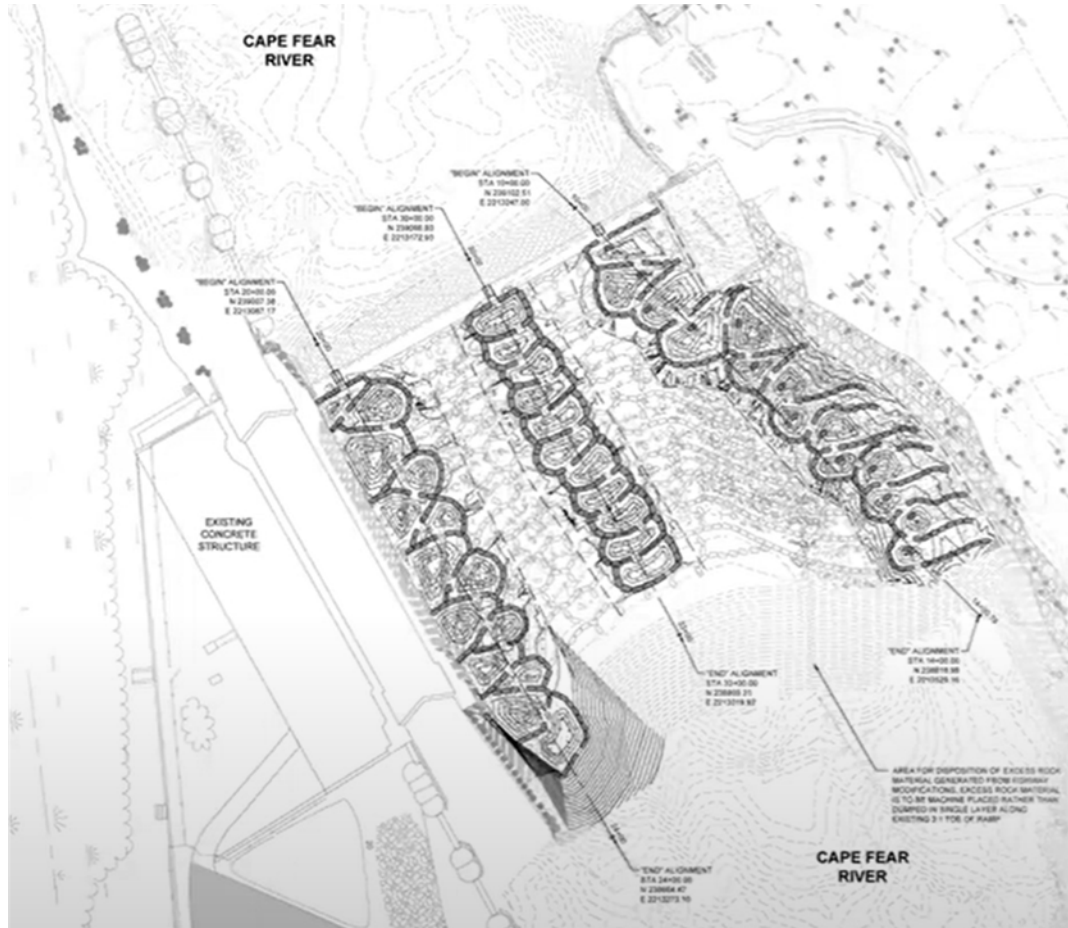


# Ultrafine-scale anadromous non-salmonid movement patterns pre- and post- modification to a large nature-like fishway (LD1)



# Research objectives

- 1) Quantify two-dimensional movement patterns of diadromous fish in the immediate downstream and upstream vicinity of the rock arch passage structure
- 2) Relate movement patterns to in situ habitat and flow measurements to identify staging areas and migration routes approaching the rock arch rapids
- 3) Identify movement patterns that result in successful passage of the rock arch rapids
- 4) Determine if individual (i.e., size, sex, condition) or environmental (i.e., flow, temperature) covariates influence diadromous passage success

\*all of this in context to pre- and post-modification to LD1

# Study Design

## Acoustic array

- 24 total HR3-307 kHz receivers all set to HTI mode
- 7 upstream array; 17 downstream array
- 3 reference tags of each tag type (HTI-495LY and HTI-495LF) were placed within each array
- Same design and placement in both years (2021 pre-mod & 2022 post-mod) unless processing and analysis says otherwise – adaptive approach

# Study Design

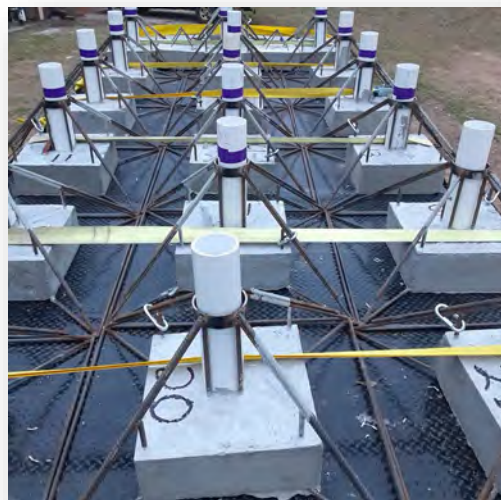
## Tagging regime

- American shad (EF & Angling)
  - HTI-495LF-307 kHz + V9-69 kHz + dart reward tag
  - Gastric insertion - adaptive double-tagging approach given lab findings
- Striped bass (EF & Angling)
  - HTI-495LY-307 kHz + V9-69 kHz + DMF external tag + fin clip (DNA)
  - Surgical
- Atlantic sturgeon (Gillnetting)
  - HTI-495LY-307 kHz + V9/V16-69 kHz + T-bar tag + fin clip (DNA)
  - Surgical



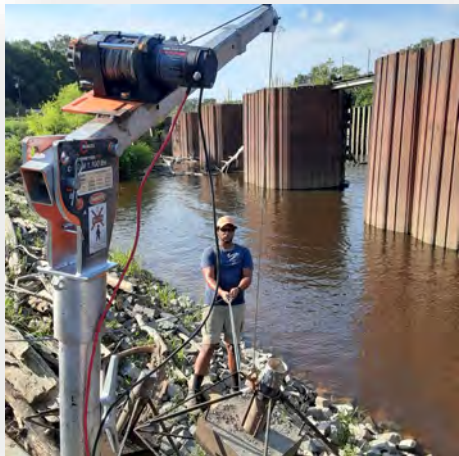


# HR3 array deployment



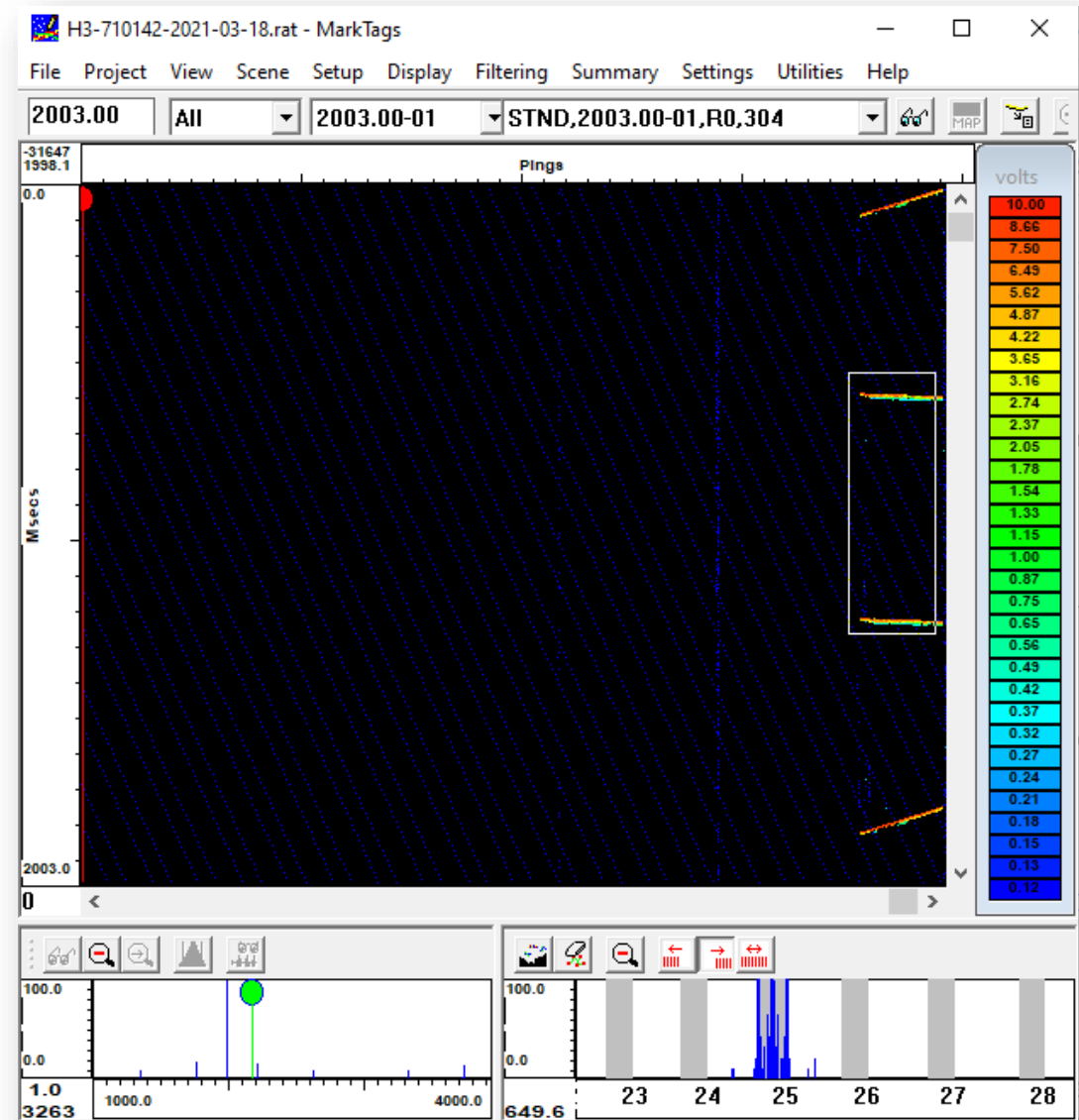


# HR3 array recovery



# Analysis

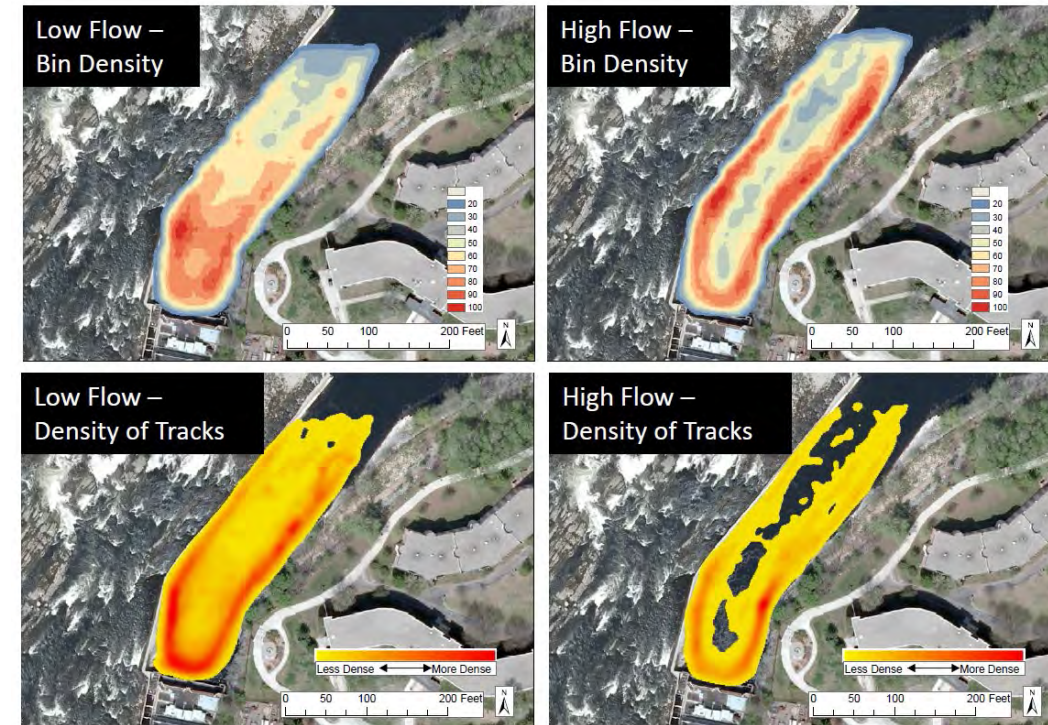
- Complex workflow for preparing tag data using HTI Program MarkTags
  - Assign tag IDs to pulse images
  - Time-sync receiver data
  - Merge all time-synced data across receivers
- Ultra-fine scale tag positioning occurs in HTI's AcousticTag Software Program
  - Proprietary algorithm to triangulate submeter positions
  - ID specific tracks





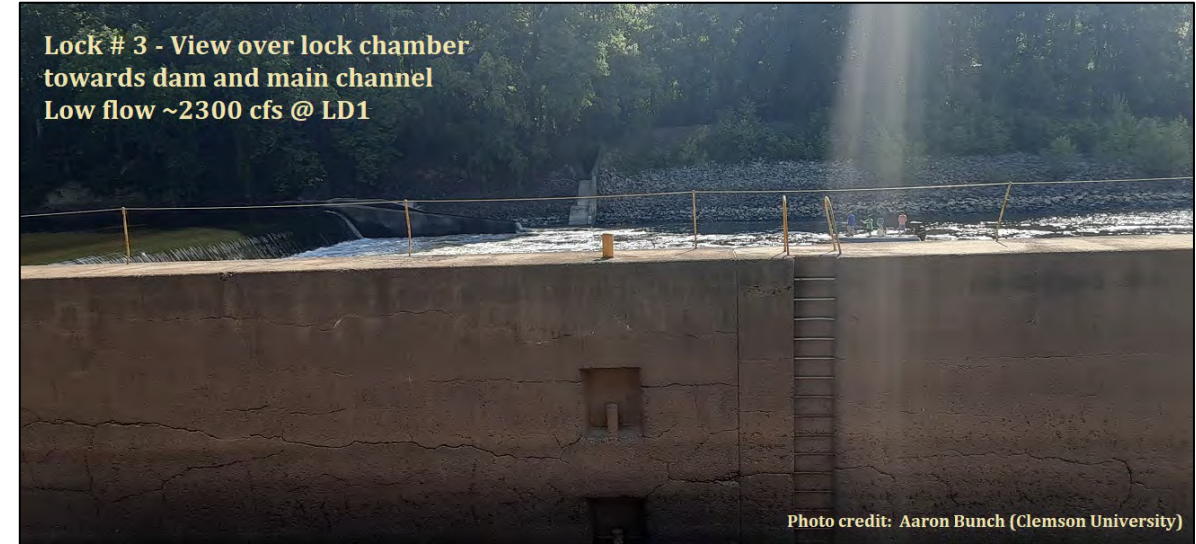
# Analysis

- Manual-marking (incredibly time consuming)
- Post-processing raw detections
  - Kernel density or similar hotspot analysis individually and by species to show movement patterns
  - Overlay over bathymetry, surface flow
  - Relate movements to pre-mod/post-mod, within-year flow levels, lock usage, tide schedule
  - Pathway choice model (probability-based) based on exit from downstream to entry of upstream? How probabilities change based on covariates mentioned above (Not fully explored)





# Flow related passage at LD2 and LD3 (experimental and natural regime)



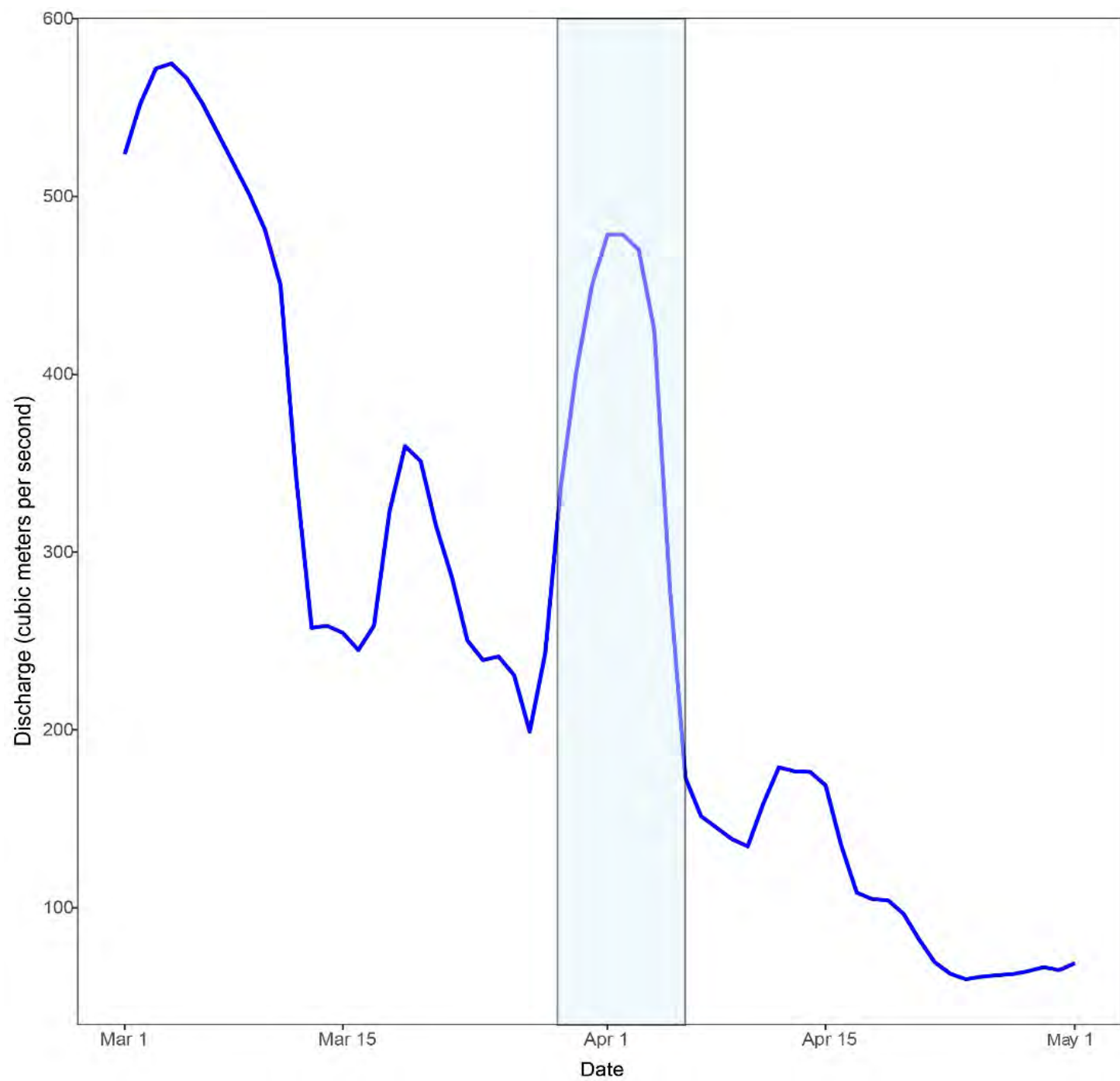
# Research objectives

1. Compare eDNA, acoustic detections, electrofishing, gillnetting data to determine species presence of American Shad and Atlantic Sturgeon above and below each LD structure throughout the spawning runs in 2021 and 2022.

\*all of this in context to submerging 2 and 3 natural or experimental; applied piece

\*developing probes and testing them; field validation



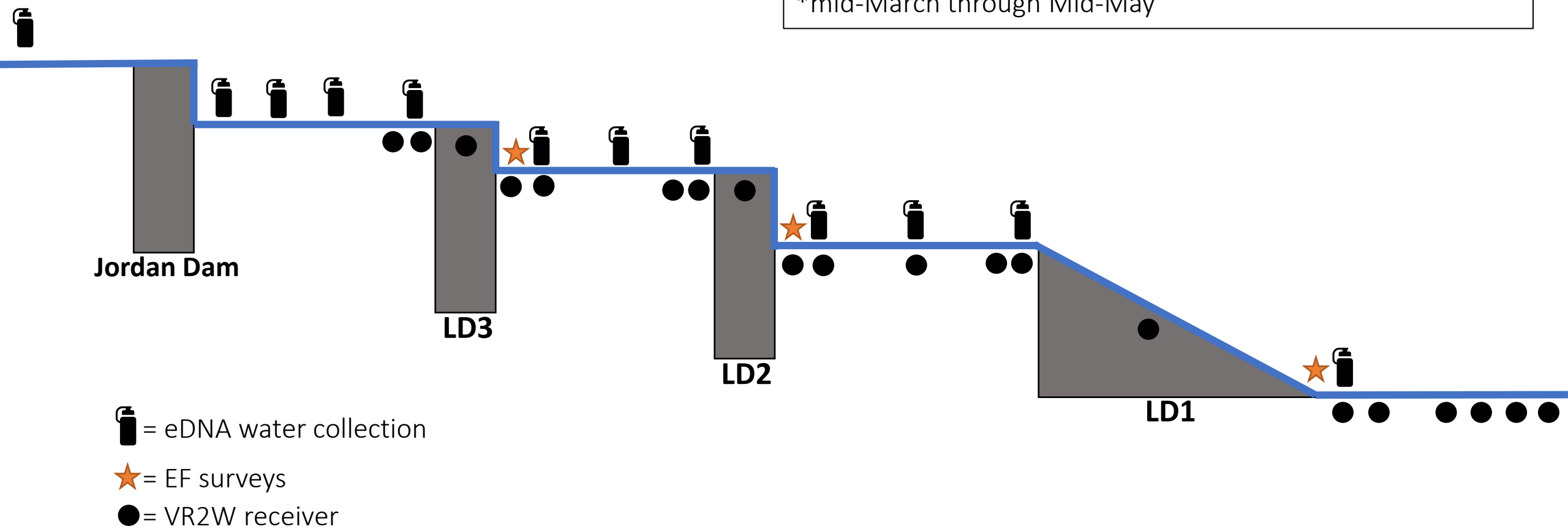


# 2022 Design: eDNA collections

Sampling protocol followed established guidelines from the “Quality assurance project plan eDNA monitoring of bighead and silver carps” which included sterilization practices, field collection methods, and preservation (USFWS, 2020)

\*weekly sampling at all locations

\*mid-March through Mid-May





# Study Design: eDNA analysis

## Process

- Water filtration, DNA homogenation & amplification
- qPCR-probe assays to detect Atlantic sturgeon and American shad from the water samples described above
- Plough et al. (2021) developed and tested a new quantitative PCR (qPCR) assay to detect Atlantic sturgeon eDNA in water samples with upcoming plans for American shad
- Targeted Cytochrome B which showed no amplification of other related and co-occurring fishes.



# Study Design: Analysis

## Standard

- Abacus plots
- Passage efficiency
- Time-to-event analysis (Castro-Santos & Perry 2011)

## Model structure

- Multiscale occupancy model developed for eDNA analysis
- EDNAOCCUPANCY R package (Dorazio & Erickson 2017)

## EDNAOCCUPANCY: An R package for multiscale occupancy modelling of environmental DNA data

Robert M. Dorazio<sup>1</sup> | Richard A. Erickson<sup>2</sup>