# U.S. Fish & Wildlife Service

## eDNA Metabarcoding Results Summary Report

*Downeast Maine, 2022*

This report is intended to provide a general summary of the 2022 Downeast Maine eDNA metabarcoding project results. A total of 24 sites were surveyed and 63 water filtration samples were collected (Table 1). The mitochondrial 12s gene, a commonly used sequence for biodiversity monitoring, was used for this analysis. Reads, copies of DNA sequences, and other sample processing information is retained in the metadata and associated with each identification. The primers, which amplify rRNA barcoding genes, used for this analysis are also recorded in the metadata and presented below (Table 2).

Samples analyzed from this project resulted in a total richness of 22 taxa. Taxa was separated into categories (Dominant, Common, Occasional, and Rare) based on their presence across all sampling to provide a simple assessment of the identification results (Table 3). Identification results that exceeded a threshold value of 0.001 or 0.01% of the total sample reads is reported within this summary to mitigate false positives.

Table 1: Total sample effort and average taxa richness.

| | Number of | | Average per Sample | |
| Project | Sites Surveyed | Samples Collected | Taxa | Reads |
|---|---|---|---|---|
| Downeast Maine | 24 | 63 | 8.1 | 175,970 |

Table 2: Primer and primer sequence information.

| | Primer Information | |
| Direction | Name | Sequence |
|---|---|---|
| Forward | Tele02-F | AAACTCGTGCCAGCCACC |
| Reverse | LUF-R | GCATAGTGGGGTATCTAATCC |

Table 3: eDNA metabarcoding identification results.

| Common Name | Scientific Name | Detections[a] | Proportion[b] | Read Frequency[c] |
|---|---|---|---|---|
| **Dominant** | | | | |
| American Eel | *Anguilla rostrata* | 53 | 0.88 | 0.07 |
| White Sucker | *Catostomus commersonii* | 53 | 0.88 | 0.11 |
| **Common** | | | | |
| Brown Bullhead | *Ameiurus nebulosus* | 41 | 0.68 | 0.08 |
| Common Shiner | *Luxilus cornutus* | 31 | 0.52 | 0.08 |
| Fallfish | *Semotilus corporalis* | 45 | 0.75 | 0.29 |
| Golden Shiner | *Notemigonus crysoleucas* | 33 | 0.55 | 0.07 |
| Pumpkinseed Sunfish | *Lepomis gibbosus* | 35 | 0.58 | 0.11 |
| Smallmouth Bass | *Micropterus dolomieu* | 33 | 0.55 | 0.06 |
| **Occasional** | | | | |
| Creek Chub | *Semotilus atromaculatus* | 24 | 0.40 | 0.21 |
| Redbreast Sunfish | *Lepomis auritus* | 27 | 0.45 | 0.19 |
| White Perch | *Morone americana* | 16 | 0.27 | 0.13 |
| Yellow Perch | *Perca flavescens* | 25 | 0.42 | 0.07 |
| **Rare** | | | | |
| Atlantic Salmon | *Salmo salar* | 2 | 0.03 | 0.01 |
| Alewife | *Alosa pseudoharengus* | 13 | 0.22 | 0.09 |
| Banded Killifish | *Fundulus diaphanus* | 6 | 0.10 | 0.08 |
| Blacknose Dace | *Rhinichthys atratulus* | 13 | 0.22 | 0.06 |
| Blueback Herring | *Alosa aestivalis* | 5 | 0.08 | 0.34 |
| Brook Trout | *Salvelinus fontinalis* | 10 | 0.17 | 0.07 |
| Chain Pickerel | *Esox niger* | 6 | 0.10 | 0.07 |
| Lake Chub | *Couesius plumbeus* | 3 | 0.05 | 0.10 |
| Largemouth Bass | *Micropterus salmoides* | 13 | 0.22 | 0.07 |
| Striped Bass | *Morone saxatilis* | 1 | 0.02 | 0.01 |

*Note:*

The bolded categories are general thresholds that denote whether that taxas presence was Dominant (>75%), Common (75-50%), Occasional (50-25%), or Rare (<25%) across the entirety of sampling.

[a] Detections refer to samples where eDNA of the specified taxa was present.

[b] The proportion is the fraction of samples which eDNA was present across the entirety of sampling.

[c] Read Frequency represents the mean read frequency per positive detection sample.