Fisheries Session

Mitochondrial DNA Polymorphism of Striped Bass in the Southeastern United States[1]

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Abstract: Striped bass (*Morone saxatilis*) from the Apalachicola River, Florida; Chattahoochee-Flint River, Georgia; Ogeechee River, Georgia; Savannah River, Georgia; Santee-Cooper River, South Carolina; Tallapoosa River, Alabama; and Chesapeake Bay, Maryland, were examined for polymorphism in their mitochondrial DNA (mtDNA) genotype. The Xba I site loss that is supposed to identify individuals with maternal lineage from Gulf Coast stocks was found in some fish from the Apalachicola and Chattahoochee-Flint rivers, as well as one individual from the Ogeechee River. Additionally, a unique Bgl I site gain was found in these same populations. Several rare genotypes found in the Apalachicola-Chattahoochee-Flint system were also rare genotypes in Chesapeake Bay. Several unique genotypes of low frequency were found in the Ogeechee River. Fish from the Santee-Cooper River were fixed for a unique Dra I genotype. The only other population exhibiting this Dra I genotype was found in the Tallapoosa River, confirming stocking history of Santee-Cooper fish into this system. Composite genotypes were distinctive for most of the fish sampled in the Apalachicola River and all individuals from the Santee-Cooper River.

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Controversy exists with respect to the propagation and distribution of striped bass (*Morone saxatilis*) populations especially in regard to the Gulf Coast strain

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(Wooley and Crateau 1983). Several state and federal hatcheries are expending large efforts to identify and propagate this strain of striped bass. Degradation of habitat and introductions of non-native striped bass and hybrid bass (*M. saxatilis* x *M. chrysops*) have also complicated identification and propagation of the Gulf Coast and other strains.

Genetic data on striped bass are needed for management of other populations of striped bass as well as for the Gulf Coast strain. Little genetic data exist for striped bass, and initial isozyme surveys on populations in the Chesapeake Bay revealed low levels of biochemical genetic variability (Morgan et al. 1973, Grove et al. 1976, Sidell et al. 1980). Since natural spawning of striped bass is declining and artificial propagation with limited number of brood fish is becoming more prevalent, the loss of potentially valuable genotypes through genetic drift becomes more likely. One management strategy might be to identify genetic variation in striped bass and selectively propagate the fish to ensure that this genetic variation is maintained until its importance is better understood.

Analysis of mitochondrial DNA (mtDNA) is one technique that may help ascertain genetic variation in striped bass. Variability in sequences of mtDNA has been identified as a powerful tool to distinguish strains of fish and measure genetic variability (Chapman et al. 1982, Bermingham and Avise 1986). When sufficient differences in mtDNA sequence exist, individuals from different populations can be identified when mixed. When the 2 populations begin to interbreed, however, the parentage of the progeny becomes uncertain since mtDNA is inherited maternally. Contribution from the midpiece of the sperm is less than 5% and difficult to detect (Chapman et al. 1982). Genetic variation in mtDNA can still be observed in mixed populations, but only maternal lineage can be positively traced. The objective of this study was to identify variation in mitochondrial DNA in populations of striped bass in the Southeastern United States.

Materials and Methods

Samples of either liver, milt, or ovaries were obtained from striped bass from the Apalachicola River, Florida; Chattahoochee-Flint River, Georgia; Ogeechee River, Georgia; Savannah River, Georgia; Santee-Cooper River, South Carolina; Tallapoosa River, Alabama; and Chesapeake Bay, Maryland. Sample sizes were 8, 9, 37, 12, 17, 5, and 63, respectively (Table 1). Samples were collected, and tissues were excised and shipped to Auburn University on ice where the samples were partially processed with procedures of Chapman and Powers (1984). Then the samples were sent to Chesapeake Bay Institute for completion of analysis with procedures of Chapman and Powers (1984).

Samples of mtDNA from each fish were digested separately with 10 restriction enzymes: Bcl I, Bgl I, Dra I, Eco RI, Eco RV, Hind III, Pvu II, Sst I, Sst II, and Xba I. Nomenclature of genotypes was that of Chapman (1987). Size polymorphisms were designated A = 17.5 kb, B = 17.6 kb, C = 17.7 kb, D/E = 17.65/

17.75 kb and F = 17.8 kb. The common digest profile was designated N. M indicated a restriction site loss; 0, a restriction site gain; and P, 2 restriction site gains (Table 1).

Results and Discussion

Genetic variation was observed using all restriction enzymes except Pvu II, Sst I, and Sst II (Table 1). Some of this variation was due to size polymorphisms and would be detected using more than 1 enzyme. Restriction site losses were found for Xba I. Restriction site gains were found for both Bgl I and Eco RI. Both size and restriction site changes were observed for Dra I. Twelve different composite genotypes were observed (Table 2).

Size polymorphisms

All populations exhibited 3 to 5 size polymorphisms except for Santee-Cooper and Tallapoosa (Tables 1, 2). The A genotype was most common in Ogeechee and Savannah populations. The B genotype was frequent in Georgia populations and the Chesapeake Bay population. The C size polymorphisms were at highest frequency in Apalachicola, Santee-Cooper, and Tallapoosa populations. A rare D/E genotype was found in 3% of the Chesapeake Bay population. The F size polymorphisms were found in the Apalachicola-Chattahoochee-Flint system and in the Chesapeake Bay.

Restriction site gains

One restriction site gain was found for Bgl I. This gain was found in 75%, 11%, and 3% of the Apalachicola, Chattahoochee-Flint, and Ogeechee individuals examined, respectively (Table 1). The Ogeechee population also exhibited 2 site gains for Eco RI; 5% had the double site gain.

Restriction site losses

The Xba I site loss previously identified (Wirgin et al. 1989) as indicative of maternal lineage from the Gulf Coast strain was found in the Apalachicola and Chattahoochee-Flint populations, as well as 1 individual in the Ogeechee population (Table 1). Eighty-eight percent of the individuals from the Apalachicola River and 22% from the Chattahoochee-Flint system had this deletion.

A site loss (C-1) for Dra I was found in all individuals from the Santee-Cooper system and 4 of 5 individuals examined from the Tallapoosa River. The 4 individuals from the Tallapoosa River with the site loss probably have maternal lineage from the Santee-Cooper population. Fish from the Santee-Cooper system were transferred to Tennessee and then the state of Alabama obtained fish from Tennessee for brood stock. One individual from the Chesapeake Bay population also had a unique Dra I site loss, B-1.

Table 1. Mitochondrial DNA genotype frequencies for 7 populations of striped bass.

Restriction enzyme	Genotype	Genotype frequency (*N*)[a]						
		A(8)	CF(9)	0(37)	S(12)	SC(17)	T(5)	CB(63)
Bcl I	A	0.13	0.11	0.38	0.50	0.00	0.00	0.19
	B	0.00	0.44	0.51	0.33	0.00	0.20	0.44
	C	0.75	0.22	0.11	0.17	1.00	0.80	0.32
	D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	F	0.13	0.22	0.00	0.00	0.00	0.00	0.02
Bgl I	N	0.25	0.89	0.97	1.00	1.00	1.00	1.00
	O	0.75	0.11	0.03	0.00	0.00	0.00	0.00
Dra I	A	0.13	0.11	0.38	0.50	0.00	0.00	0.19
	B	0.00	0.44	0.51	0.33	0.00	0.20	0.42
	B-1	0.00	0.00	0.00	0.00	0.00	0.00	0.02
	C	0.75	0.22	0.11	0.17	0.00	0.00	0.32
	C-1	0.00	0.00	0.00	0.00	1.00	0.80	0.00
	D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	F	0.13	0.22	0.00	0.00	0.00	0.00	0.02
Eco RI	A	0.13	0.11	0.38	0.50	0.00	0.00	0.19
	B	0.00	0.44	0.46	0.33	0.00	0.20	0.44
	C	0.75	0.22	0.11	0.17	1.00	0.80	0.32
	D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	F	0.13	0.22	0.00	0.00	0.00	0.00	0.02
	P	0.00	0.00	0.05	0.00	0.00	0.00	0.00
Eco RV	A	0.13	0.11	0.38	0.83	0.00	0.00	0.19
	B	0.00	0.44	0.51	0.00	0.00	0.20	0.54
	C	0.75	0.22	0.11	0.17	1.00	0.80	0.22
	D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	F	0.13	0.22	0.00	0.00	0.00	0.00	0.02
Hind III	A	0.13	0.11	0.38	0.50	0.00	0.00	0.19
	B	0.00	0.44	0.51	0.33	0.00	0.20	0.44
	C	0.75	0.22	0.11	0.17	1.00	0.80	0.32
	D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
	F	0.13	0.22	0.00	0.00	0.00	0.00	0.02
Pvu II	N	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Sst I	N	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Sst II	N	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Xba I	M	0.88	0.22	0.03	0.00	0.00	0.00	0.00
	N	0.12	0.78	0.97	1.00	1.00	1.00	1.00

[a]A = Apalachicola River, CF = Chattahoochee-Flint River, O = Ogeechee River, S = Savannah River, SC = Santee-Cooper River, T = Tallapoosa River, CB = Chesapeake Bay.

Table 2. Composite mitochondrial DNA genotype frequencies for 7 populations of striped bass.

Composite genotype	Genotype frequency (*N*)[a]						
	A(8)	CF(9)	O(37)	S(12)	SC(17)	T(5)	CB(63)
A	0.13	0.11	0.38	0.50	0.00	0.00	0.19
B	0.00	0.44	0.43	0.33	0.00	0.20	0.43
B-1	0.00	0.00	0.03	0.00	0.00	0.00	0.00
B-2	0.00	0.00	0.03	0.00	0.00	0.00	0.00
B-3	0.00	0.00	0.03	0.00	0.00	0.00	0.00
C	0.00	0.22	0.11	0.17	0.00	0.00	0.32
CA	0.75	0.00	0.00	0.00	0.00	0.00	0.00
C-1	0.00	0.00	0.00	0.00	1.00	0.80	0.00
D/E	0.00	0.00	0.00	0.00	0.00	0.00	0.03
F	0.00	0.00	0.00	0.00	0.00	0.00	0.03
F-1	0.13	0.11	0.00	0.00	0.00	0.00	0.00
F-2	0.00	0.11	0.00	0.00	0.00	0.00	0.00

[a]A = Apalachicola River, CF = Chattahoochee-Flint River, O = Ogeechee River, S = Savannah River, SC = Santee-Cooper River, T = Tallapoosa River, CB = Chesapeake Bay.

Composite genotypes

Twelve composite genotypes from all 10 restriction enzymes were observed (Table 2). The CA genotype was found only in the Apalachicola population. The F-1 genotype was observed in the Apalachicola-Chattahoochee-Flint system, and the F-2 genotpye in 1 individual in the Chattahoochee-Flint River. Several unique genotypes—B-1, B-2, and B-3—were exhibited only by the Ogeechee population. The C-1 genotype identified all individuals from the Santee-Cooper population and individuals in the Tallapoosa River that probably shared common maternal ancestry. Rare D/E (3%) and F genotypes (3%) were observed only in the Chesapeake Bay population.

In conclusion, genetic variation existed within and among populations of striped bass in the Southeastern United States. The only homozygous population was found in the Santee-Cooper River, and these fish had a unique genotype that differentiated them from other populations.

The Xba I site loss indicative of maternal lineage from the Gulf Coast strain was found in the Apalachicola-Chattahoochee-Flint system and in 1 individual from the Ogeechee population. The 1 individual from the Ogeechee River is either a contaminant or the Xba site loss is not naturally restricted to the Apalachicola-Chattahoochee-Flint system. Individuals that lack the Xba site loss are not necessarily of Atlantic Coast origin since the original genotypic frequencies were not determined prior to stocking of Atlantic Coast strains. Since the mtDNA is a small portion of the total genome and is primarily of maternal origin, nuclear genetic markers should be sought to supplement data on mtDNA or striped bass.

The data indicate that genetically distinct populations of striped bass exist. Populations should not be further mixed until more extensive genetic data are col-

lected, the relationships between these genetic differences and stocking histories determined, and the significance of this genetic variation established. Performance traits of these striped bass populations should be measured and their relationship to the genetic markers determined.

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