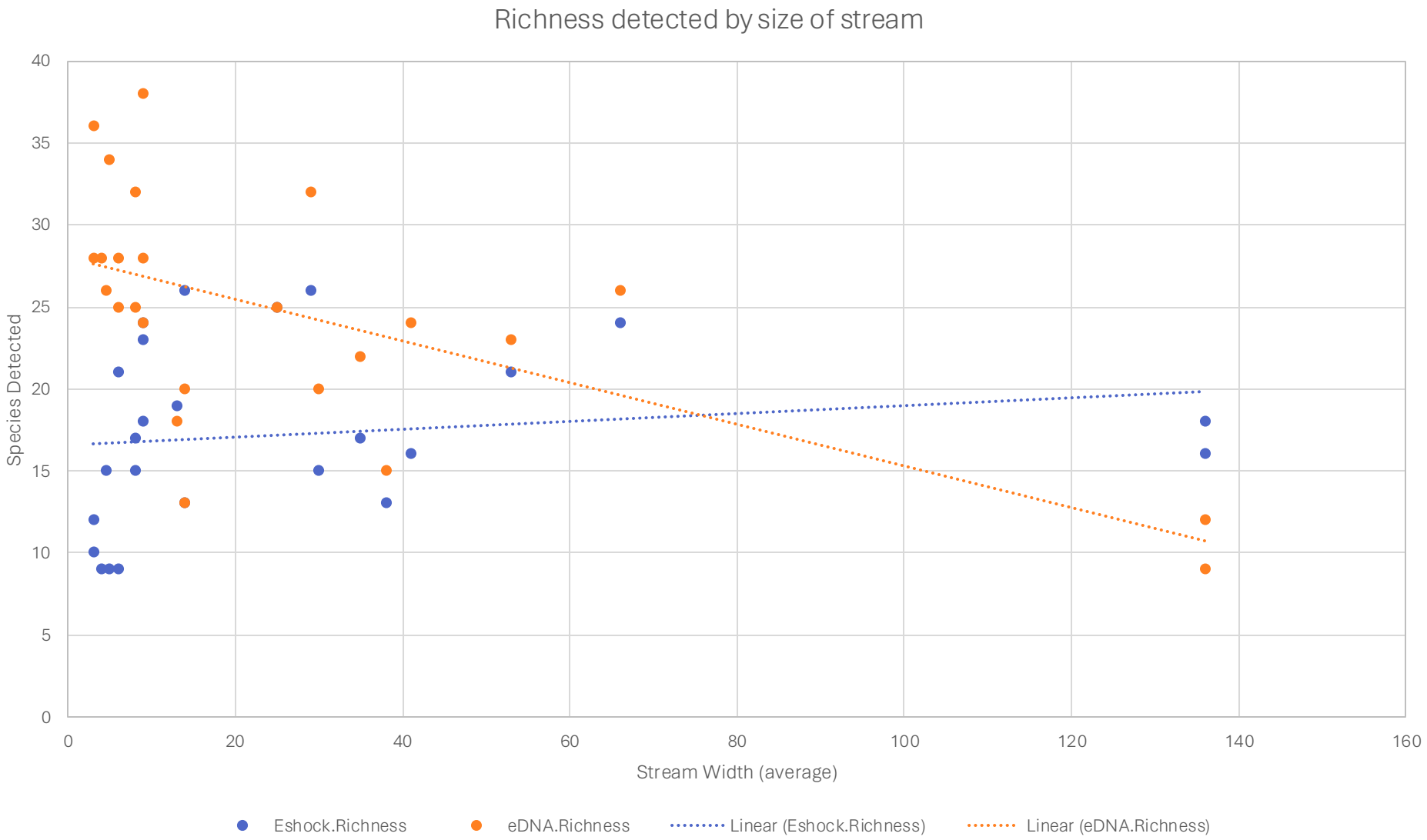
RESULTS – eDNA vs electroshocking





One-way ANOSIM p-value: 0.0001

RESULTS – sites and eDNA detection



Linear Regression

eShock p-value

0.435969

eDNA p-value

0.000636

DISCUSSION

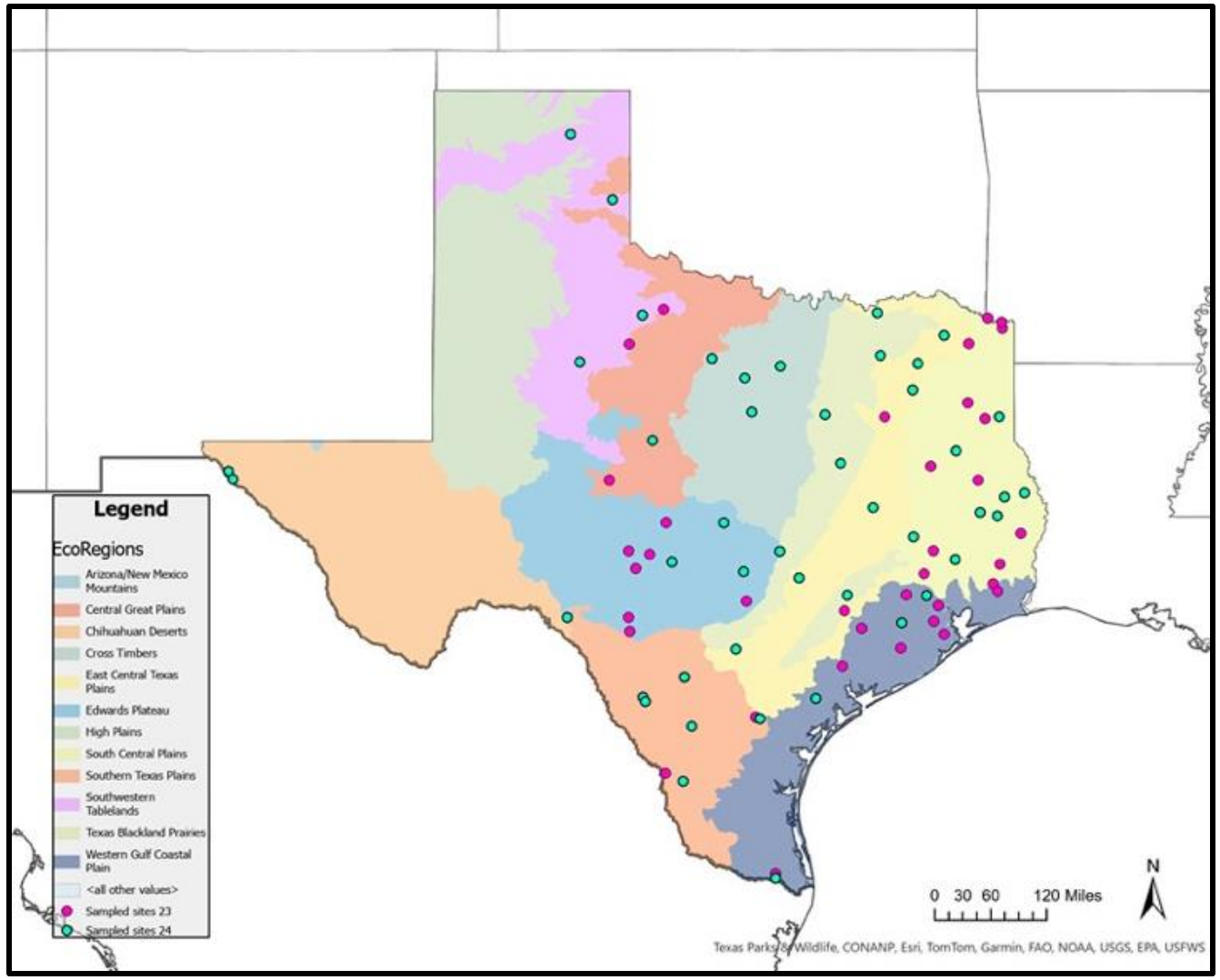
- FIL vs COM
  - It is unnecessary to collect the sample across the reach.
  - Having multiple samples; however, was useful in detecting more species.
- 12S vs 16S
  - Using multiple primers helps to detect more species and reduce biases that may occur with one.
- eDNA vs electroshocking
  - eDNA has repeatedly detected more species than traditional methods across studies.
  - This study found that eDNA did not detect more species in large rivers but was complementary.

DISCUSSION and CONCLUSION

- Each method has limitations and the addition of eDNA will help better study fish assemblages
- eDNA metabarcoding will need a lot more work done with completing genomic libraries before these studies can be widely used.

CONCLUSION – next steps

- Samples from an additional 47 sampling events
  - Greater sample sizes
  - Better spread of sites and site types
- Completion of genetic library for Texas fishes



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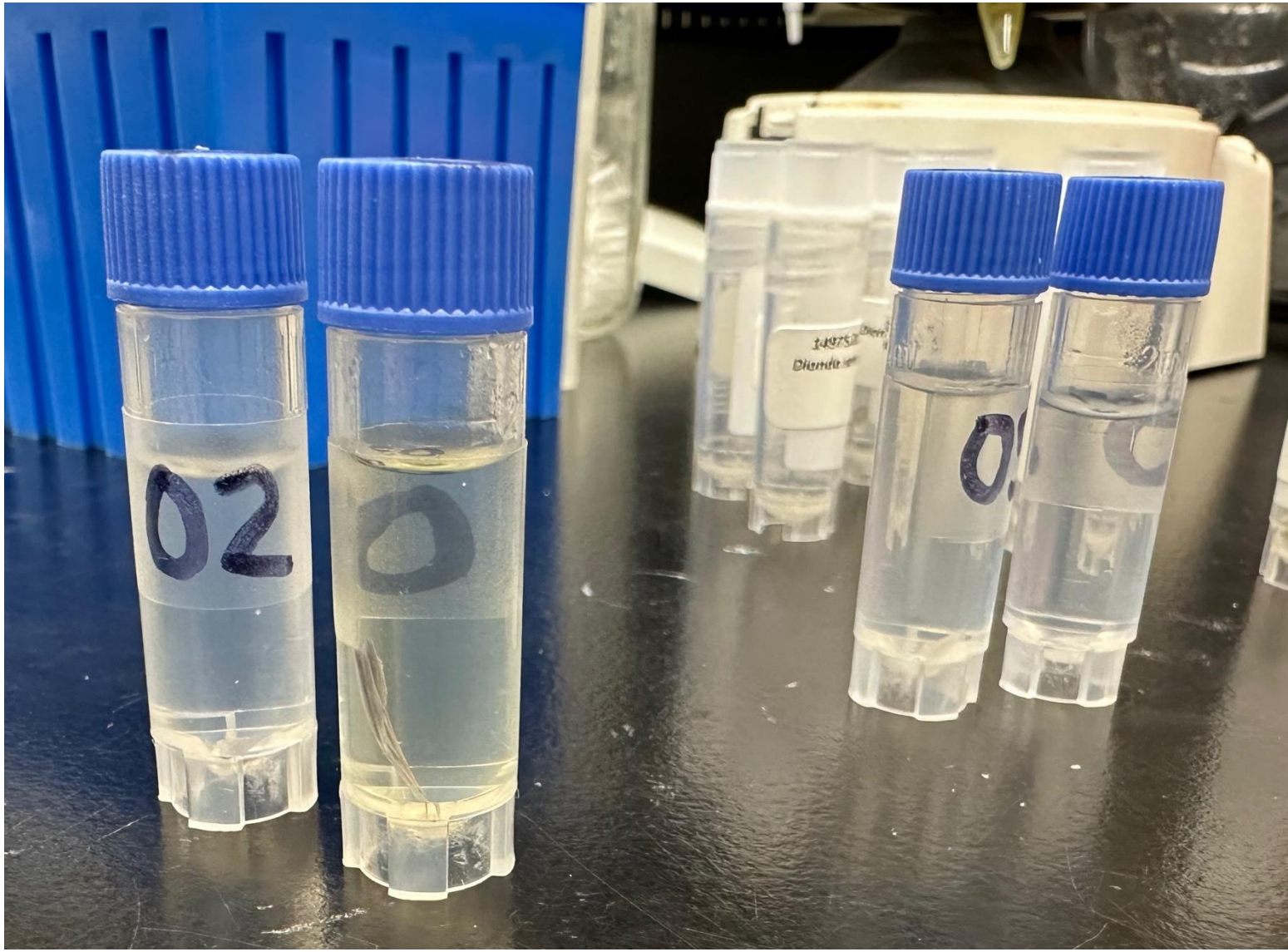

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Questions