

# Genetic Structure of Atlantic Sturgeon Population Based on Mitochondrial DNA Control Region Sequences

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## Background



- Atlantic sturgeon
  - large, long-lived, and anadromous, reaching weights approaching 300 kg and ages of 60 years (Smith and Clugston 1997)
  - an historically important commercial species because of their valuable roe (caviar) and meat
  - some populations in United States in danger of extinction

- DNA sequence analysis of the mtDNA control region
  - a sensitive tool in elucidating the stock structure of fishes because of their rapid evolution of that portion of the genome (Wirgin and Waldman 1994; Stepien 1995)

- Study area
  - fish collected from 6 Atlantic coast river systems; Hudson (NY,NJ), Delaware (NY, PA, NJ, DE), Altamaha (GA), Chesapeake Bay (VA), Great Pee Dee (NC), Neuse (SC)

## Methods

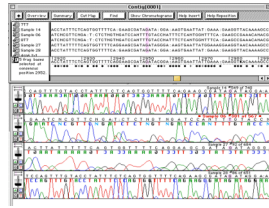
- Sample collections – fin clip or barbell from collected fish were obtained and stored in 95% ethanol or SDS-urea buffer, pH 6.8.

- DNA extraction – standard phenol-chloroform extractions and recovered by alcohol precipitations

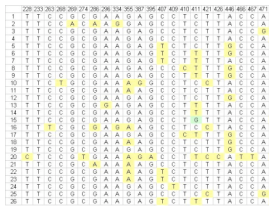
- Sequence analysis of the mitochondrial DNA control region – a 300-bp stretch of the mtDNA control region from 109 individuals

- Data Analysis
  - Pileup program in GCG for multiple alignment
  - TFGPA (tools for population genetic analysis) software to construct a UPGMA (unweighted pair-group method with arithmetic averages) phenogram (Kumar et al. 1993): A pairwise matrix of interpopulation nucleotide diversity indices (Nei 1987) among the rivers was used.

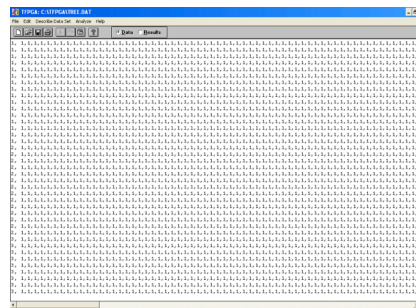
\* Miller, Mark P. 1997. Tools for population genetic analyses (TFGPA) 1.3: a windows program for the allozyme and molecular population genetic data. Computer software distributed by author. ([http://www.marksgeneticssoftware.net/\\_vti\\_bin/shtml.exe/tfpga.htm](http://www.marksgeneticssoftware.net/_vti_bin/shtml.exe/tfpga.htm))



Pileup and polymorphic nucleotide site searching



26 Atlantic sturgeon haplotypes (leftmost column) identified based on 27 polymorphic nucleotide sites (White: most abundant base, Yellow: second abundant base, Green: third abundant base)



Example of data set for TFGPA analysis

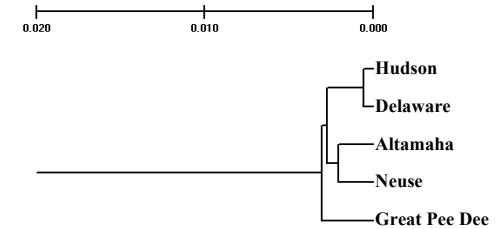
(Each line - each individual, Each column – each locus, First column - population identifier)

Location	N	Haplotype destination																										
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
Hudson	48	7	3	11	13	1	1	1	1	2	1	1	1	1	4													
Delaware	13	1	1	2	2	1	1	1	1	1	1	1	1	1	1	4												
Altamaha	28																											
Chesapeake Bay	1			1	2																							
Great Pee Dee	9																											
Neuse	6																											

Atlantic sturgeon haplotype frequencies

## Results

- 26 mtDNA haplotypes were identified based on 27 polymorphic nucleotide sites in 109 Atlantic Sturgeon specimens.
- 16 of the 26 (62%) haplotypes were unique to a particular river (ex. haplotypes 20 for Great Pee Dee). However, 13 of those haplotypes were observed as only one or two specimens in their respective collections.



A UPGMA tree of the interpopulation nucleotide diversity indices for mtDNA control region sequencing data from Atlantic sturgeon population of 5 Atlantic coast rivers

- The UPGMA tree generated from the interpopulation nucleotide diversity indices clustered the 5 population samples included in this analysis into one major branch that separated the two northern populations (Hudson and Delaware) from those in the south (Altamaha and Neuse). The Great Pee Dee population occupied discrete branches.

(Because only one individual was obtained from Chesapeake Bay, this population was not included in this analyses)

## References

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- Nei, M. 1987. Molecular evolutionary genetics. Columbia University Press. New York.
- Smith, T. L., and J. P. Clugston. 1997. Status and management of Atlantic sturgeon, *Acipenser oxyrinchus*, in North America. Environmental Biology of Fishes 48:335-346.
- Stepien, C. A. 1995. Population genetic divergence and geographic pattern from DNA sequences: examples from marine and freshwater fishes. Pages 263-287 in J.L. Nielson, editor. Evolution and the aquatic ecosystem: defining unique units in population conservation. American Fisheries Society, Symposium 17, Bethesda, Maryland.
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