



Practicality of Using eDNA to Assess Anadromous Herring Stream Spawning Habitat



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Background

Stream Ichthyoplankton (IP) surveys have been the standard for determining combined presence of Herring (Alewife, Blueback Herring, and Hickory Shad) eggs or larvae in non-tidal streams¹. Recent environmental DNA (eDNA) studies detected Herring species² and evaluated relative abundance of Herring in non-tidal streams of the Chesapeake Bay region^{3,4}. To supplement a long running Stream IP sampling program in Mattawoman Creek, we collected eDNA samples in tandem with 2025 Stream IP sampling to evaluate proportion of samples with Herring eggs or larvae (P_{herr}) and to determine practicality of this method for sampling anadromous Herring spawning habitat.

Objectives: 1. Use eDNA to differentiate three species of Herring and determine spatiotemporal use of spawning habitat. 2. Determine if P_{herr} from eDNA (presence of eDNA from at least one of the three species) can duplicate Stream IP.

SPECIES OF INTEREST



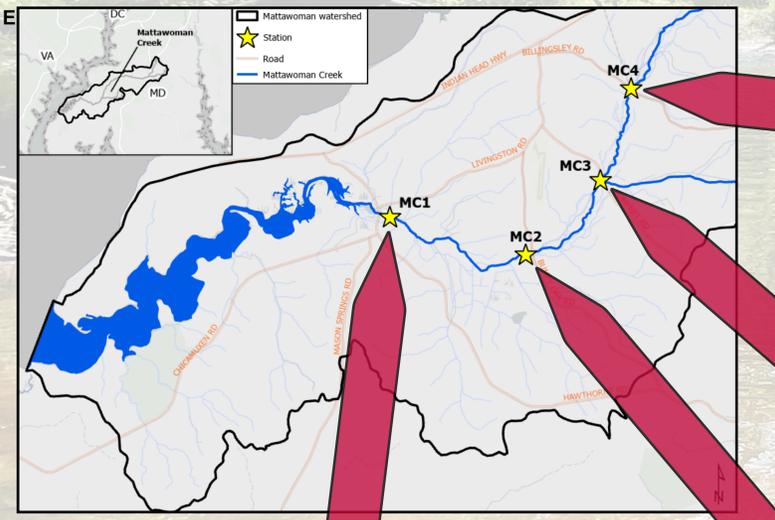
Photos: ncfishes.com

Methods

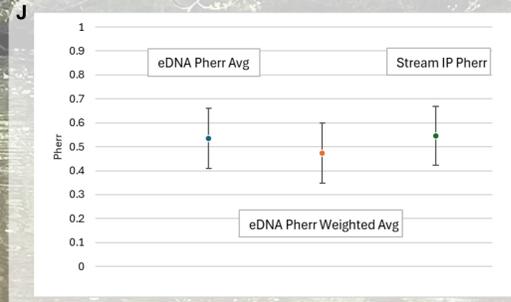
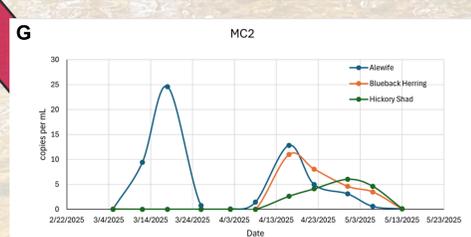
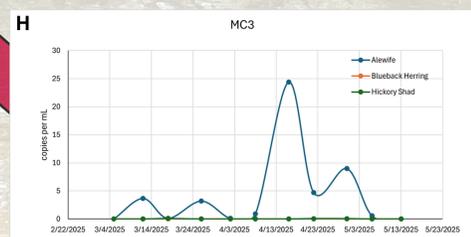
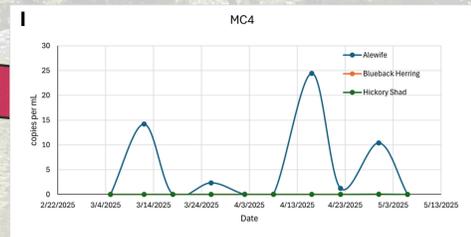
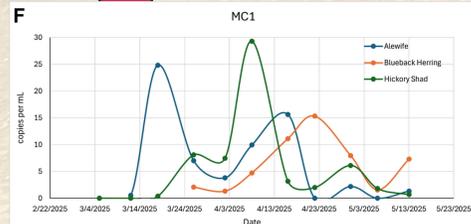
Collection of eDNA samples occurred weekly at four sites in Mattawoman Creek during March-May, 2025 with a Smith-Root eDNA sampler that filtered 2.0 liters of water with 5.0 um self-preserving filters. The eDNA samples were sent to Jonah Ventures for metabarcoding processing. Stream IP samples at each site were collected using a 360-micron mesh net attached to a square frame held on the bottom in the current for five minutes. Samples were preserved for lab processing. P_{herr} was calculated from Stream IP samples, the average of eDNA presence, and weighted average of eDNA presence.



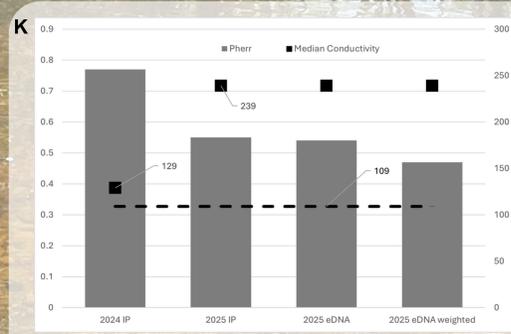
(A) A DNR biologist collects a Stream IP sample from Mattawoman Creek, (B) the collection net and jar in use during Stream IP sampling, (C) a DNR biologist collects an eDNA sample from the creek, and (D) the Smith-Root eDNA sampler in use while collecting a sample.



(E) Map of sampling sites on Mattawoman Creek with corresponding spatiotemporal use of spawning habitat by the three Herring species (i.e., Alewife, Blueback Herring, Hickory Shad) at (F) MC1, (G) MC2, (H) MC3, and (I) MC4 in 2025.



(J) P_{herr} estimates derived from Stream IP and eDNA sampling in 2025 with 90% confidence intervals.



(K) P_{herr} estimates from Stream IP (2024-2025) and eDNA (2025) with conductivity measurements from Mattawoman Creek. The dashed line represents the baseline conductivity for Coastal Plain streams.

Conclusions

1. Estimates of P_{herr} for Stream IP and eDNA sampling were similar based on 90% confidence intervals.
2. eDNA results allowed for identification of Herring to species level.
3. Alewife migrated the furthest upstream, followed by Hickory Shad then Blueback Herring.
4. Timing of migration followed previously established patterns for these anadromous species (Alewife first, Hickory Shad second, Blueback Herring last).
5. Variations of estimates of P_{herr} between 2024 and 2025 may be a response to conductivity fluctuations (i.e., road salt, pictured below) in Mattawoman Creek. A negative response by anadromous fish to conductivity has been determined from combined data from nine streams sampled during 2005-2024⁵.



(L), (M) Road salt on the bridge crossing at site MC2.

Literature Cited

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Future Considerations

1. Develop a cost analysis for Stream IP sampling versus eDNA sampling. How do the costs compare?
2. What does the historical data have to say about spawning migration and habitat use?
3. Is water quality having an impact on the spatiotemporal use of spawning habitat by the three Herring species?