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CHANGES IN THE POPULATION STRUCTURE OF MALE STRIPED BASS, *MORONE SAXATILIS*, SPAWNING IN THE THREE AREAS OF THE CHESAPEAKE BAY FROM 1984 TO 1986

The striped bass, *Morone saxatilis*, supported important commercial and recreational fisheries until recently. Population declines over the past 15 years have prompted fishing restrictions in most states along the Atlantic coast of the United States and a complete moratorium in Maryland. Spawning success of *M. saxatilis* has been poor since 1970, except for 1982 when the juvenile index reported by the Maryland Department of Natural Resources which was near the 50-yr average for Chesapeake stocks (Boone and Uphoff 1983).

Knowledge of the population structure of the striped bass is important to restoration efforts. Many attempts have been made to identify distinct stocks along the Atlantic coast and within Chesapeake Bay. Morphological studies have found evidence of discrete stocks within the Chesapeake system (c.f. Setzler et al. 1980 for review), while studies of allozyme variation have been ambiguous (Morgan et al. 1973; Grove et al. 1976; Sidell et al. 1980). Electrophoretic studies have found only limited allozyme variation and, thus, discrimination of stocks has been problematical. To further understand the reproductive patterns of striped bass in the Chesapeake Bay, an analysis of mitochondrial DNA (mtDNA) genotypes among spawning individuals was initiated in 1984. For the most part, mtDNA is maternally inherited and and provides information concerning matriarchal ancestry. The results of this analysis for the overall striped bass fishery will be reported elsewhere, but support the conclusion that distinct stocks exist in the Chesapeake Bay. As part of this survey, it was deemed important to examine the distribution of mtDNA genotypes of striped bass among 1982 year class individuals as they recruited into reproducing populations and to determine if the distribution of these genotypes changed in subsequent years. I report here on the distribution of mtDNA genotypes in 1982 year class males during their first (1984) and third spawning seasons (1986).

Methods

Striped bass were gill netted from the Chesapeake Bay at the mouth of the Sassafras River (Worton Point, 23, 24, 26 April 1984 and 7, 9 May 1986), the Potomac River (2 May 1984 and 29 April 1986) and Choptank River (9 May 1984 and 13 May 1986) during the spawning season. Age and sex determinations were made by counting scale annuli and visually inspecting the gonads, respectively. The accuracy of scale annuli for aging striped bass was reviewed by Setzler et al (1980). MtDNA was isolated from the livers according to the methods of Chapman and Powers (1984) and digested with the restriction endonucleases *Hind* III, *Eco* RI, and *Bcl* I. The digested mtDNA fragments were separated on 0.8% agarose gels. To insure consistent scoring of genotypes, 1984 samples were rerun against 1986 samples. Homogeneity of mtDNA frequencies within localities and among years was tested by G^2 tests with pooling of expected classes less than five (c.f. Sokal and Rolf 1969).

Results and Discussion

Variation in *M. saxatilis* mtDNA was characterized by fragment length polymorphisms that can be

divided into 14 distinct matriarchal clones. For this report, I consider only the five mtDNA size groups that account for more than 95% of the variation in Chesapeake Bay specimens. Molecular weight estimates for the size groups (Fig. 1) were A = 17.5 kilobases (kb), B = 17.6 kg, C = 17.7 kb, D/E = 17.65/17.75, and F = 17.8. The D/E genotype indicated individuals with two distinct molecules. These genotypes were easily distinguished by the migration of the lowest molecular weight fragment produced by digestion with the enzymes mentioned above.

The distribution of mtDNA genotypes in males taken from each of the collecting localities changed dramatically from 1984 to 1986 (Table 1). In 1984, the B genotype was found in more than 75% of the specimens (81% in the Potomac, 53% in the Choptank, and 100% in the Worton Point area). In 1986 this genotype represented about 30% of the spawning 1982 year class males (21% in the Potomac, 23% in the Choptank, and 42% in the Worton Point area). The C genotype represented 15% of the specimens in 1984, but was more common in 1986 (49%). The D/E and F genotypes were not observed in 1984, but combined to represent 17% of the specimens taken in 1986. The changes in mtDNA genotype frequencies from 1984 to 1986 are highly significant in the combined data and in the Worton Point and Potomac spawning areas (Table 1). The nonsignificant result in the Choptank may be due to the effects of pooling and inadequate sample size.

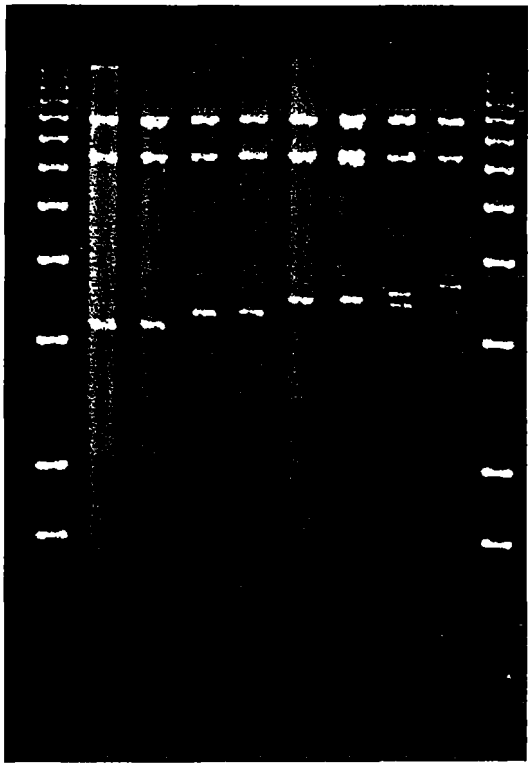

FIGURE 1.—*BclI* digestion patterns of *Morone saxatilis* mtDNA showing size fragment variation for genotypes A = 17.5 kg, lanes 2, 3; B = 17.6 kb, lanes 4, 5; C = 17.7 kb, lanes 6, 7; D/E = 17.65/17.75, lane 8; and F = 17.8 kb, lane 9. Lanes 1 and 10 are 1 kb ladder standards purchased from BRL, Inc. (Reference to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.)

Year to year variation in the frequencies of various mtDNA genotypes found among spawning individuals could arise from changes in the age composition. Previously spawning individuals may die and new recruits may be descendants of different females. These possibilities are not concerns here because data are reported only upon the 1982 year class males. The changes in mtDNA frequencies within spawning members of this group can be explained by either of three hypotheses. First, the abundance of B genotypes in the 1984 sample may be an overestimation of their actual frequency, but the age at which male striped bass join spawning aggregations may depend upon genetic factors that are marked by (or perhaps linked to) mtDNA genotypes. As the remaining genotypes became sexually mature, mtDNA frequencies among spawners more accurately reflected the frequencies in the 1982 year class. Second, the 1984 data may actually reflect genotype frequencies during that year, but differential mortalities from 1984 to 1986 substantially altered the frequencies. This does not necessarily imply selective mortalities because aggregations of B genotypes following the spawning season may have been more susceptible to fishing pressure. Third, the increase in the C, D/E, and F genotypes may be the result of migration from other areas. The survey of Chapman and Powers (unpubl. data) did not find significant concentrations of these genotypes in the Chesapeake Bay, but this survey did not include the York and James Rivers in the Chesapeake Bay or the Hudson River. If these rivers are the source of most of the C, D/E, and F genotypes found in this study, it would require a migration rate of 50% among Chesapeake Bay and/or the Hudson River stocks to produce the frequency changes noted here.

Migratory patterns of *M. saxatilis* vary from region to region along the Atlantic coast. Populations from southern North Carolina to the St. John's River, FL, are essentially riverine and do not under-

TABLE 1.—The distribution of mtDNA genotypes and G^2 tests (Sokal and Rohlf 1969) for random distributions in the Potomac River, the Choptank River and the Worton Point area in 1984 and 1986. The expected values are in parentheses.

		Genotype					
		A	B	C	D/E	F	G^2
Potomac	1984		13 (6.9)	3 (7.2)	0 (0.7)	0 (1.1)	7.12 $P < 0.01$
	1986		6 (12.1)	17 (12.7)	2 (1.2)	3 (1.9)	
Choptank	1984	3 (1.5)	7 (5.5)	3 (4.0)	0 (1.0)	0 (1.0)	2.85 $0.1 > P > 0.05$
	1986	0 (1.5)	3 (5.5)	6 (4.0)	2 (1.0)	2 (1.0)	
Worton Point	1984	0 (0.5)	11 (6.2)	0 (3.4)		0 (0.8)	10.51 $P < 0.01$
	1986	2 (1.4)	12 (15.8)	11 (8.6)		3 (2.2)	
Combined	1984	3 (1.8)	31 (18.7)	6 (14.7)	0 (1.5)	0 (3.9)	26.62 $P < 0.01$
	1986	2 (3.1)	21 (32.3)	34 (25.3)	4 (2.5)	8 (5.1)	

take coastal migrations (c.f. Setzler et al. 1980). In the Chesapeake Bay and Hudson River, tagging studies suggest that individuals less than age 2 do not migrate extensively from their natal tributaries (c.f. Setzler et al. 1980). After this sedentary period, females begin to leave the Chesapeake Bay for coastal waters and virtually all females older than age 4 return only to spawn (Kohlenstein 1980). Females do not mature sexually until age 3 at the earliest and most do not mature until age 4 or 5 (Jones et al. 1977). In contrast, few males leave the Chesapeake Bay until age 4 or 5 and virtually all age 2 are sexually mature. Tagging studies by Manseuti (1961) suggest that larger males (ages 3-4) moved greater distances within the Chesapeake than small males (ages 0-2). Massman and Pacheco (1961) supported this conclusion and also found that James and York River fish tended to migrate northward in the bay proper. These migration studies fit nicely with the data presented here, if indeed the changes in mtDNA frequencies were due to immigration from the James and York Rivers.

Further study of striped bass population dynamics are needed to test the hypotheses outlined above. Of particular importance will be an assessment of populations from the James and York Rivers. Whatever the outcome, the data presented here will need to be considered in management plans for this economically important species.

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