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# Using eDNA metabarcoding to assess fish assemblages in the rivers and streams of Texas

Kylie Perkins<sup>1,2</sup>, Jenny Oakley<sup>1</sup>, Erik Pilgrim<sup>3</sup>

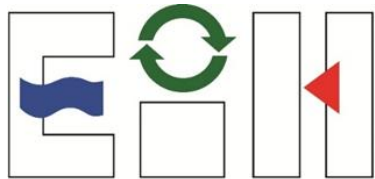
<sup>1</sup> University of Houston – Clear Lake, Environmental Institute of Houston, Houston, TX

<sup>2</sup> University of Houston – Clear Lake, College of Science and Engineering, Houston, TX

<sup>3</sup> Environmental Protection Agency, Office of Research and Development, Cincinnati, OH



University  
of Houston  
Clear Lake



Environmental Institute of Houston

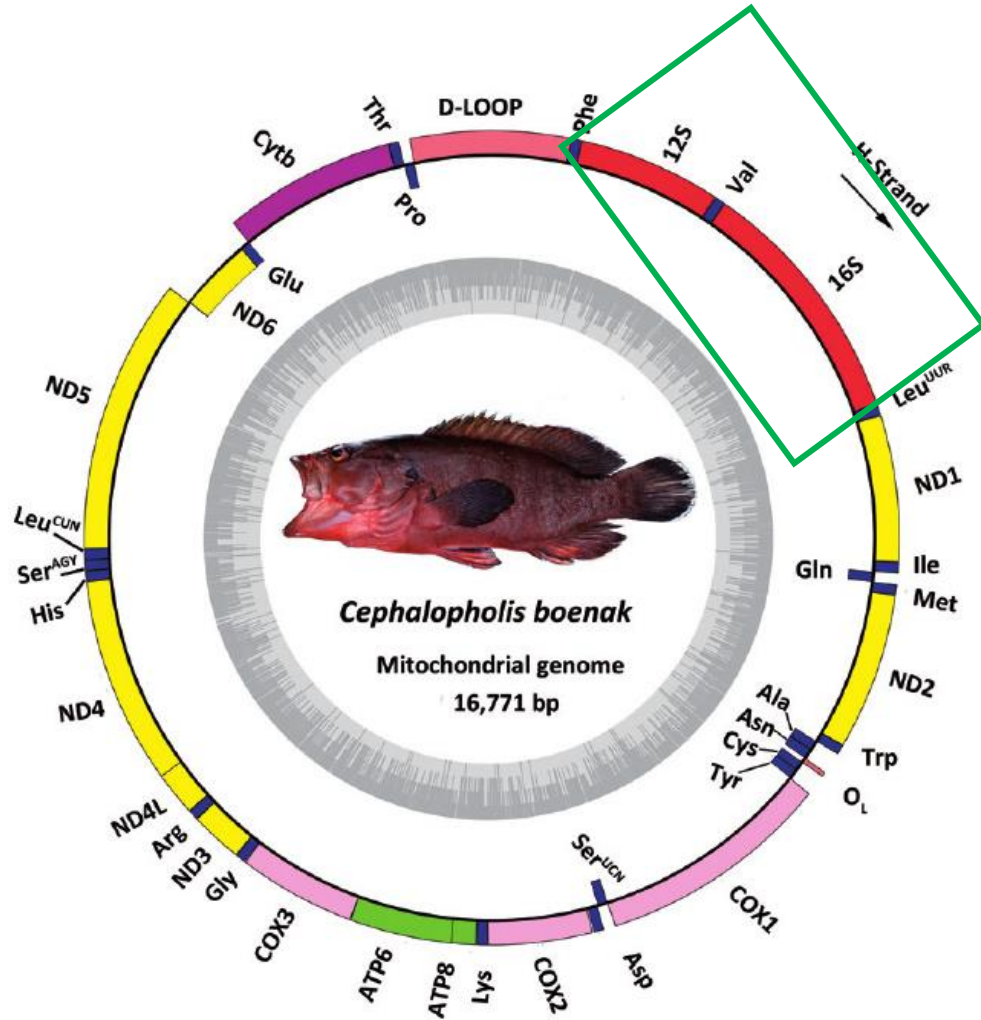
Texas Chapter of the American Fisheries Society  
Nacogdoches, TX  
February 23, 2024



eDNA – What is it?



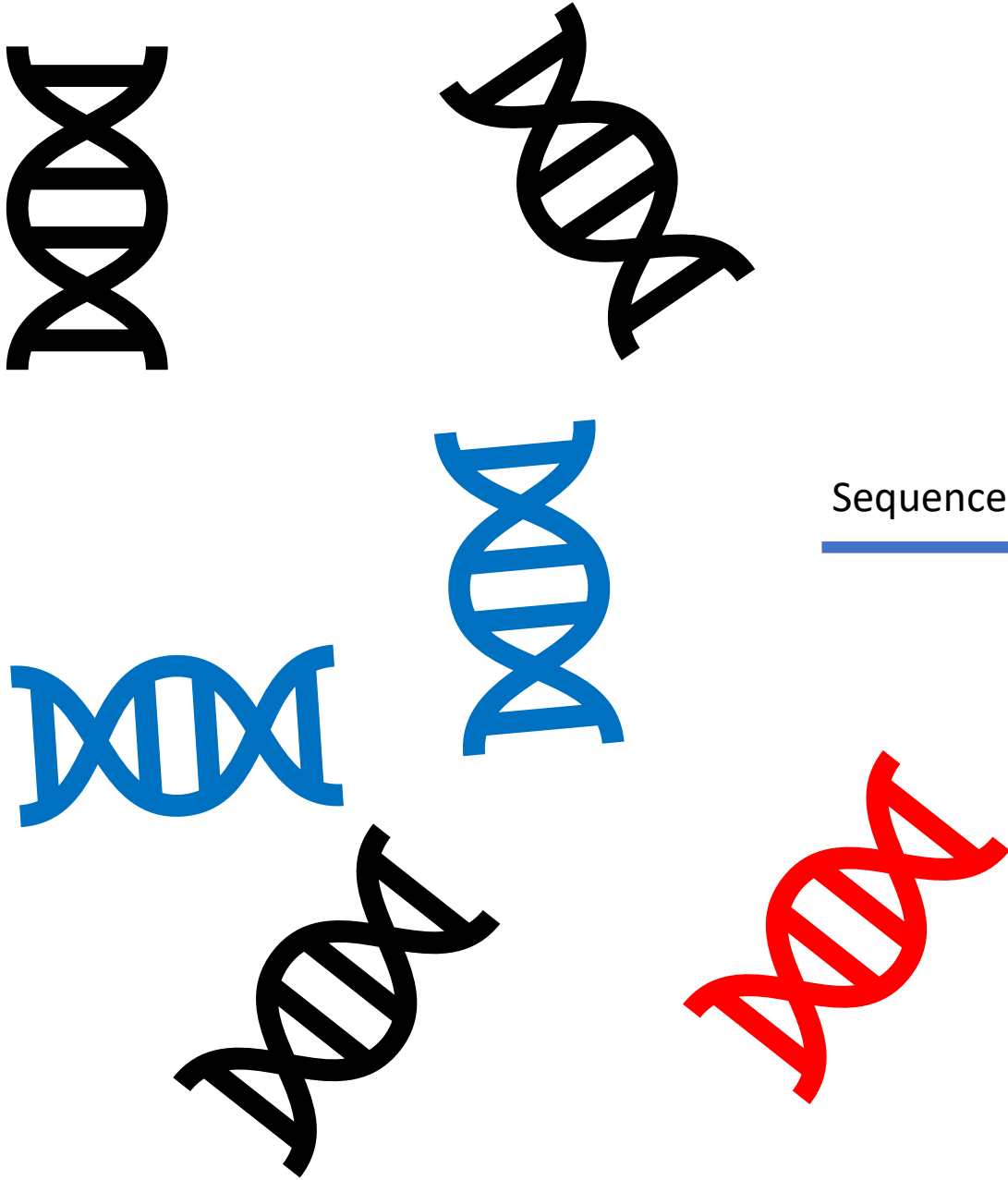
# eDNA Metabarcoding



Primers

A black arrow pointing from the large DNA structure to the smaller DNA structure, indicating the process of PCR amplification using primers.





Read count	Fish
1	Red fish
2	Blue Fish
3	Black Fish

# Pros and Cons of eDNA metabarcoding

Pros	Cons
<p>Minimally-invasive</p> <p>Cheaper than traditional methods – equipment, labor, time</p> <p>Detecting of rare or cryptic species</p> <p>May reduce bias with other methods: mesh size, net size, fish physiology, habitat</p>	<p>Many sensitive steps</p> <p>Cross contamination of samples</p> <p>Unknowns with persistence of DNA and environment</p> <p>Contamination from other sources</p> <p>*Need a complete genetic database</p>

# Motivation

Habitats are degrading and changing quickly.

Tracking widespread species assemblages regularly, and easily could play an important role in future management decisions.

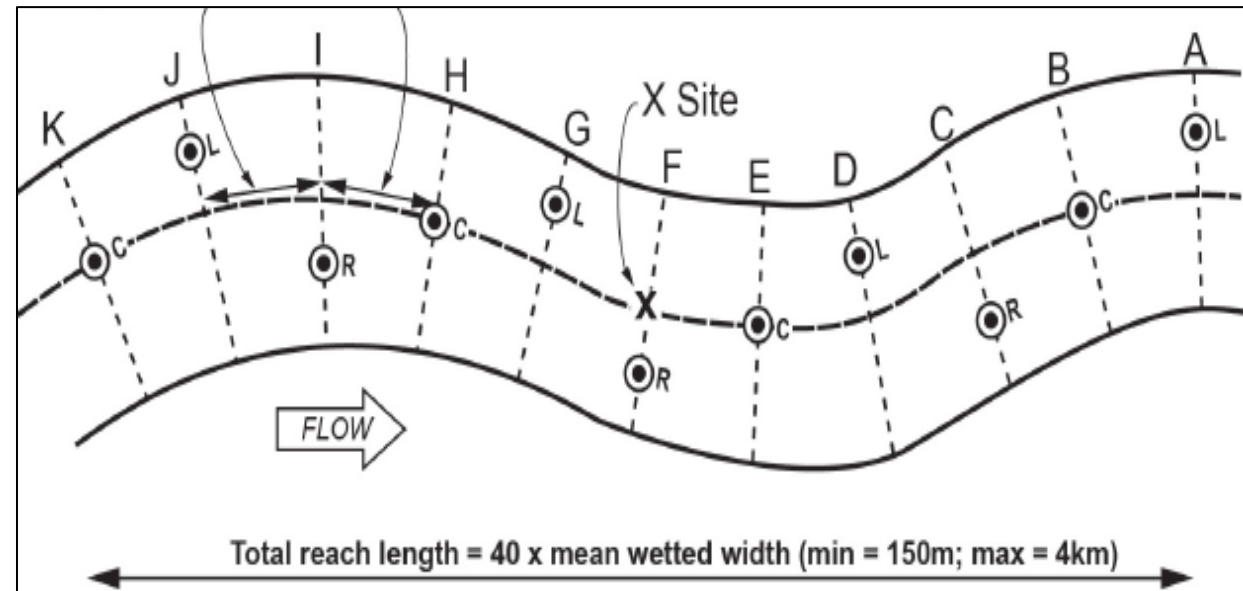
eDNA could help in those processes.



# Study Design

Follows the EPA's National Rivers and Streams Assessment standards.

- Rapid assessment
  - Involves collection of data for environmental conditions, habitat within stream and riparian zones, and general stream measurements
- Random sites (80+)
  - Small Streams
  - Large Streams
  - Rivers





# Traditional Methods

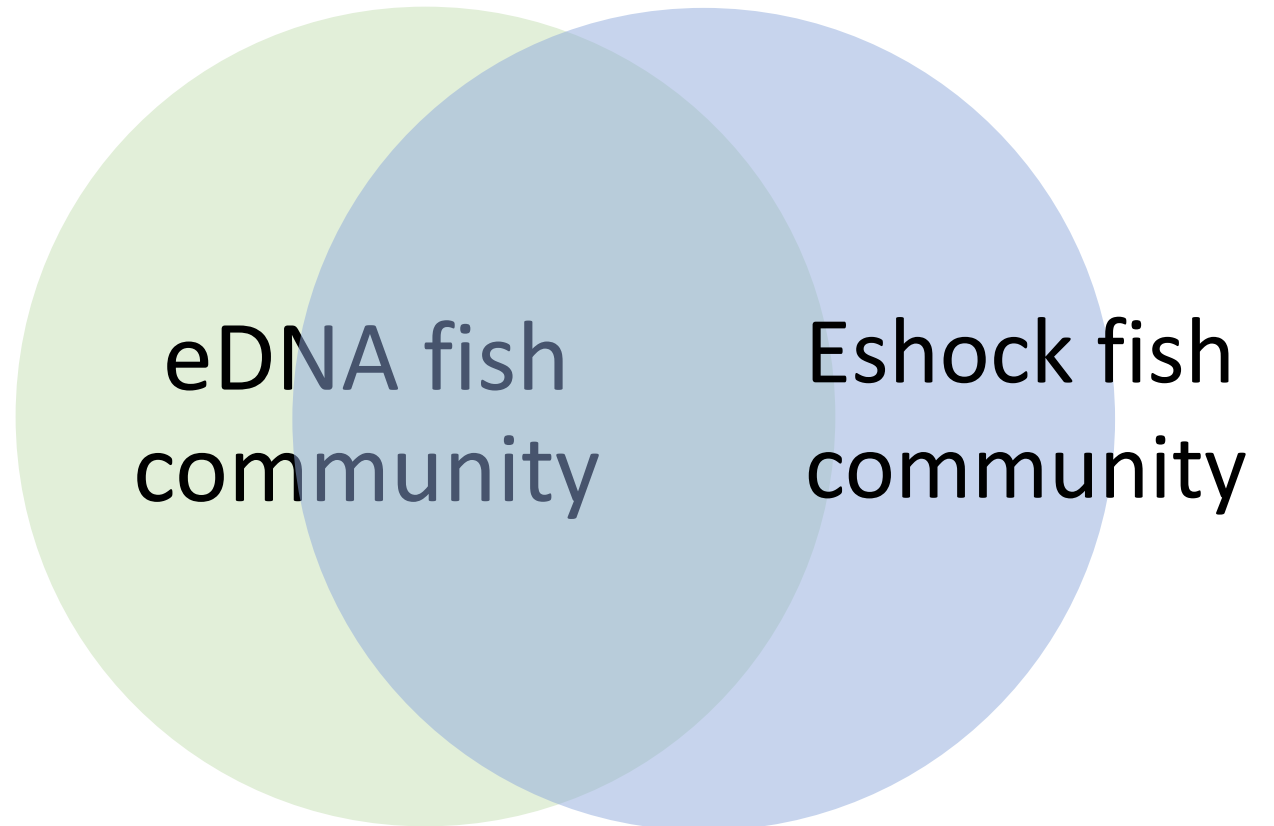
- Electrofishing

Pros	Cons
Compare data	Time intensive
Data on individual fish	Invasive to the ecosystem
Abundance and diversity data	Highly skilled crew



# Study Snapshot

1. Take water samples for eDNA
2. Collect fish data via electroshocking
3. Compare the results



# Objectives

- Compare fish assemblage from eDNA metabarcoding to fish assemblage from electroshocking
- Discover efficacy of using eDNA across a wide variety of stream/river sizes and classes, watersheds, substrate types, and other environmental variables
- Compare methods of eDNA collection and processing to retrieve the most DNA

# Sites

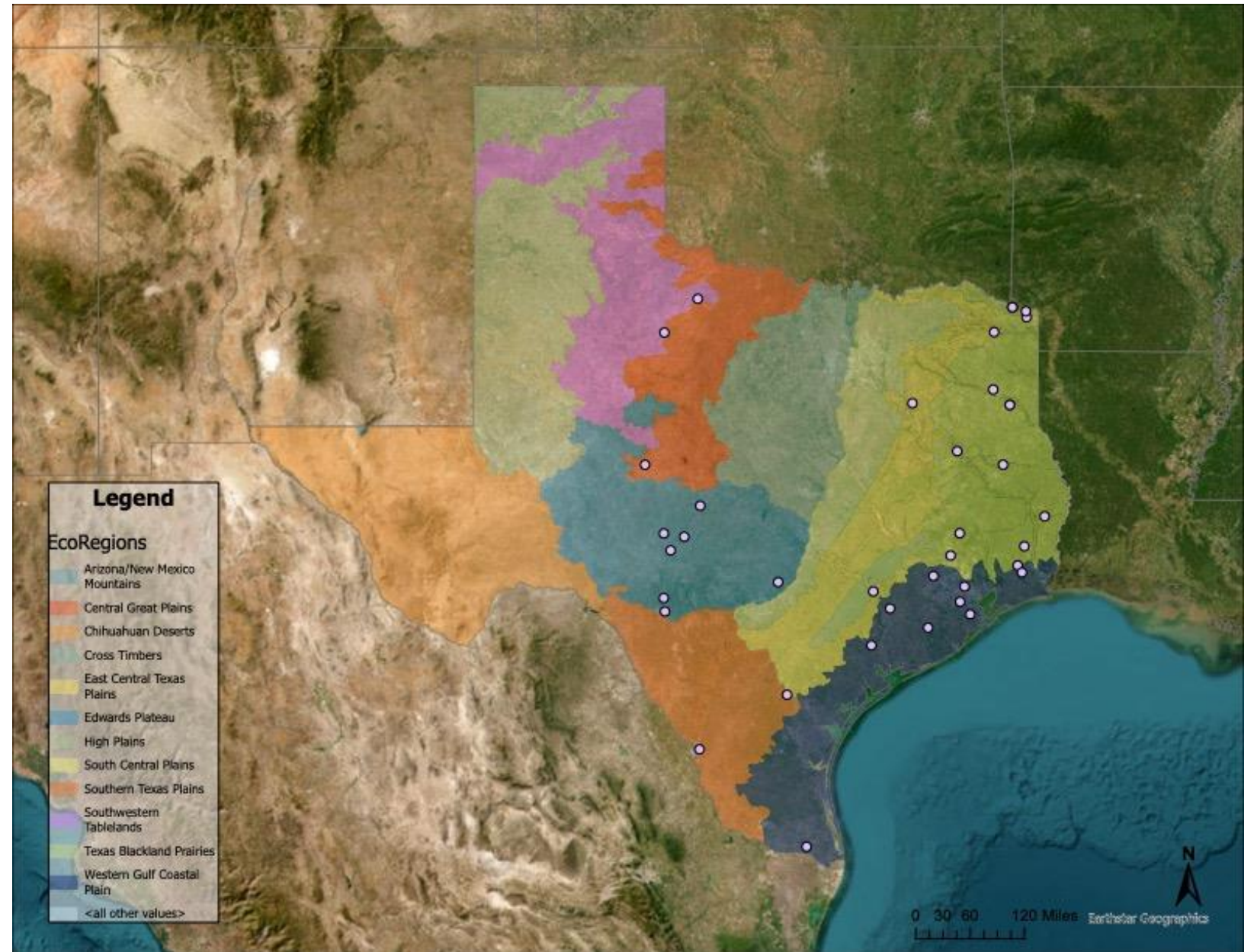
Completed:

38 Sampling events  
at 36 Sites (43%)

(5 SS, 10 LS, 22 R)

To sample:

49 sampling events  
at 47 sites

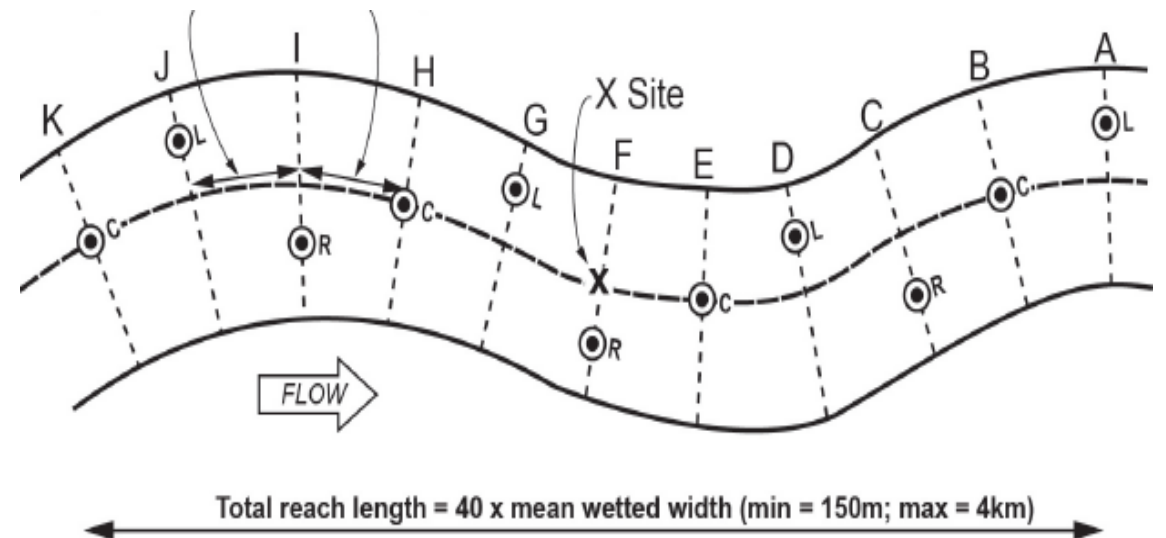


# eDNA collection

1- A 1 L water sample at designated location

2- A 1 L composite sample. ~100 mL taken at 11 evenly spaced transects along reach

3- A control sample taken from a live well with species, and size recorded for every individual. (select sites)



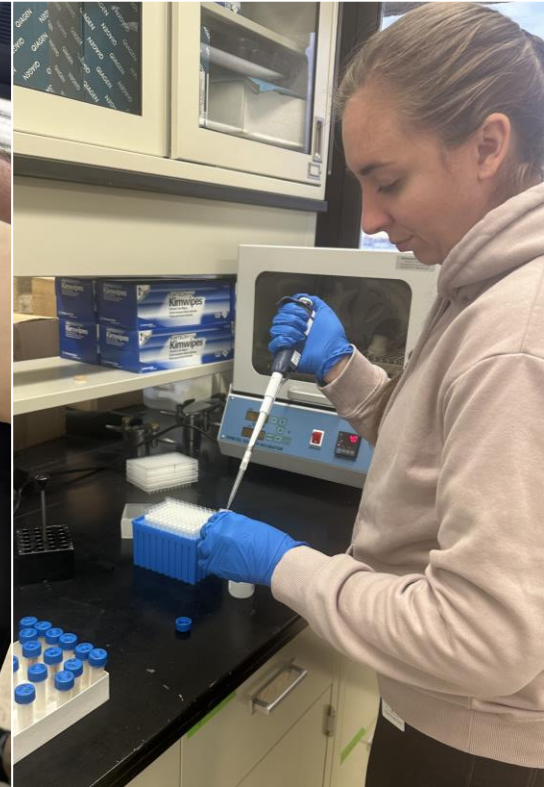
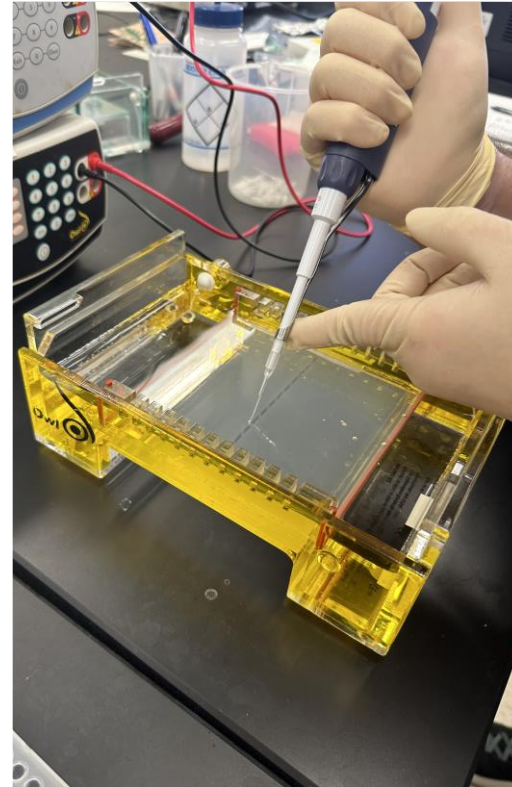
# Fishing

- Electrofishing was the only traditional method used for this survey
  - Every fish caught was ID'd and counted by size class
- If width < 12m = fish entire reach
- If width > 12m = fish until at least 500 fish were caught and 50% fished



# eDNA processing

- Water was filtered same day through a 3 micron, ISOPORE™ Membrane Filter using a peristaltic pump.
- At the lab, DNA then went through an extraction and purification process before being amplified with PCR and checking for DNA with gel electrophoresis.
- Currently on final rounds of PCR to then be sequenced.





## Outcomes:

From electrofishing we caught a total of

- 104 species
- 16,927 individuals

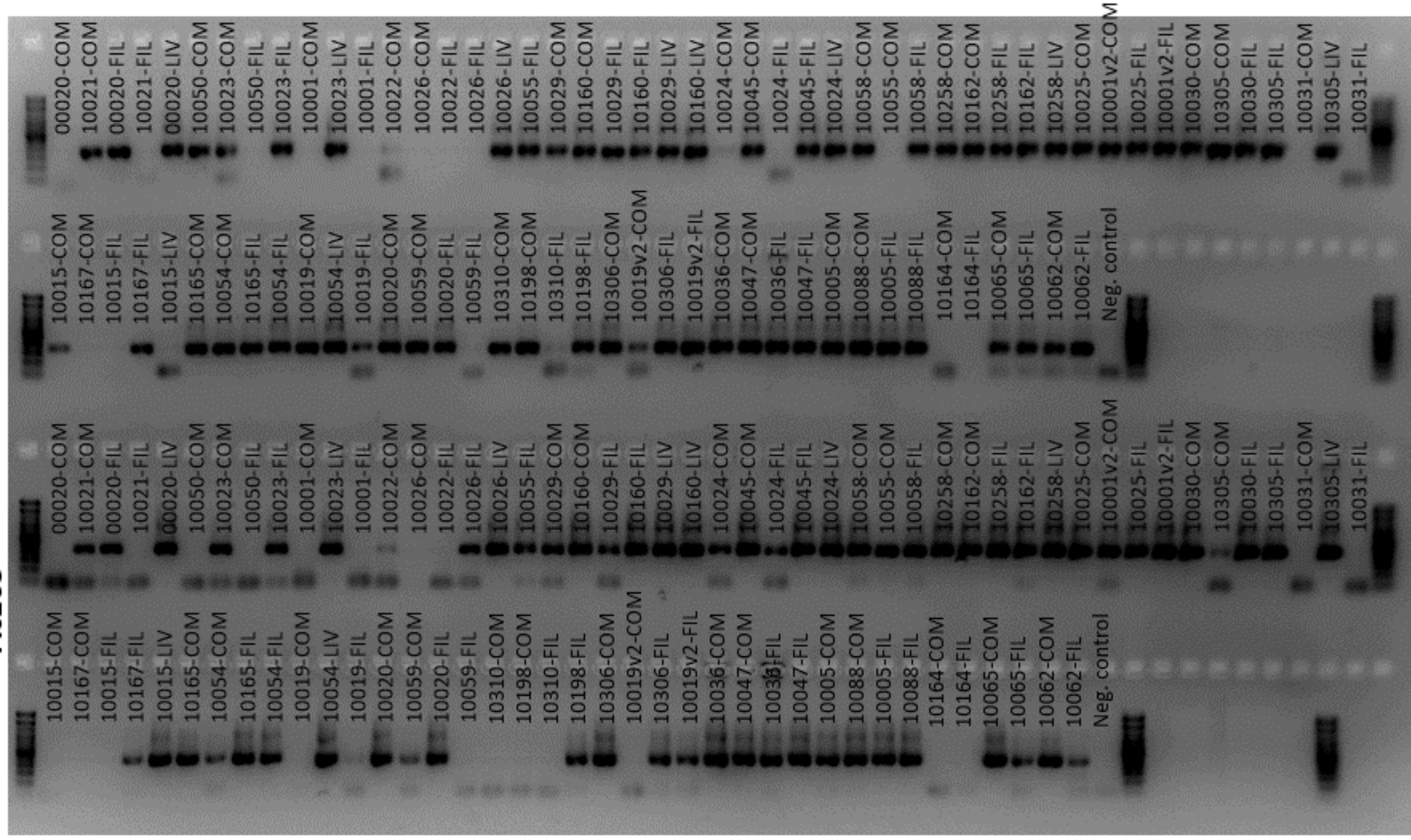
Collected:

Paired data for 36 sites



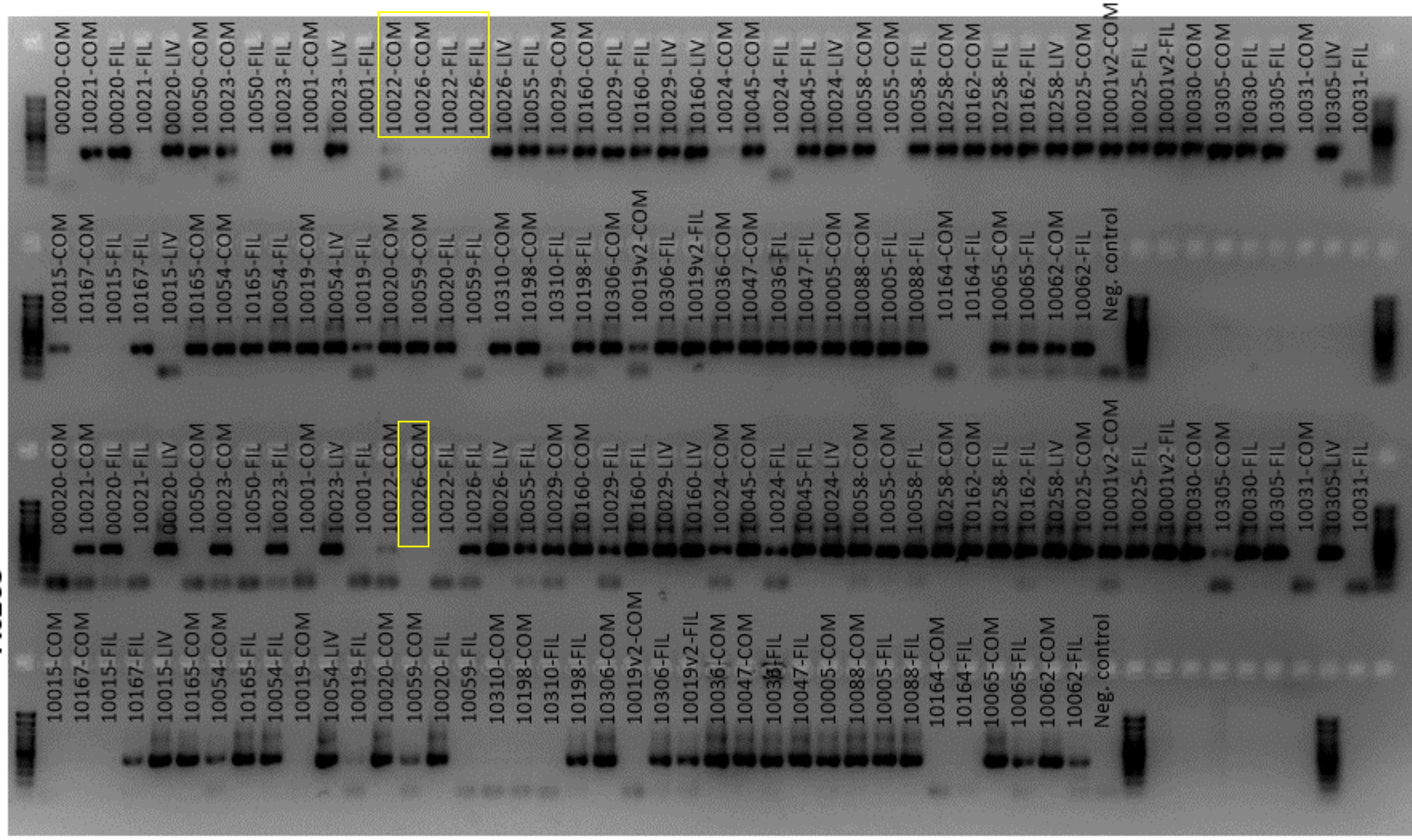
## Ac16S

## Am12S



## Ac16S

## Am12S





# Pros and Cons of eDNA metabarcoding

Pros	Cons
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# Genetic Library

2023

Texas FW Fish count: 242

Genetic data available: 152

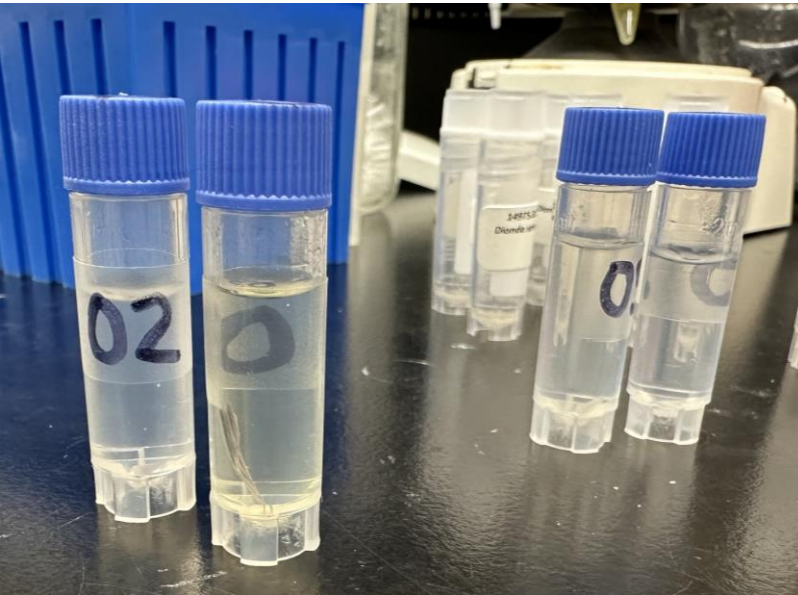


Completed:

Field Collected: 76 clips

Biodiversity Research and Teaching  
collections at Texas A&M: 199 fin clips

For a total of 59 additional species



2024

Still no data or fin clips for 37 species

# Acknowledgements

The EPA – Office of Research and Development

UHCL – Environmental Institute of Houston field team:

- Noah Daun, Angelica Castillo, Mandi Gordon, Gabrielle Hammerbach, Heather Hinchliffe, Aurora Alvarez, Kaylei Chau, Danielle DeChellis, Ashlyn Sak, Erica Underwood, Jenny Oakley



Contact Info:

Kylie Perkins

Graduate Research Assistant

Environmental Institute of Houston

[perkinsky@uhcl.edu](mailto:perkinsky@uhcl.edu)



# Species with no genetic data

- **Amistad gambusia** - *Gambusia amistadensis*
- **Big Bend gambusia** - *Gambusia gaigei*
- **Blotched gambusia** - *Gambusia senilis*
- **Bluehead shiner** - *Pteronotropis hubbsi*
- **Chestnut lamprey** - *Ichthyomyzon castaneus*
- **Clear Creek gambusia** - *Gambusia heterochir*
- **Clown goby** - *Microgobius gulosus*
- **Cypress minnow** - *Hybognathus hayi*
- **Darter goby** - *Ctenogobius boleosoma*
- **Fountain darter** - *Etheostoma fonticola*
- **Freshwater goby** - *Ctenogobius shufeldti*
- **Golden redhorse** - *Moxostoma erythrurum*
- **Goldstripe darter** - *Etheostoma parvipinne*
- **Highfin goby** - *Gobionellus oceanicus*
- **Leon Springs pupfish** - *Cyprinodon bovinus*
- **Lyre goby** - *Evorthodus lyricus*
- **Mexican goby** - *Ctenogobius claytonii*
- **Mud darter** - *Etheostoma asprigene*
- **Pecos bluntnose shiner** - *Notropis simus pecosensis*
- **Peppered chub** - *Macrhybopsis tetranema*
- **Phantom shiner** - *Notropis orca*
- **Redfin darter** - *Etheostoma whipplei*
- **Rio Grande bluntnose shiner** - *Notropis simus simus*
- **Rio Grande chub** - *Gila pandora*
- **Rio Grande silvery minnow** - *Hybognathus amarus*
- **River goby** - *Awaous tajasica*
- **San Marcos gambusia** - *Gambusia georgei*
- **Skipjack herring** - *Alosa chrysochloris*
- **Spinycheek sleeper** - *Eleotris pisonis*
- **Swamp darter** - *Etheostoma fusiforme*
- **Tex-Mex gambusia** - *Gambusia speciosa*
- **Texas silverside** - *Menidia clarkhubbsi*
- **Toothless blindcat** - *Trogloglanis pattersoni*
- **West Mexican redhorse** - *Moxostoma austrinum*
- **Western creek chubsucker** - *Erimyzon claviformis*
- **Western sand darter** - *Ammocrypta clara*
- **Western starhead topminnow** - *Fundulus blairae*
- **Widemouth blindcat** - *Satan eurystomus*