Supplementary Material

# Supplementary Data Analysis Methods

# We conducted statistical analyses to assess which habitat and environmental variables had a statistically significant (p<0.05) or marginally significant (p=0.05–0.10) effect on fish abundance, biomass, community composition, and predation potential per unit effort (fyke net or trotline soak time expressed in hours). For the fyke net data, analyses of fish community structure using both abundance (i.e., fish community abundance) and biomass (i.e., fish community biomass) data were made with a multivariate approach, while analyses of total fish abundance and biomass, diversity indices, and individual species abundances used a univariate approach. The number of worms eaten was based on the number of worms missing at the end of trotline soak times and were also analyzed with a univariate approach. We conducted all statistical analyses in R (R Core Team, 2019) version 3.5.1 (2018-07-02) with packages “vegan” (Oksanen et al., 2019), “reshape” (Wickham, 2007) and “ggplot2” (Wickham, 2016).

# Fish community abundance data consisted of a matrix of 27 samples (two samples had zero fish caught and were excluded from the fish community analysis) for each of 12 captured species: threadfin shad (*Dorosoma petenense*), warmouth (*Lepomis gulosus*), bluegill (*Lepomis macrochirus*), brown bullhead (*Ameiurus nebulosus*), gizzard shad (*D. cepedianum*), seminole killifish (*Fundulus seminolis*), golden silverside (*Labidesthes vanhyningi*), dollar sunfish (*Lepomis marginatus*), redear sunfish (*Lepomis microlophus*), spotted sunfish (*Lepomis punctatus*), coastal shiner (*Notropis petersoni*), and black crappie (*Pomoxis nigromaculatus*). Environmental data (i.e., both habitat and site characteristics and measurements) consisted of a matrix of the 27 samples and eight variables: sampling time of day, the continuous wind speed at each site (m/s), the estimated size of SAV patch sampled (index of 0–5, as described in the main text), the estimated distance from the center of each habitat sampled to the shoreline (m), the habitat type (*P. illinoensis* n=8, *V. americana* n=8, mix n=3, or bare n=10), the presence (n=11) or absence (n=18) of *Hydrilla*, water temperature (°C), and the water depth (m). Salinity (ppt) and secchi depth (m) were fairly consistent across all sites (0.16–0.18 ppt and 0.30–0.55 m respectively) and dissolved oxygen (mg/L) was highly dependent on time of day, so they were excluded from the analysis (Table 2-2).

# Seven of the twelve fish species sampled were rare (only present in one sample each), but because they were largely the sunfishes (*Lepomis* spp.) and are of particular interest for restoration due to recreational value, they were not excluded from the community analysis. We used the function decostand() to perform a Hellinger transformation on all of the abundance data as it performs well with zero-inflated abundance datasets (Legendre and Gallagher, 2001). All non-categorical environmental data were left-skewed, so we log-transformed the data. The coefficient of variation among all of the environmental variables was greater than 50, so we scaled the data with the scale() function. We checked for multicollinearity using the cor() function. Habitat type and SAV patch size expressed multicollinearity (>0.7 correlation value), but because they were both of interest, we included them both in the statistical tests, then ran the statistical tests with each one missing.

# To determine the optimal constrained ordination method, we performed a detrended correspondence analysis using the decorana() function. Because one axis had a value greater than 3, the species abundances showed a unimodal relationship with the underlying gradient that was confirmed by plotting, meaning a canonical correspondence analysis (CCA) was appropriate for the data. We ran the CCA with the cca() function on all 12 species and all eight variables. Eight variables are too many for a CCA, so we conducted forward selection using the ordiR2step() function with a relaxed ⍺ of 0.1 to better allow for variable selection and capture marginally statistically significant results (⍺=0.1) in addition to traditionally significant results (⍺=0.05). The only variable that was selected was SAV patch size. The result was the same when habitat type was excluded as a variable because of the multicollinearity. When SAV patch size was excluded, habitat type was selected in the forward selection, but because when both were included, SAV patch size was the one selected, that is the variable we chose to focus on in the results. We performed the same transformation, scaling, and analysis on fyke net fish community biomass data.

# We calculated the Shannon and Simpson diversity indices of the fyke net catches with the diversity() function. We used linear regression with the lm() function to evaluate how the Shannon diversity index, Simpson diversity index, and individual species fyke net abundances changed with SAV patch size to further describe the change in fish community abundance. We used multiple linear regression with forward selection (⍺=0.05) with the lm() function to evaluate how total biomass per soak time hour, total abundance per soak time hour, and the worms missing from trotlines per soak time hour changed with the same transformed and scaled environmental variables as the fish community data analysis. We examined the most abundant species in the fyke nets, threadfin shad, using the simper() function to run a Similarity Percentage (SIMPER) analysis of their contribution to Hellinger-transformed community structure in the Bray Curtis dissimilarity index.

# References

Legendre, P., and Gallagher, E. D. (2001). Ecologically meaningful transformations for ordination of species data. *Oecologia* 129, 271–280. doi: 10.1007/s004420100716

Oksanen, J., Blanchet, F. G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D., et al. (2019). vegan: community ecology package. R package version 2.5-6.

R Core Team (2019). R: a language and environment for statistical computing.

Wickham, H. (2007). Reshaping data with the reshape package. *J. Stat. Softw.* 21. doi: 10.18637/jss.v021.i12

Wickham, H. (2016). ggplot2: elegant graphics for data analysis.

# Supplementary Tables

**Supplementary Table 1.** Location and characteristics of each sampling habitat. SAV patch sizes were estimated based on an index of 0–5, with 0 being a bare habitat and each increase of 0.5 in the index being equivalent to an approximated increase in patch size of 0.75 m by 0.75 m*.*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Site | Latitude | Longitude | Habitat Type | SAV Patch Size | Distance from shore (m) | *H. verticillata* present? |
| AP6 | 28.63007 | -81.55045 | *P. illinoensis* | 1 | 1.5 | no |
| AP6 | 28.62968 | -81.55025 | *V. americana* | 3 | 1.5 | no |
| AP6 | 28.62934 | -81.55025 | bare | 0 | 0 | no |
| AP9 | 28.58646 | -81.58089 | *P. illinoensis* | 2 | 18.3 | yes |
| AP9 | 28.58641 | -81.58020 | bare | 0 | 0 | no |
| AP9 | 28.58584 | -81.58060 | *V. americana* | 1 | 1.5 | yes |
| AP9 | 28.58664 | -81.58033 | *V. americana* | 1 | 21.3 | no |
| AP9 | 28.58680 | -81.58081 | *V. americana* | 3.5 | 6.1 | no |
| AP9 | 28.58616 | -81.58092 | bare | 0 | 15.2 | no |
| AP20 | 28.63542 | -81.55254 | *P. illinoensis* | 2.5 | 15.2 | yes |
| AP20 | 28.63420 | -81.55190 | bare | 0 | 0 | yes |
| AP20 | 28.63332 | -81.55151 | *V. americana* | 3 | 6.1 | no |
| AP2 | 28.67760 | -81.62418 | bare | 0 | 9.1 | yes |
| AP2 | 28.67804 | -81.62373 | mix | 4 | 0 | yes |
| AP2 | 28.67815 | -81.62311 | *P. illinoensis* | 3.5 | 0 | yes |
| AP5 | 28.63650 | -81.55537 | *P. illinoensis* | 4.5 | 15.2 | yes |
| AP5 | 28.63733 | -81.55464 | *P. illinoensis* | 2 | 3.0 | yes |
| AP5 | 28.63672 | -81.55589 | bare | 0 | 6.1 | yes |
| AP3 | 28.66890 | -81.59624 | bare | 0 | 91.4 | no |
| AP3 | 28.66850 | -81.59546 | mix | 5 | 30.5 | no |
| AP3 | 28.66713 | -81.59569 | *V. americana* | 5 | 61.0 | no |
| AP20 | 28.63336 | -81.55204 | mix | 3 | 6.1 | no |
| AP20 | 28.63459 | -81.55206 | bare | 0 | 0 | no |
| AP20 | 28.63487 | -81.55231 | *P. illinoensis* | 2 | 6.1 | no |
| AP21 | 28.64246 | -81.56198 | *P. illinoensis* | 5 | 3.0 | no |
| AP21 | 28.64235 | -81.56126 | bare | 0 | 3.0 | no |
| AP8 | 28.60192 | -81.56991 | *V. americana* | 4 | 0 | no |
| AP8 | 28.60312 | -81.56866 | *V. americana* | 5 | 0 | no |
| AP8 | 28.60376 | -81.56788 | bare | 0 | 0 | no |

**Supplementary Table 2.** The mean, standard deviation, and range of the six continuous environmental variables used in the data analysis, as well as the three that were chosen to be excluded. Fyke net and trotline sampling days were combined to calculate values. SAV patch sizes were estimated based on an index of 0–5, with 0 being a bare habitat and each increase of 0.5 in the index being equivalent to an approximated increase in patch size of 0.75 m by 0.75 m*.*

|  |  |  |
| --- | --- | --- |
| Environmental Variable | Mean (± SD) | Range |
| Time of day | 9:23 am (± 1h:9m) | 8:00–11:20 am |
| Continuous wind speed (m/s) | 1.29 (± 1.04) | 0–2.3 |
| SAV patch size | 2.09 (± 1.92) | 0–5 |
| Distance from shore (m) | 11.08 (± 20.03) | 0–91.4 |
| Water temperature (°C) | 29.78 (± 1.44) | 27.1–32.3 |
| Secchi depth (m) | 0.37 (± 0.10) | 0.30–0.55 |
| Dissolved oxygen (%) | 79.3 (± 17.2) | 49.2–120.0 |
| Salinity (ppt) | 0.18 (± 0.01) | 0.16–0.18 |

**Supplementary Table 3.** The mean and standard deviation catch-per-hour of the five fish species caught in more than one fyke net. SAV patch sizes were estimated based on an index of 0–5, with 0 being a bare habitat and each increase of 0.5 in the index being equivalent to an approximated increase in patch size of 0.75 m by 0.75 m*.*

|  |  |  |  |
| --- | --- | --- | --- |
| Species | SAV Patch Size Bare (0) | SAV Patch Size Small (1–3) | SAV Patch Size Large (3.5–5) |
| Threadfin shad | 4.47 (± 7.47) | 17.36 (± 37.54) | 2.40 (± 2.94) |
| Warmouth | 0 (± 0) | 0.18 (± 0.46) | 0.25 (± 0.32) |
| Bluegill | 0.42 (± 0.46) | 0.19 (± 0.59) | 0.58 (± 1.16) |
| Coastal shiner | 0.07 (± 0.11) | 0.94 (± 1.22) | 0.62 (± 1.85) |
| Seminole killifish | 0.07 (± 0.23) | 0 (± 0) | 0.22 (± 0.66) |

**Supplementary Table 4.** The catch-per-hour of the eight fish species caught in only one fyke net and the SAV patch size they were caught in. SAV patch sizes were estimated based on an index of 0–5, with 0 being a bare habitat and each increase of 0.5 in the index being equivalent to an approximated increase in patch size of 0.75 m by 0.75 m*.*

|  |  |  |
| --- | --- | --- |
| Species | Abundance per Hour | SAV Patch Size |
| Brown bullhead | 0.38 | 2.5 |
| Gizzard shad | 0.37 | 3.0 |
| Golden silverside | 0.34 | 3.5 |
| Dollar sunfish | 0.35 | 3.5 |
| Redear sunfish | 0.38 | 2.5 |
| Spotted sunfish | 0.50 | 5.0 |
| Black crappie | 0.46 | 5.0 |

# Supplementary Figures

# A close up of a map Description automatically generated

**Supplementary Figure 1.** Locations of field sampling sites in Lake Apopka, Florida (USA), created with Google My Maps. Site names were kept consistent with the ongoing restoration efforts.



**Supplementary Figure 2.** Number of fyke nets or trotlines deployed at each SAV patch size. SAV patch sizes were estimated based on an index of 0–5, with 0 being a bare habitat and each increase of 0.5 in the index being equivalent to an approximated increase in patch size of 0.75 m by 0.75 m*.*



**Supplementary Figure 3.** Catch accumulation curves for the fyke net and two trotlines deployed for pilot testing. The sampling equipment in the legend are listed in the order they appear on the right side of the figure.