Abstract.—Restriction-fragment length polymorphism analysis of mitochondrial DNA (mtDNA) was used to investigate the genetic basis of stock structure of the bluefish *Pomatomus saltatrix* along the U.S. mid-Atlantic coast, and to determine the degree of genetic differentiation between mid-Atlantic bluefish and Australian conspecifics. A total of 472 young-of-the-year (YOY) and yearling bluefish collected in New Jersey, Virginia, and North Carolina over a period of 3 years, and 19 YOY bluefish collected in New South Wales, Australia were analyzed with 9 informative restriction endonucleases. Despite considerable mtDNA variation within samples of U.S. mid-Atlantic bluefish, no significant genetic differentiation was detected among spring-spawned and summer-spawned (YOY) bluefish, YOY and yearling bluefish from different geographic locations along the mid-Atlantic coast, or yearling bluefish collected at the same location in different years. Mid-Atlantic bluefish differed from their Australian conspecifics by three or more restriction site differences, or a mean nucleotide sequence divergence of 1.96%. In addition, Australian bluefish demonstrated greatly reduced levels of mtDNA variation relative to the mid-Atlantic samples. The results of this study suggest that bluefish along the mid-Atlantic coast comprise a single genetic stock and that significant differentiation occurs among geographically disjunct populations of this widely distributed marine fish.

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Stock structure of the bluefish *Pomatomus saltatrix* along the mid-Atlantic coast*

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The bluefish *Pomatomus saltatrix* is broadly distributed in temperate and warm-temperate coastal waters of the world's oceans (Briggs 1960), although it is absent from the eastern Pacific (Smith 1949). In the United States, bluefish occur along the Atlantic and Gulf coasts, supporting large recreational and commercial fisheries.

The movements and biology of the bluefish, like many fishes along the Atlantic coast, are closely tied to large seasonal fluctuations in water temperature (reviewed in Wilk 1977). Spawning appears to be concentrated in two spatially and temporally distinct events: a spring spawn at the inside edge of the Gulf Stream in the south Atlantic bight, and a summer spawn in the shelf waters of the mid-Atlantic bight (Kendall and Walford 1979). However, the presence of eggs and larvae indicates that some spawning occurs throughout the year, especially in the southern portion of the south Atlantic bight (Kendall and Walford 1979, Collins and Stender 1988). Presumably, eggs and larvae are transported by cross-shelf currents to estuaries along the Atlantic coast which serve as nursery grounds for the young bluefish.

The discrete temporal nature of the two spawning events is evidenced by a bimodal size distribution of juvenile bluefish within the estuaries during the middle and late summer (Nyman and Conover 1988, McBride 1989), a difference that is still evident in yearling fish and may persist until fish reach 4 years of age (Lassiter 1962). The extent to which each of the major spawning events contributes juveniles to specific areas appears to vary annually (Chiarella and Conover 1990).

A general mixing of bluefish from different coastal areas may occur at the end of the first summer. Tagging studies indicate that as water temperatures cool, young bluefish move out of the estuaries in a southerly direction and probably overwinter in the south Atlantic bight (Lund and Maltezos 1970, Wilk 1977), while adults move further offshore (Wilk 1977). As temperatures along the mid-Atlantic coast warm in the spring, there is a general movement of bluefish up the Atlantic coast, with larger bluefish making more extensive migrations into northern waters (Wilk 1977).

Although the seasonal movements of bluefish may be conducive to a mixing of fish from different coastal areas, mark and recapture studies suggest that a large fraction of bluefish are recaptured in the same general area in which they were tagged (Lund and Maltezos 1970, Wilk 1977). The degree to which this fidelity affects stock structure is not known.

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Table 1
Sample size, date, location, and age of bluefish *Pomatomus saltatrix* collected and analyzed in this study. YRL = yearling; YOY = young-of-the-year.

Sample	*n*	Date	Location	Age
VA88	100	7/88	York River VA	YRL
VA89	102	7/89	York River VA	YRL
VA90	39	7/90	York River VA	YRL
NC88	83	7/88	Hatteras NC	YRL
NC89	57	7/89	Hatteras NC	YRL
NC90	40	7/90	Hatteras NC	YOY
NJ90-Sp	26	8/90	southern NJ	YOY
NJ90-Su	25	8/90	southern NJ	YOY
AU91	19	2/91	Port Stephens, N.S.W., Australia	YOY

The genetic basis of population structure of the bluefish is poorly understood. Based on studies of morphological and scale characteristics, Wilk (1977) suggested that two populations exist along the mid-Atlantic coast. These populations correspond to the fish which spawn off North Carolina in the spring, and those that spawn in the northern mid-Atlantic during the summer. Lund and Maltezos (1970) also concluded on the basis of mark and recapture analysis that several populations are present along the mid-Atlantic coast. Chiarella and Conover (1990) used scales from summer-spawning fish in the New York Bight to back-calculate length at age-1 and found that most summer-spawning fish had lengths corresponding to a spring birthdate, a result not consistent with spring- and summer-spawning stocks. They concluded that the morphological and life-history differences found between spring- and summer-spawned bluefish are probably ecophenotypic in nature, and suggested that a direct genetic analysis of stock structure was warranted.

In this paper, we present the results of a restriction-fragment length polymorphism (RFLP) analysis of bluefish mitochondrial DNA (mtDNA) among bluefish collected along the mid-Atlantic coast over a period of 3 years. We employed RFLP analysis of mtDNA to evaluate genetic differentiation between spring- and summer-spawned bluefish collected at a single location at the same time, among similarly-sized bluefish collected at the same location over several years, and among bluefish collected during the same year from the north and south mid-Atlantic coast, as well as from a disjunct population in Australia.

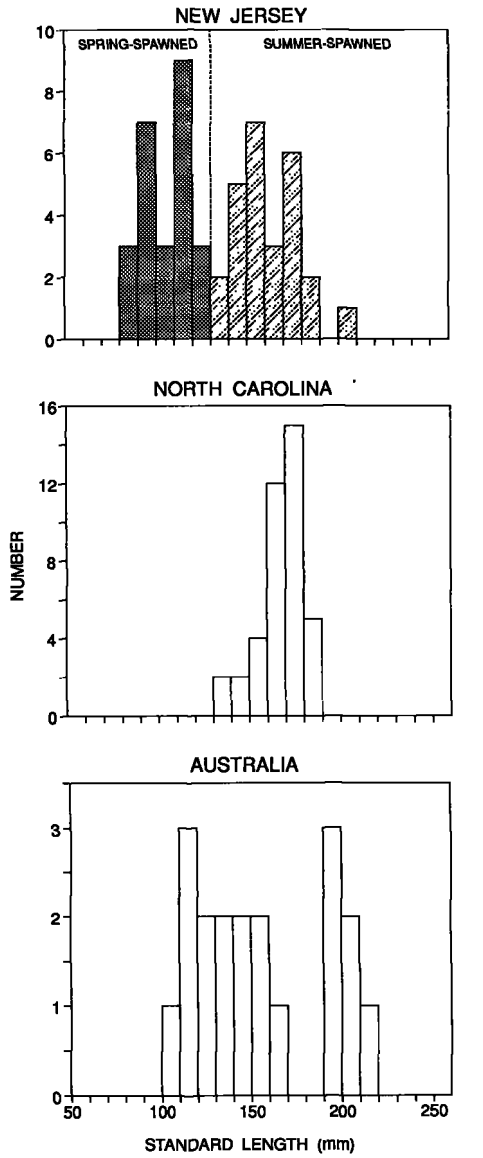

Figure 1
Frequency distribution of standard lengths among YOY bluefish *Pomatomus saltatrix* collected in New Jersey, North Carolina, and Port Stephens, N.S.W., Australia. The New Jersey fish were separated into spring- and summer-spawned groups based upon their standard length on the date of capture relative to a standard length of 125 mm (Nyman and Conover 1988, McBride 1989).

Materials and methods

Experimental design and collections

Bluefish were collected along the mid-Atlantic coast during 1988–90, and in Australia during 1991 (Table 1). To test the hypothesis that spring- and summer-spawned bluefish represent genetically distinct stocks, young-of-the-year bluefish were collected by trawl on New Jersey state survey cruises during August 1990 (NJ90-Sp, NJ90-Su, Table 1). Fish were classified as spring- or summer-spawned based on the date of capture using a standard length of 125 mm used as the cut-off between the two groups in August (Nyman and Conover 1988, McBride 1989). The distribution of lengths is presented in Figure 1.

To obtain an estimate of the degree of temporal genetic variation between bluefish year-classes at a single collection location, 1-year-old (yearling) bluefish were purchased from commercial fishermen on the York River, Virginia during July 1988 (VA88), 1989 (VA89), and 1990 (VA90), and in Hatteras, North Carolina during 1988 (NC88) and 1989 (NC89). The distribution of lengths of the Virginia and North Carolina samples is presented in Figure 2.

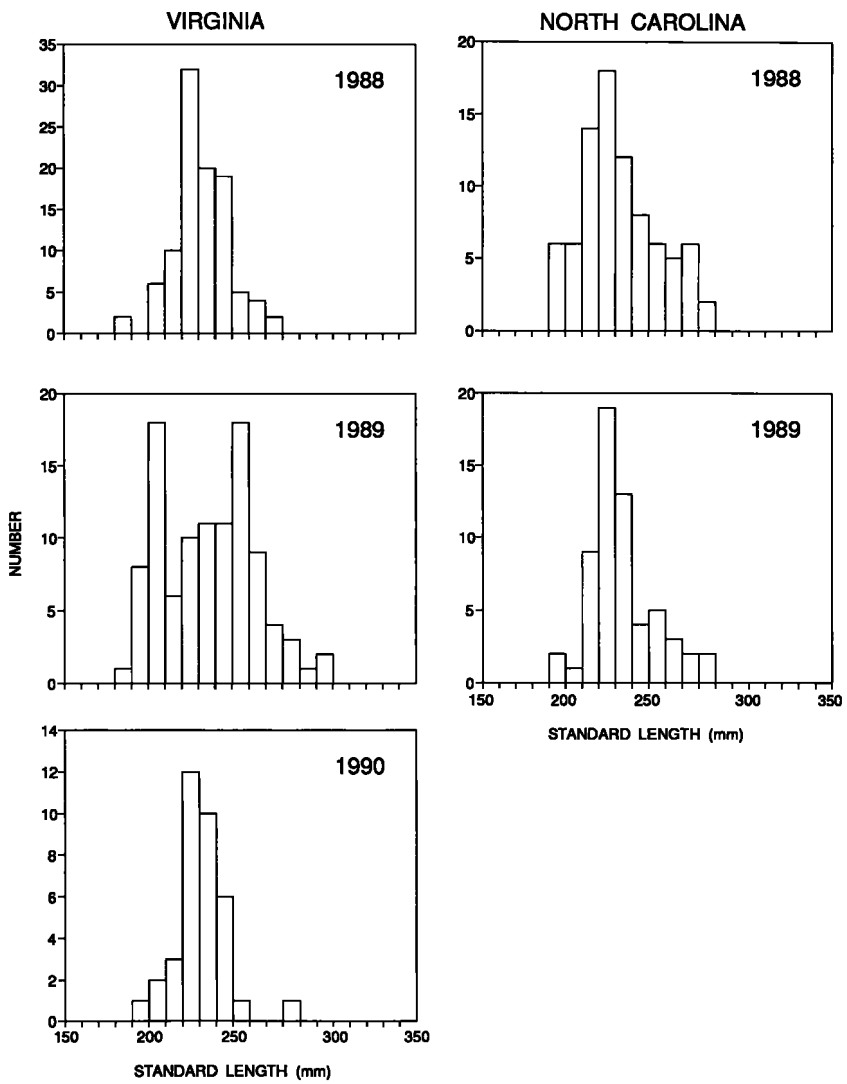

Figure 2
Frequency distribution of standard lengths among yearling bluefish *Pomatomus saltatrix* collected in (left) the York River, VA during summer 1988, 1989, and 1990, and (right) Hatteras, NC during summer 1988 and 1989.

An analysis of geographic population structure of highly vagile fishes, like the bluefish, is problematic. The presence of an adult bluefish in one geographic location is not very meaningful, as the fish could easily travel to another location several hundred kilometers away within a few weeks. If discrete geographic stocks of bluefish exist, such stocks might be expected to separate at the time of spawning. However, collection of adults at this critical time is difficult since bluefish spawn at the edge of the continental shelf during the spring and in the middle of the shelf during the summer (Kendall and Walford 1979). Thus we decided to focus our study on their products, YOY bluefish. Although some mixing probably occurs during cross-shelf transport, the genetic composition of YOY bluefish should reflect the composition of the offshore spawning population.

To determine genetic differentiation among bluefish along the mid-Atlantic coast, samples of YOY individuals were collected during summer 1990 in New Jersey (described above) and purchased from commercial fishermen in Hatteras, North Carolina (NC90). In addition, to obtain an estimate of the degree of mtDNA differentiation between isolated bluefish populations, a sample of 19 YOY bluefish was collected by hook-and-line in Port Stephens, N.S.W., Australia during February 1991 (AU91). The size composition of all YOY collections is presented in Figure 1.

mtDNA analysis

Depending on size and quality of the bluefish, three different procedures were used to analyze bluefish mtDNA. The rapid isolation procedure of Chapman and Powers (1984) was used to obtain mtDNA from samples of lateral red muscle from the yearling bluefish collected in 1988 and 1989. After digestion, restriction fragments were separated electrophoretically on 0.8–1.5% agarose gels run at 2 volts/cm overnight and visualized directly with ethidium bromide staining. For those samples in which there was not sufficient mtDNA

for direct visualization, restriction digestions were endlabeled before electrophoresis with a mixture of all four ^{35}S nucleotide triphosphates using the Klenow fragment (Maniatis et al. 1982). After electrophoresis, gels were treated with a scintillation enhancer, dried, and autoradiographs exposed at −70°C for 5 days.

Mitochondrial DNA was purified from YOY and yearling bluefish collected in 1990 and 1991 following the protocols of Lansman et al. (1981) and ^{35}S-end-labeled restriction fragments were visualized autoradiographically after electrophoresis. Due to the thermal history of many of these specimens, yields of supercoiled mtDNA were low. In those instances, the nuclear band containing both nuclear DNA and relaxed mtDNA was collected and dialyzed as described for mtDNA bands in Lansman et al. (1981), or mtDNA was reisolated following the Chapman and Powers (1984) protocol. For these samples, the Southern transfer and

Table 2

Distribution of mtDNA genotypes among bluefish *Pomatomus saltatrix* samples. Each letter represents the fragment pattern for a particular restriction endonuclease: from left to right, *Ava*I, *Hin*dIII, *Pvu*II, *Dra*I, *Eco*RV, *Sst*I, *Pst*I, *Sst*II, and *Nci*I. A description of all fragment patterns and sizes is available from the authors upon request.

Composite genotype	VA88	VA89	VA90	NC88	NC89	NC90	NJ90-Sp	NJ90-Su	AU91	Total
AAAAAAAAA	44	45	24	50	33	17	20	18	0	250
AAAAAAAAB	0	0	0	1	1	1	0	0	0	3
AAAAAAAAC	1	2	0	1	1	0	0	2	0	7
AAAAAAAAD	6	1	0	0	0	0	0	0	0	7
AAAAAAAAG	0	1	1	0	1	0	0	0	0	3
AAAAAAAAH	0	0	1	0	0	0	0	0	0	1
AAAAABAAA	0	0	1	0	0	0	0	1	0	2
AAAABAAAA	11	11	1	5	3	5	1	1	0	38
AAAABAAAB	0	0	0	0	1	0	0	0	0	1
AAAABAABA	0	1	0	1	0	0	0	1	0	3
AAAACAAAA	6	6	3	2	3	2	2	0	0	24
AAAACAAAC	0	0	0	0	0	1	0	0	0	1
AAAACAABA	0	0	0	0	0	1	0	0	0	1
AAAADAAAA	7	13	3	4	2	4	1	1	0	35
AAABAAAAA	0	0	1	0	1	0	0	0	0	2
AAACAAAAA	1	1	0	1	0	0	0	0	0	3
AAAEEAAAD	0	0	0	0	0	0	0	0	18	18
AAAEFAAAD	0	0	0	0	0	0	0	0	1	1
AABAAAAAA	0	2	0	1	1	0	0	0	0	4
AABABAAAA	3	4	0	2	1	3	1	0	0	14
AABABAAAB	1	0	0	0	0	0	0	0	0	1
AABABAAAC	0	0	0	0	1	0	0	0	0	1
AABABAAAE	0	2	0	2	0	1	0	0	0	5
AACAAAAAA	1	0	0	2	1	0	0	0	0	4
AACACAAAA	2	2	0	0	0	0	0	0	0	4
BAAAAAAAA	6	2	0	4	3	2	0	1	0	18
BAAAAAAAC	0	1	0	0	0	0	0	0	0	1
BAAACAAAA	5	1	0	2	0	0	0	0	0	8
BAAACAAAD	1	0	0	0	0	0	0	0	0	1
BAAACBAAA	0	1	0	0	0	0	0	0	0	1
BAAADAAAA	0	0	0	1	1	0	0	0	0	2
BADAAAAAA	1	0	0	0	0	0	0	0	0	1
BADACAAAA	0	0	0	1	0	0	0	0	0	1
CAAAAAAAA	1	1	0	0	1	0	0	0	0	3
CAAAAAAAC	3	1	1	0	0	2	0	0	0	8
CAAABAAAC	0	1	0	0	0	0	0	0	0	1
DAAAAAAAA	0	2	0	1	1	1	0	0	0	5
DAAACAAAA	0	1	0	0	0	0	0	0	0	1
DACAAAAAA	0	0	0	0	1	0	0	0	0	1
EAAAAAAAF	0	0	0	1	0	0	0	0	0	1
FAAAAAAAA	0	1	0	1	0	0	0	0	0	2
Totals	100	102	36	83	57	40	26	25	19	469

hybridization protocols of Maniatis et al. (1982) were followed after digestion and electrophoresis. Highly purified bluefish mtDNA, nick translated with biotin-7-dATP, was used as a probe for mtDNA fragments. Hybridization filters were visualized after strigency washes using the BRL BlueGene Nonradioadtive Nucleic Acid Detection System.

All mtDNA samples were digested with the following nine restriction endonucleases used according to the manufacturers' instructions: *Ava*I, *Dra*I, *Eco*RV, *Hin*dIII, *Nci*I, *Pst*I, *Pvu*II, *Sst*I, and *Sst*II. The different restriction-fragment patterns produced by each restriction endonuclease were assigned a letter, and a composite mtDNA genotype, consisting of nine letters representing the fragment patterns generated by each of the restriction endonucleases, was constructed for each individual. The nucleon diversity (Nei 1987) was calculated for each sample and for the pooled samples. The nucleotide sequence divergence among mtDNA genotypes was estimated by the site approach of Nei and Li (1979). The mean nucleotide sequence diversity within samples and mean nucleotide sequence divergence between samples were calculated following the method of Nei (1987), with the latter value being corrected for within-group diversity (Nei 1987). The distribution of genotypes was evaluated for homogeneity among collections using the G-test (Sokal and Rohlf 1981); however, as several of the genotypes were represented by one individual, we employed the Roff and Bentzen (1989) Monte Carlo approach to estimate the significance of heterogeneity χ^2 values determined from the raw data.

Results

The analysis of 472 mid-Atlantic bluefish with 9 restriction endonucleases revealed 40 mtDNA genotypes, and 2 mtDNA genotypes were encountered among 19 Australian bluefish. A total of 77 restriction fragments was visualized, and the average individual was scored for 34 fragments, accounting for approximately 1.4% of the mtDNA genome. The restriction endonucleases, *Hin*dIII and *Pst*I, revealed no variant fragment patterns, while the remaining seven enzymes revealed from two (*Sst*I and *Sst*II) to eight (*Nci*I) different fragment patterns. Restriction-site gains or losses were inferred from completely additive changes in fragment patterns.

Considerable RFLP variation was detected within Atlantic bluefish samples (Table 2). The most common mtDNA genotype, AAAAAAAAA, ranged in frequency from 0.43 (NC 1990 YOY) to 0.75 (NJ 1990 YOY). The large number of variant genotypes resulted in nucleon diversities ranging from 0.416 to 0.798 (Table 3). Because many of the variant genotypes differed from the common genotype by several site changes, the within-sample mean nucleotide sequence diversities were also relatively high, varying from 0.63% to 1.49%. In contrast to the mid-Atlantic bluefish, the Australian sample was quite depauperate of variation. Of the 19 fish in the sample, 18 shared a common mtDNA genotype (AAAEEAAAD), and one fish had a genotype differing from the common type by a single site change (Table 2). The lack of variation in the Australian sample was reflected in a low nucleon diversity (0.105) and a within-sample mean nucleotide sequence diversity of 0.07%.

Significant genetic differentiation was not found between the samples of spring- and summer-spawned YOY bluefish collected in New Jersey during the summer of 1990. The corrected mean nucleotide sequence divergence between the two samples was extremely small (0.02%), indicating that average sequence divergence between two individuals randomly drawn from either the spring- or summer-spawned sample was the same as the divergence between two individuals randomly drawn from each group.

Table 3

Genetic variation within bluefish *Pomatomus saltatrix* samples expressed as nucleon diversity and mean nucleotide sequence diversity. The spring- and summer-spawned NJ YOY bluefish collections were pooled (NJ90 combined) for comparison with the NC90 YOY sample, and all NJ, VA, and NC bluefish collections were pooled (mid-Atlantic combined) for comparison with the AU91 YOY sample. YRL = yearling; YOY = young-of-the-year.

Sample	Age	*n*	Nucleon diversity	Mean nucleotide sequence diversity
VA88	YRL	100	0.781	1.34%
VA89	YRL	102	0.777	1.41%
VA90	YRL	36	0.565	0.89%
NC88	YRL	83	0.632	1.15%
NC89	YRL	57	0.663	1.20%
NJ90-Sp	YOY	26	0.416	0.72%
NJ90-Su	YOY	25	0.467	0.63%
NJ90 combined	YOY	51	0.438	0.67%
NC90	YOY	40	0.798	1.49%
mid-Atlantic combined		372	0.696	1.23%
AU91	YOY	19	0.105	0.07%

Considerable genetic differentiation was not detected among samples of yearling bluefish collected at the same site in different years. The mean nucleotide sequence divergences (Table 4) among the VA88, VA89, and VA90 collections, and between the NC88 and NC90 samples, were of the same magnitude as the within-sample mean nucleotide sequence diversities (Table 3). Consequently, when adjusted for within-sample diversity (Nei 1987), the corrected mean nucleotide sequence divergences among samples were nearly zero (Table 4).

Table 4

Mean nucleotide sequence divergences (%) among selected bluefish *Pomatomus saltatrix* collections. Values are presented with and without correction for within-sample variation.

Collections	Uncorrected	Corrected
Among collections at a single location over 2 or more years		
VA88 vs. VA89	1.39	0.11
VA88 vs. VA90	1.20	0.18
VA89 vs. VA90	1.20	0.05
NC88 vs. NC89	1.18	0.01
Between spring- and summer-spawned bluefish		
NJ90-Sp vs. NJ90-Su	0.69	0.02
Between mid-Atlantic YOY fish		
NJ90-combined vs. NC90	1.19	0.11
Between mid-Atlantic and Australian bluefish		
mid-Atlantic combined vs. AU91	2.60	1.96

Analysis of YOY bluefish from the northern and southern mid-Atlantic bight revealed little mtDNA genetic differentiation. The corrected mean nucleotide sequence divergence between the combined NJ90 YOY sample and the NC90 YOY collection was 0.11%, suggesting little population structuring along the mid-Atlantic coast. This inference was further supported by an analysis of heterogeneity which demonstrated no significant differences in the distribution of six major mtDNA genotypes (those occurring in 10 or more of the 472 fish) and the pooled rare genotypes among the seven mid-Atlantic collections ($G_H = 39.5$, $0.25 < P < 0.50$). Heterogeneity χ^2 analysis of the distribution of all genotypes, including those represented by a single individual, was performed using the Monte Carlo simulation of Roff and Bentzen (1989). A total of 320 of the 1000 randomizations produced χ^2 values greater than the original data set, indicating no significant heterogeneity.

The low levels of mtDNA differentiation among mid-Atlantic bluefish collections contrasted with the substantial difference encountered between the combined mid-Atlantic bluefish and the Australian sample. The average mid-Atlantic bluefish could be distinguished from its Australian conspecific by three or more restriction-site changes. Two of the site changes were unique to the Australian sample, and the third (*Nci*I pattern D) occurred at a low frequency (0.01) in the combined mid-Atlantic sample. The corrected mean nucleotide sequence divergence between the Australian sample and the combined mid-Atlantic bluefish samples was 1.95%. Significant heterogeneity was noted among the pooled samples when the Australian sample was included with the mid-Atlantic bluefish ($G_H = 177$, $p < 0.001$).

A sample of 10 yearling bluefish was analyzed from the northeast Gulf of Mexico (Panama City, FL). Unlike the Australian bluefish, all of the mtDNA genotypes found in the Gulf of Mexico mtDNA individuals were also present in the mid-Atlantic samples, and 7 of the 10 Gulf of Mexico bluefish had the common mid-Atlantic mtDNA genotype. Because of the small size of the Gulf of Mexico sample, it was not appropriate to test for frequency differences between bluefish from the mid-Atlantic coast and the Gulf of Mexico.

Discussion

Mid-Atlantic bluefish demonstrated considerable mtDNA genotypic variation. It is difficult to directly compare the nucleon diversities calculated in this study with those from other studies because the value is sensitive to the number of restriction sites surveyed, and analyses employing larger numbers of restriction endonucleases typically have higher nucleon diversities. The value of 0.696 for the pooled mid-Atlantic bluefish samples is higher than those reported for many marine fishes surveyed with a larger number of enzymes (Avise et al. 1989, Gold and Richardson 1991), and indicates a relatively high degree of genetic variation within the bluefish. This trend becomes more apparent when mean nucleotide sequence diversities, a measure of intrasample diversity that is much less sensitive to the number of restriction sites surveyed, are compared. The value calculated in this study for the pooled mid-Atlantic samples, 1.23%, is higher than values reported for many other marine fishes (Ovenden 1990).

The Australian bluefish demonstrated much less variation than their mid-Atlantic conspecifics. The sample of 19 Australian bluefish had a nucleon diversity five times lower than the combined Atlantic samples, and a mean nucleotide sequence diversity that was an order of magnitude lower (Table 3). A similar difference in the level of mtDNA variation between

conspecific populations has been noted between Atlantic and Pacific blue marlin (Graves and McDowell, unpubl. data). The striking lack of variation within the Australian sample could be the result of a smaller effective population size of females resulting from population bottlenecks, or may simply reflect a period of isolation sufficient for the sorting of gene trees (Nei 1987, Avise et al. 1988, Chapman 1990, Bowen and Avise 1990).

We found little evidence to support the hypothesis that genetically distinct stocks of bluefish exist along the mid-Atlantic coast. Although appreciable mean nucleotide sequence divergences were found between sampling locations (Table 4), when corrected for within-group variation the values became extremely small, indicating that most of the observed differentiation could be accounted for by variation within the samples. The lack of population structuring was also supported by the homogeneous distribution of all genotypes and the fact that the level of genetic divergence among sampling locations was not appreciably greater than the level of divergence among samples taken at any one location in different years.

The extent of gene flow among populations can also be inferred from the frequency distribution of rare alleles (Slatkin 1989). An inspection of Table 2 indicates that almost all mtDNA genotypes that occurred more than once were found in different collections, suggesting significant gene flow among sampling locations. For example, the genotype AAAABAABA, which was present in three individuals, occurred in the VA89, NC88, and NJ90-Su collections. An exception to this pattern was presented by the genotype AAAAAAAAD, which occurred seven times: in six individuals of the VA88 sample and one individual of the VA89 sample. However, an examination of bluefish mtDNA genotypes not included in this analysis—because the individuals were greater than one year old, or because they came from a sample that was too small for inclusion in this analysis—suggests that the observed distribution of the AAAAAAAAD genotype may be an artifact of sampling error. The genotype was present in two bluefish collected in 1988 (one in New York and one in Connecticut) and in six bluefish collected in 1989 (two in New York, two in Virginia, and two in North Carolina).

In contrast to the genetic similarity among mid-Atlantic samples, a large, consistent genotypic difference was noted between the mid-Atlantic bluefish and a conspecific population in Australia. The corrected mean nucleotide sequence divergence of almost 2% is more than an order of magnitude larger than the values detected among mid-Atlantic samples, and is similar to values reported between northwest Atlantic and Barents Sea capelin populations (Dodson et al. 1991) or among populations of freshwater fishes of different river systems (Bermingham and Avise 1986).

While significant genetic differentiation was found between mid-Atlantic and Australian bluefish, no major differences were detected between mid-Atlantic bluefish and a small sample from the Gulf of Mexico. Consistent restriction-site differences have been reported between Gulf of Mexico and mid-Atlantic populations of a number of marine organisms, including horshoe crabs *Limulus polyphemus* (Saunders et al. 1986), oysters *Crassostrea virginica* (Reeb and Avise 1990), and black sea bass *Centropristis striata* (Bowen and Avise 1990). These preliminary results suggest that bluefish from the Gulf of Mexico and the mid-Atlantic are not as genetically isolated as many other coastal marine species, although much larger samples will have to be surveyed to determine if significant mtDNA genotypic frequency differences exist between the two areas. Considering the high vagility of bluefish and their continuous distribution around Florida, this result is not unexpected.

The lack of significant genetic differentiation between spring- and summer-spawned bluefish is consistent with the results of Chiarella and Conover (1990), who found no correlation between the season in which an adult bluefish spawned and the hatch-date of an individual. These data suggest that the bimodal distribution of YOY bluefish in mid-Atlantic estuaries results from two major spawning events of the same population of bluefish, rather than the participation of different stocks. The morphological differences found between spring- and summer-spawned bluefish are probably ecophenotypic, resulting from early-life-history development in appreciably different environments. Similar morphological plasticity has been demonstrated in many other marine fishes (Barlow 1961).

The high degree of genetic homogeneity detected within mid-Atlantic bluefish is also consistent with the results of tag and recapture studies. While many bluefish return to the same site for several years (Lund and Maltezos 1970), migratory habits appear to change with age (Wilk 1977). Thus, the potential exists for considerable interchange, and it is important to note that even small levels of exchange can prevent the accumulation of genetic differentiation (Hartl 1988).

The results of this study cannot disprove the null hypothesis that bluefish along the mid-Atlantic coast share a common gene pool. There appears to be sufficient gene flow to prevent the accumulation of even slight genetic differences. Determining the magnitude of exchange between geographic regions would require an extensive tag and recapture program. Until such data are available, the resource should be managed as assumed in the Fishery Management Plan for the Bluefish—as a single, genetically homogeneous stock.

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