Environmental DNA Analysis of Forage Fish Diversity and Distribution in the Indian River Lagoon

Emily Farrell, Girish Kumar, and Michelle R. Gaither
Department of Biology | Genomics and Bioinformatics Cluster
University of Central Florida

Background

Indian River Lagoon:
The Indian River Lagoon (IRL) is home to over 400 species of fishes, making it one of the most species rich estuaries in the United States. These inhabitants include many forage fish species and their key predators, both of which are critically important to local marine food webs.

Florida Fish and Wildlife Conservation Commission (FWC) has been conducting monthly seine and trawl surveys in the IRL for over 25 years, generating the data on which most state fisheries resource management and conservation decisions are based. However, these surveys systematically miss many key species due to gear bias and the inability to sample hard bottom habitat, resulting in data deficiencies.

Environmental DNA:
Environmental DNA (eDNA) is the genetic material shed by organisms into their environment. When filtered from small volumes of seawater, eDNA has been found to be highly accurate in detecting and characterizing species composition in freshwater and marine systems without the need to directly observe or capture organisms and can be collected across all habitats.

The Gaither lab at the University of Central Florida has optimized eDNA protocols and shown that water sampling in the IRL captures information about both forage fish species and predators of interest (Table 1) (Kumar et al. in prep[a,b]).

Table 1. eDNA detections of forage fish species in the IRL

Scientific Name	Common Name
Forage Fish Species	
Brevoortia tyrannus	Menhaden
Brevoortia patronus	Menhaden
Mugil cephalus	Mullet
Mugil curema	Mullet
Mugil rubrioculus	Mullet
Diapterus auratus	Mojarra
Sardinella aurita	Sardinella
Anchoa hepsetus	Anchovy
Anchoa mitchilli	Anchovy
Forage Fish Predators	
Centropomus undecimalis	Snook
Trachinotus carolinus	Pompano
Sciaenops ocellatus	Redfish
Cynoscion nebulosus	Spotted sea trout
Mycteroperca microlepis	Gag grouper
Scomberomorus cavalla	King mackerel

Indian River Lagoon

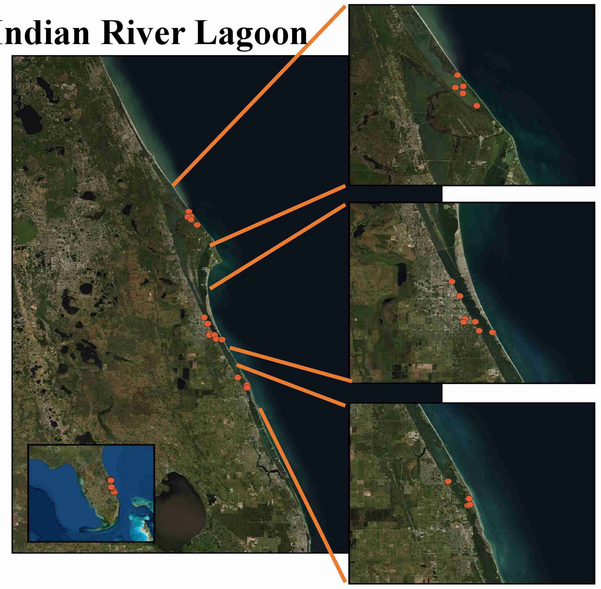

Figure 1. Map of Sampling Locations
Sampling was conducted at the locations marked on the map over three days in September 2020.

Objectives

(1) Optimize existing lab protocols for long-term eDNA monitoring to provide a cost-effective tool that will complement existing fisheries assessment methods
(2) Conduct eDNA field sampling alongside FWC collections for a direct comparison of the methods.
(3) Evaluate differences in species composition between FWC and eDNA datasets to identify the relative biases and strengths of each technique.
(4) Integrate FWC and eDNA datasets in a spatially explicit framework to serve as a baseline for future efforts.
(5) Develop species hotspot maps for forage fishes and their predators.
(6) Alongside FWC scientists, optimize protocols combining traditional survey techniques with eDNA sampling to reduce the time and monetary cost of monitoring efforts

References

Kumar, G., Reaume, A., Farrell, E., Gaither, M.R. (In Prep[a]). Universal fish primers for aquatic eDNA analyses: Which to choose? In Prep for December 2020 submission to Environmental DNA.
Kumar, G., Farrell, E., Reaume, A., Gaither, M.R. (In Prep[b]). Optimizing protocols for the field sampling and extraction of environmental DNA from water samples. In Prep for December 2020 submission to Environmental DNA.

Acknowledgements

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Methods

eDNA sample collection: At two time points (fall and spring), water samples will be collected at sites across the IRL in conjunction with FWC's monthly surveys. Five replicate 500 mL water samples are taken 2" below the surface just before seine nets are deployed. Samples are stored on ice and filtered using 0.45 µm pore size MCE filters within 6 hours of collection. Filters are stored at -20° C in Longmire's buffer.

Next-generation DNA sequencing:
A two-PCR step protocol, using a 16S primer set for fishes, will be used to prepare libraries. Resulting libraires will be sequenced using a MiSeq reagent Kit v3 (2×300 cycles)

Species identification and data analyses:
After quality control, reads will be collapsed into amplicon sequence variants and queried against a reference DNA sequence database. Taxonomic identities will be assigned based on thresholds of 97% match for genus level designations and 99% for species-level. Species communities at each site and habitat type will be evaluated using taxon-dependent and independent approaches.

Project Status

Fall water sample collection (Fig. 1) and filtration was completed over three days in September 2020. Extraction for these samples is in progress.