

An American Shad Story: Using Geneious and Cervus for Allele Analysis Internship Experience

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Introduction

American Shad (*Alosa sapidissima*) is a fish in the herring family that can be found on the east coast from Newfoundland to Florida. American Shad mainly inhabit saltwater environments but return to freshwater environments to spawn (reproduce). These fish play important roles in sport and commercial fisheries (NCWRC).

American Shad populations have diminished over time through over-fishing and the construction of dams that block the spawning sites from the Shad (NCWRC). In the United States, the federal government holds a partial responsibility in keeping up with conservation efforts of these fish. The U.S. government works in collaboration with other groups, such as state agencies, to create management practices that will facilitate restoration of the fish populations (USFWS).

Aquaculture-based fisheries enhancement is a current management technique that is being investigated to maintain adequate populations levels of American Shad. This involves releasing cultured fish from hatcheries into natural populations, which could possibly pose a threat to the genetic diversity of wild populations. A genetically diverse population is important to ensure the species can adapt to changing environments. Broodstock, or fish hatchery populations, need to be as diverse as wild populations in order to avoid losing genetic diversity or increase inbreeding (Cushman et al., 2018).

In this internship, which I started on January 11th and will continue to April 30th, I am analyzing genetic diversity of American Shad from six rivers in North and South Carolina. It was initially chosen because it would allow for experience working in the field of conservation while also applying knowledge of genetics to analyses. The specific goals for this internship are to gain organizational skills and experience with data analysis techniques that pertain to the visualization of allelic data collected from the lab and parentage analyses. This internship was sponsored by the North Carolina Museum of Natural Sciences (NCMNS), which is located in Raleigh, NC and is one of many state-sponsored museums.

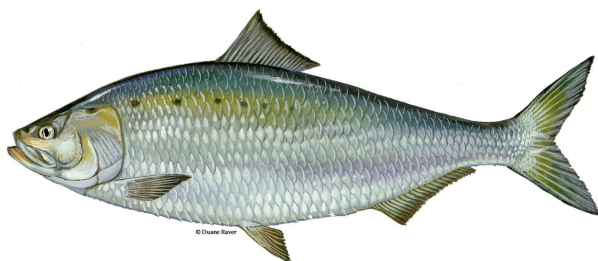


Figure 1. Illustration of American Shad.

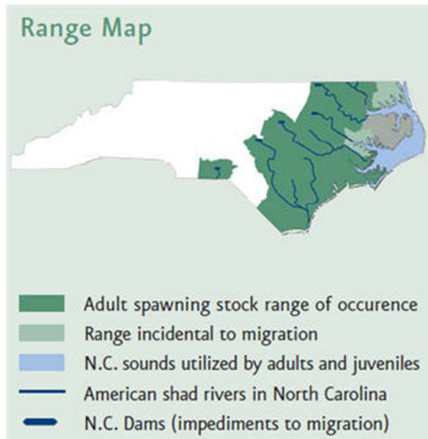


Figure 2. Range of American Shad in North Carolina.

Experience

For this internship, I am currently aiding a conservation geneticist (Dr. Heather Evans) who is employed by the North Carolina Wildlife Resources Commission (NCWRC) but works for NCMNS. I am analyzing microsatellite sequences in American Shad to inform conservation efforts. Microsatellites are repetitive sequences in the DNA that do not code for anything. They can be used as markers instead to track inheritance through families (*Microsatellite*).

This internship is completely virtual; everything is being done through a computer and . The software application Geneious was used to analyze microsatellite sequences in American Shad. The data obtained from Geneious was entered and organized in a master Excel sheet to keep track of data. The application software Cervus will be used to conduct parentage-based analyses, which is a statistical software program that uses allelic data to predict how likely it is that an offspring is related to a parent that is in the database.

I learned how to use Geneious to analyze allelic data that comes from an electropherogram, which is a way to measure the length of DNA fragments that have been previously separated. A lot of it required me using my own judgement to determine what peak calls (peaks measuring DNA fragment size) were real and what might have been a reading error, so asking my supervisor questions was very important. I am also currently learning how to use Cervus for parentage-based analyses, but I have not run any analyses yet. I also had to use my knowledge of Microsoft Excel to organize an extensive amount of allelic data from Geneious in the master sheet.

Contributions to Institution

NCMNS sponsored my internship, but I am really contributing to conservation efforts at NCWRC for American Shad (which uses labs at the museum to carry out research). Having this data is crucial to making decisions about management practices for American Shad in North and South Carolina (such as restocking waterways with more fish or choosing not to do so).

Conclusions

This experience has allowed me to gain insight into the field of conservation genetics. It is/was tough learning the principles and concepts behind what I am doing in an online environment (normally an intern in a similar position would be able to help in the museum lab, but I could not because of Covid regulations). However, this is a good internship for the circumstances we are in.

I believe my original goals have/are being achieved. Keeping the data organized through Excel and in Geneious has been tough but I think I have found better ways to stay organized. I have also learned how to use Geneious, how it functions, and I am currently in the process of understanding the basis of Cervus, both giving me experience with data analysis. I did not realize how much conservation geneticists do in terms of actual work (Dr. Evans works on many projects at a time) and I have realized just how underappreciated this field is.

While I highly appreciate the work I did and the experience I am gaining from this internship, I do not know if this field is for me.. I would still like to keep up with advancements in the field, though, since it is rapidly changing.

Acknowledgements

I would like to say thank you so much to Dr. Traci Porter at Salem College for being my internship sponsor and for her guidance through much of this process. I would also like to thank Dr. Evans at NCMNS for her insight and guidance on the analyses. Finally, I would like to thank the North Carolina Museum of Natural Sciences for providing these opportunities to interns. This poster template comes from gengraphics.com.

Image Citations

1. Brown, J. (2007). [Range of American Shad in North Carolina]. NCPedia. <https://www.ncpedia.org/american-shad-nc-wins>
2. Raver, D. (n.d.). [Illustration of American Shad]. U.S. Fish and Wildlife Service. https://www.fws.gov/fisheries/freshwater-fish-of-america/american_shad.html

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2. American shad. (n.d.). U.S. Fish and Wildlife Service. Retrieved April 9, 2021, from https://www.fws.gov/fisheries/freshwater-fish-of-america/american_shad.html
3. Cushman, E. L., Evans, H. K., Moyer, G. R., Raley, M. E., Williams, A. S., & Darden, T. L. (2018). Development of a Standardized Molecular Tool and Estimation of Genetic Measures for Responsible Aquaculture-Based Fisheries Enhancement of American Shad in North and South Carolina. *Transactions of the American Fisheries Society*, 148(1), 148–162. <https://doi.org/10.1002/tafs.10127>
4. Microsatellite. (n.d.). National Human Genome Research Institute. Retrieved April 9, 2021, from <https://www.genome.gov/genetics-glossary/Microsatellite>