Project Overview

Environmental DNA (eDNA) is DNA from an environmental sample such as water, soil or air. eDNA can come from entire microorganisms (like algae or bacteria) or fragments of tissue. eDNA methods can identify what species are in a system without requiring field researchers to capture and identify living organisms.

There are two common methods of analyzing eDNA for species identification: metabarcoding and single species PCR.

Metabarcoding identifies multiple species, but is more complex to interpret.

Single species PCR (qPCR or dPCR), is quicker and cheaper, but limited to one species at a time.

Objectives

Advanced eDNA monitoring provides an effective, low cost method of evaluating the impact of tidal boundaries on aquatic species’ migration and biodiversity. We will assess the presence of American eel and river herring at fish ladders and upstream locations, and compare the results to existing sampling and assessment programs. Various eDNA methods will be compared as well. The results will support development of protocols to provide effective and reliable information on fish passage.

Sampling and analysis steps

Collect field sample
Filter and extract DNA
Analyze for target species

Tracking Fish Returns

In May 2018, we began collecting water samples from sites on the Oyster and Lamprey Rivers. We collect samples at the head of tide dams above and below the dams. There are three sites on the Lamprey River; two above the McCallan dam and one below. There are six sites on the Oyster River; one directly above the Mill Pond dam, two below, and three farther upstream.

American eel and river herring are of particular interest because they move between freshwater and the ocean throughout their lifetime. NH Fish and Game manages a fish ladder at the McCallan dam and they count river herring that go up the river. NH Fish and Game also counts river herring that pass the Mill Pond fish ladder. NH Sea Grant collaborates with Fish and Game at the Mill Pond dam where volunteers count glass eels and move them over the dam so they can continue their journey up the river.

Initial Results

We compared our eDNA results to the fish counts recorded by NH Fish and Game. We began detecting river herring at the same time they began to migrate in May, and continued to detect them after Fish and Game stopped detecting them, which is likely due to fish living upstream. American eel were mostly detected in the Oyster River. We identified them throughout the sampling period, while Fish and Game saw a peak during the glass eel migration in spring. eDNA methods cannot distinguish between eels at different stages in their lifecycle.

Digital PCR vs. Metabarcoding

Digital PCR (dPCR) quantifies DNA of a target species in a sample. We designed a primer set to amplify American eel DNA only. dPCR provides quicker results that require less bioinformatic analysis.

The table to the right shows the results of a trial on a subset of samples to compare the detection of American eel. The samples used here are all from Site 1 on the Oyster River, which is below the dam. The check marks indicate that American eel DNA was detected in the sample. Given this small dataset, dPCR and metabarcoding seem to yield very similar detection results.

Next Step: Quantifying Species in eDNA with Quantitative PCR

Quantitative PCR (qPCR) is another species-specific quantification method. qPCR machines are more widely available than dPCR machines. Once qPCR is optimized to use with the American eel primers, the results will be compared to metabarcoding and dPCR. qPCR will be a valuable tool if the results are sufficient for fish monitoring.