CONTRIBUTION OF THE HUDSON RIVER STRIPED BASS POPULATION TO THE MIXED COASTAL RECREATIONAL HARVEST AT MONTAUK POINT, NY

A Final Report of the Tibor T. Polgar Fellowship Program

Eva H. Hasegawa

Polgar Fellow

New York University School of Medicine
New York, NY

Project Advisor:

Isaac Wirgin, PhD
Department of Environmental Medicine
New York University School of Medicine
New York, NY 10010

Hasegawa, E.H., I. Wirgin, L. Maceda, and N. Roy. 2021. Contribution of the Hudson River Striped Bass Population to the Mixed Coastal Recreational Harvest at Montauk Point, NY. Section IV: 1-32 pp. *In* S.H. Fernald, D.J. Yozzo, and H. Andreyko (eds.), Final Reports of the Tibor T. Polgar Fellowship Program, 2020. Hudson River Foundation.

ABSTRACT

Striped bass, *Morone saxatilis,* support one of the most lucrative recreational and commercial fisheries along the Atlantic Coast of the U.S. Yet, today, striped bass numbers are down significantly along the Atlantic Coast and new management initiatives have been implemented in 2020 to reduce the catch coastwide. In the middle of its range along the Atlantic coast of the U.S., striped bass are seasonally migratory, ranging from the Bay of Fundy, Canada, to the Outer Banks of North Carolina. This coastal migratory stock of striped bass is primarily supported by spawning populations in the Hudson River and Chesapeake Bay, with smaller contributions from the Delaware River and Roanoke River populations. Spawning success and recruitment within these populations vary temporally and is often asynchronous suggesting that they likely require differing levels of protection over time. Therefore, an important prerequisite to effective management of these populations is a quantitative estimate of their relative contributions to coastal landings. Montauk Point is probably the site within New York State that hosts the largest striped bass recreational fishery and is geographically sited to host migrant striped bass from all possible populations that contribute to the coastal migratory stock. Therefore, the stability of the Hudson River contributions to the recreational harvest of striped bass at Montauk Point in 2019 were evaluated. Mixed Stock Analysis (MSA) and Individual Based Assignment (IBA) were used to test microsatellite DNA data. In the Montauk mixed-stock fishery, results showed that Chesapeake fish are the largest contributors (88%), followed by Hudson River fish (8.2%), and, lastly, Roanoke River fish (3.4%). Data from this study will be useful for NOAA managers in their stock assessment modeling for striped bass since variations in recruitment of contributing stocks vary over time, which reflects their differing population abundances.

TABLE OF CONTENTS

LIST OF FIGURES AND TABLES

INTRODUCTION

The Hudson River is home to three glamour species of fishes that are of important commercial and recreational interests. Striped bass, *Morone saxatilis*, is one of these species (the others being American shad, *Alosa sapidissima*, and Atlantic sturgeon, *Acipenser oxyrinchus*, that at one time supported lucrative commercial fisheries within the Hudson River (Limburg et al. 2006). While the Hudson River still supports a robust seasonal recreational fishery and lucrative charter fishing operations, its commercial fishery for striped bass was closed river-wide in 1976, and remains closed today because of elevated levels of PCBs in its population, exceeding the U.S. Food and Drug Administration limit of 2.0 ppm for human consumption (Ashley et al. 2000). Restoring this fishery to its full potential requires monitoring the abundance of striped bass within the river itself, but also its quantitative vulnerability to mixed stock harvests along the Atlantic Coast. In 2016, the Atlantic States Marine Fisheries Commission (ASMFC) highlighted stock composition analysis as a high priority for striped bass fishery management (ASMFC 2016). Determining the population origin of striped bass in mixed coastal fisheries such as at Montauk Point is critical in evaluating the impact of mortality in mixed coastal fisheries on individual populations, such as the Hudson River, comprising the coastal migratory stock. These results are important to the New York State Department of Environmental Conservation (NYSDEC), managers of the Hudson River component of the resource, as well as the ASMFC charged with managing the resource coastwide. This is especially important today given the precarious state of the

fishery and the stated need by the ASMFC in 2019 to significantly reduce landings and catch and release mortality in 2020 (ASMFC 2019).

Striped bass in marine waters of the northeastern U.S. are termed the coastal migratory stock and are supported by spawning in the Hudson River, eight tributaries of the Chesapeake Bay, and to a lesser extent the Delaware (Waldman and Wirgin 1994) and Roanoke rivers (Callihan et al. 2015; Wirgin et al. 2020). Striped bass spawned in these rivers are anadromous and adults seasonally migrate coastally from the Outer Banks of North Carolina to the Bay of Fundy in Atlantic Canada (Wirgin et al. 2020). The proportion of specimens from the different spawning populations at any single coastal site probably varies significantly over time depending on the relative recruitment success in the individual populations which contribute to the mixed coastal stock. Relative reproductive and recruitment success among the contributing populations may be asynchronous: one population may experience much higher success than another population in the same year. For instance, the reproductive success in the Hudson River striped bass population was noticeably higher than that of Virginia populations in 2017, with approximate geometric mean values of nine and 17, respectively (Figures 1 and 2, NYSDEC 2020; Gallagher et al. 2018). Similarly, 2011 was an outstanding year for Virginia populations (mean=27) and just average in the Hudson (mean=11). These results highlight the different dynamics experienced by these populations and suggest that these populations be managed separately rather than pooling them into one unit.

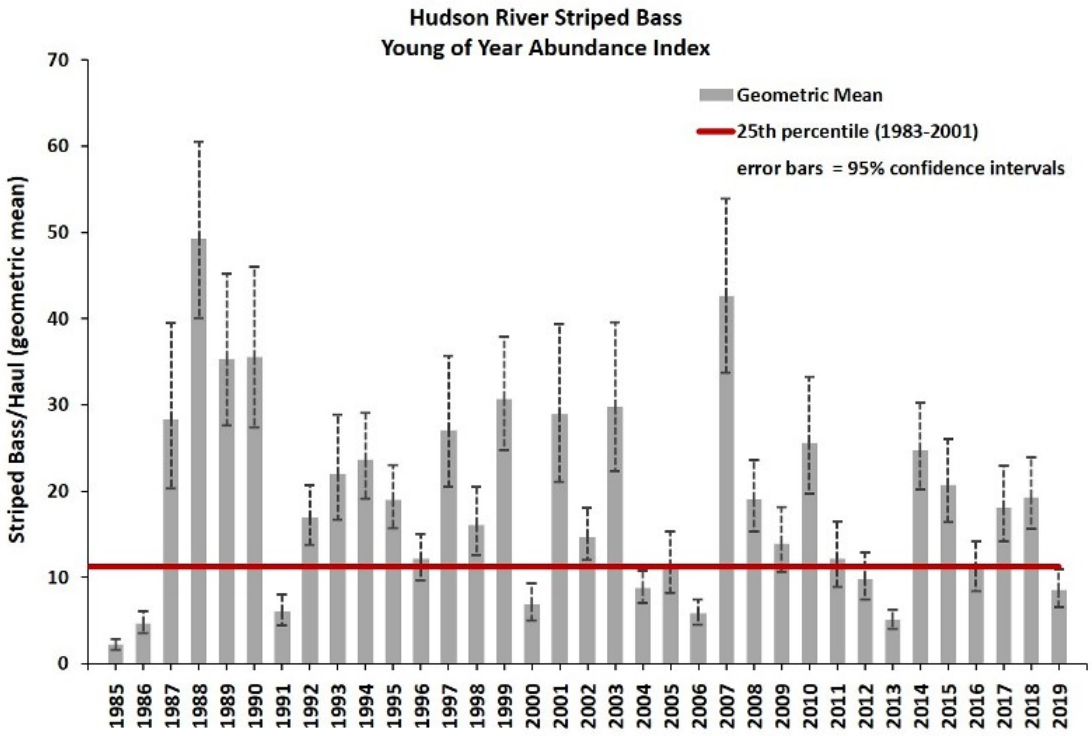

Figure 1. Reproductive success of striped bass in the Hudson River (Young of Year Striped Bass Abundance, NYSDEC 2020).

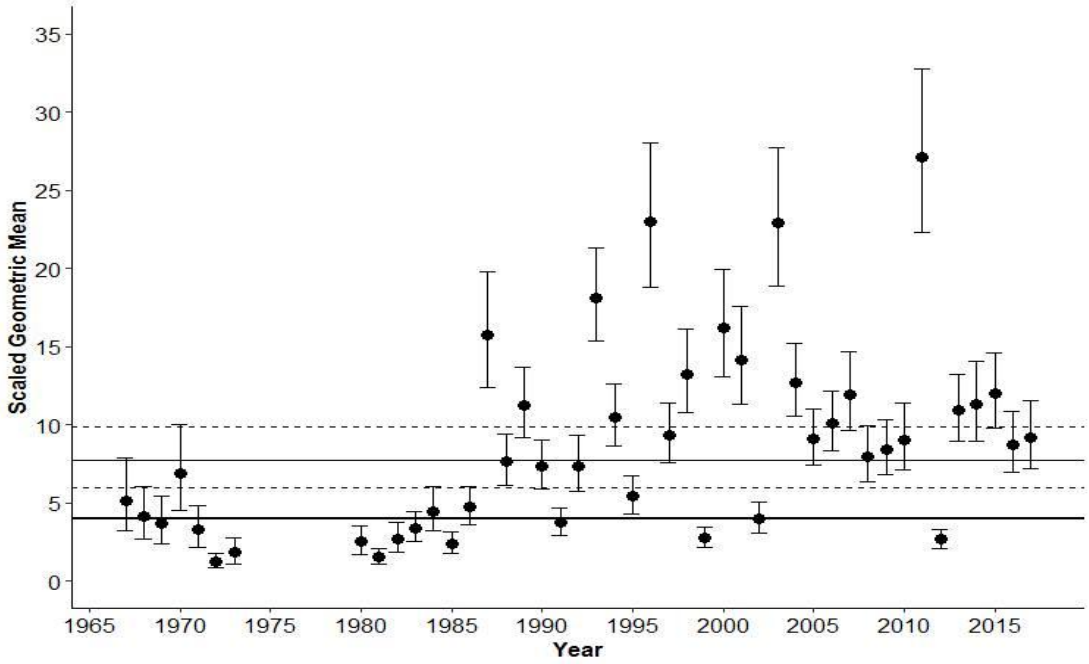

Figure 2. Reproductive success of striped bass in Virginia (Gallagher et al. 2018).

Their popularity as a sport fish and profitable commercial fishery along the Atlantic coast is a testament to how valued striped bass are as an ecosystem resource. In New York alone, $1.165 billion was added to the state's gross GDP by the recreational fishery in 2016 (Southwick Associates 2019). Striped bass spawned in the Hudson are subject to significant mortality from commercial and sport fisheries in coastal waters from North Carolina to Atlantic Canada. Based on past data, the coastal migratory stock is composed primarily of Chesapeake and Hudson River fish, with smaller contributions from other populations (Waldman et al. 1997). The abundance of striped bass populations is known to fluctuate significantly depending on spawning success, recruitment, and vulnerability of populations to within-river and coastal harvest. Reproductive success of a population is believed to be subject to a variety of physical environmental parameters and density dependent biological factors. These factors resulted in a coastwide crash of abundances of striped bass populations in the early 1980s followed by recovery in the early to mid-1990s. This was followed by two decades of recruitment success and what was considered a totally rebuilt fishery; however, the past several years witnessed alarming signs of population declines as evidenced by a significant reduction in female spawning biomass and a decrease in recruitment success (Limburg et al. 2006). As a result, severe cuts in harvest were being enacted for the year 2020 by the ASMFC, including several measures that would ensure an overall 18% decrease in fishing mortality for the coastal migratory stock (ASMFC 2019). For example, Virginia has imposed a complete moratorium on the landings of adults during the 2020 trophy spawning season and a 50% reduction of harvest during the fall season by reducing the possession limit from two to one fish (Commonwealth of

Virginia Marine Resources Commission 2020). Closures on harvests have also been declared for select populations in North Carolina (Ingram 2021).

Understanding genetic population structure is important in fisheries management because it informs fishery managers and researchers on the presence of individual reproductively isolated units within a species' distribution that may differ in: 1) reproductive and recruitment success, 2) growth, maturity, and natural mortality rates, 3) migratory behavior, and 4) exploitation rates. As a result, managers need to know the origins of fish in mixed stock fisheries to set appropriate and effective regulations to best protect the most vulnerable populations (Waldman et al. 1997); however, striped bass is still managed as a single stock coastwide despite the advantages of management on a stock specific basis and evidence that discrete stocks exist.

A sensitive method to genetically distinguish stocks from each other is needed. In this study, informative striped bass microsatellite DNA markers are used (Wirgin et al. 2020) to accurately determine the Hudson River's contribution to the Montauk mixed stock recreational fishery. Microsatellites for striped bass were isolated by Rexroad et al. (2006) and Roy et al. (2000) and were recently shown to be effective in distinguishing striped bass populations that contribute to the coastal migratory stock (Wirgin et al. 2020). Individual Based Assignment (IBA) was used to assign each individual Montauk specimen to its most likely spawning population and Mixed Stock Analysis (MSA) was used to quantify the percentage contribution of each spawning population to the Montauk harvest. This study was the first to evaluate the population composition of the Montauk fishery over an entire fishing season rather than a brief snapshot. It provides a stock composition estimate for the 2019 fishing season.

Techniques used in the past to distinguish striped bass populations and to assign individuals to specific population origins include meristics, morphometrics, scale shape, trace element composition of scales, fatty acids, and parasite assemblages (reviewed in Waldman et al. 1988), along with molecular techniques such as protein electrophoresis (Morgan et al. 1973), restriction fragment polymorphism analysis (RFLP) of mitochondrial DNA (mtDNA) (Wirgin et al. 1990), DNA fingerprinting (Wirgin et al. 1991), single nucleotide polymorphisms (SNPs) (Wirgin et al. 2005), microsatellite DNA (Robinson et al. 2004; Brown et al. 2005; Gauthier et al. 2013; Anderson et al. 2014; Wirgin et al. 2020), and next generation single nucleotide polymorphism analysis (Leblanc et al. 2018). However, some of these methods have met some challenges; for instance, allozymes did not vary substantially (Morgan et al. 1973) and mtDNA variation was very low in striped bass (Wirgin et al. 1990).

Microsatellite DNA analysis has provided a valuable tool in the identification of the population structure of many economically and ecologically important fishes. In many instances, microsatellites provided informative data in a management context for species and populations that heretofore proved refractory to other less sensitive methods of stock identification. This is because of the high levels of allelic variability often exhibited at microsatellite loci (Kumar et al. 2019). As reviewed by Abdul-Muneer (2014), microsatellite markers have been used to determine whether hatchery-raised fish are genetically differentiated from wild populations, to distinguish natural populations, analysis of pedigree, genomic variation, and studies of evolution. These highly polymorphic loci are ideal as genetic tags in aquaculture, stock discrimination, and population genetics.

Several studies have attempted to determine the relative contribution of spawning populations of striped bass to mixed coastal collections. In the most cited study, and most referred to by management, Berggren and Lieberman (1978) used a suite of five morphometric measurements to find an overwhelmingly large Chesapeake (90.2%) and small Hudson (6.6%) contribution to 1975 coastwide collections from multiple locales ranging from Cape Hatteras to Maine. In a genetic study, Wirgin et al. (1993) used RFLP analysis of mtDNA to estimate that the Hudson River contribution to a fall collection in 1989 from the eastern Long Island haul seine fishery was much larger, at 73%. Both studies suffered from shortcomings. Berggren and Lieberman's (1978) effort relied on markers that are known to be subject to environmental influence and therefore temporal instability, and Wirgin et al.'s (1993) investigation used DNA that exhibited limited levels of variation. Furthermore, given the dynamic nature of reproductive success in these populations and likely fluctuating contributions to coastal migrations, it is time to revisit this issue with a more sensitive and stable genetic technique.

An added benefit from a contemporary quantification of the relative contributions of these populations to the Montauk sport fishery contribution is more informed human health risk from the consumption of PCB-contaminated striped bass from the Hudson River. Despite six years of remediation, recent evidence suggests that striped bass from the lower Hudson River still exhibit significantly higher levels of lipid normalized total PCBs than striped bass from other systems (Klawinski and Greenberg 2017).

It is hypothesized that smaller contribution of the Hudson River population to the Montauk mixed stock recreational striped bass fishery in 2019 than in 1990 will be found. According to young-of-year striped bass surveys done by the New York State

Department of Environmental Conservation (NYSDEC), there were fewer juvenile striped bass per haul in 2019 compared to 1990 (Figure 1, NYSDEC 2020). Furthermore, it is likely that the proportional contributions to the coastal migratory stock have changed over time based on differing relative recruitment success in the contributing populations. Lastly, there is likely no significant difference in stock composition by total length or collection date.

METHODS

Montauk Specimen Collections

410 adult striped bass were collected by angling weekly from June 23 through Oct 31, 2019, and were provided by one of the captains of the Montauk charter boat fleet. Date of capture and total length were recorded for each specimen. Montauk supports a significant recreational fishery, is central to the migratory route of the coastal stock of striped bass, and may be the coastal locale where the population composition is most representative of mixed aggregations of specimens from the Hudson, Chesapeake, Delaware, and Roanoke populations.

Figure 3. Sampling locations of striped bass; Montauk Point fish were collected in 2019 and all other specimens were collected in past years. US Census 2019 Cartographic Boundary Files, Rivers of the US (National Operational Hydrologic Remote Sensing Center); Map made with ArcMap 10.8.1.

Reference Specimen Genotyping

To compare Montauk specimen genotypes to those of reference population specimens, genotypes from reference population specimens were analyzed from the Hudson River, Roanoke River, Delaware River, and the tributaries of the Chesapeake

Bay from past years. Specimens were collected from the Upper Bay, Choptank, Patuxent, Pocomoke, Nanticoke, Rappahannock, and Potomac rivers. These reference samples allowed for evaluation of temporal stability of diagnostic microsatellite genotypes in these three populations that are the major contributors to the coastal migratory stock.

DNA isolations

Due to four specimens getting lost or yielding very little DNA, a total of 406 Montauk specimens were used for analysis. 765 reference specimens were used to compare with Montauk DNA. Genomic DNA was isolated from fin clips by their incubation in hexadecyltrimethylammonium bromide buffer (CTAB) buffer and digestion with proteinase K, followed by standard phenol-chloroform extractions and alcohol precipitations. Briefly, fin clips were 1) placed in phosphate-buffered saline (PBS) for 10 min, 2) placed in water for 10 min, 3) placed in vials of CTAB and proteinase K, and 4) placed in a water bath at 37°C overnight. DNA was extracted by 1) centrifuging specimens in 180 µl of chloroform:isoamyl alcohol at a 24:1 ratio, 2) taking out the aqueous layer and adding 90 µl of phenol and centrifuging, 3) placing the aqueous layer into 90 µl of phenol, adding 90 µl of chloroform:isoamyl alcohol, then centrifuging, 4) adding 180 µl of chloroform:isoamyl alcohol and centrifuging, 5) placing the supernatant to 200 µl of isopropanol and 1.8 µl of glycogen then mixing very well, and finally 6) placing the vials in a -80°C freezer overnight. Each centrifugation was done at 13,000 rpm for 5 min.

To isolate and purify the DNA pellet, 1) vials were centrifuged 2) isopropanol was dumped out, then 200 µl of 70% ethanol was added, 3) vials were centrifuged, 4)

ethanol was removed, and vials were overturned to dry for 1 hour, and 5) 110 µl of sterile water was added, and vials were incubated at 37°C for 1 hour. Centrifugations were done at 13,500 rpm for 30 min. DNA concentrations of each sample were quantified using a Nanodrop ND-100 spectrophotometer (NanoDrop Technologies, Wilmington, Delaware) and adjusted to 25 ng/µl for standardization of subsequent procedures. Each sample had a final volume of 125 µl.

DNA analysis

Eight microsatellite loci were used in total. Four loci, MSM1357, MSM1598, MSM1584, and SB108, were selected from the battery developed by Rexroad et al. (2006). Wirgin et al. (2020) previously used these four loci to successfully distinguish spawning populations of striped bass coastwide and used MSA and IBA in determining the status and population origin of specimens in two rivers in Atlantic Canada, including the Saint John and Annapolis. Four newly developed loci, MSM1626, MSM1557, MSM1556, and MSM1592, were used since they showed efficacy in distinguishing striped bass populations. Polymerase chain reactions (PCR) were performed as described in Robinson et al. (2004). Polymerase chain reactions for MSM primers were conducted in 12.5 µl total reaction volumes in 96 well plates, where each well contained 3.5 µl of DNA, 6.6 µl of sterile water, 1.25 µl of KlenTaq1 reaction buffer (AB Peptides, Inc., St. Louis, Missouri), 0.5 µl of forward and reverse primers (1 µM stock primer) (Integrated DNA Technologies, Coralville, IA), 0.1 µl of dNTPs (250 µM stock of each) (GE Healthcare, Chicago, IL.), and 0.03 µl of KlenTaq1 enzyme (AB Peptides, Inc., St. Louis, Missouri). Polymerase chain reactions volumes for SB108 contained 3.5 µl of DNA, 5.6 µl of sterile water, 1.25 µl of Taq polymerase reaction buffer (Roche Diagnostics

Corporation, Indianapolis, IN), 0.1 µl of dNTPs, 1.0 µl of forward and reverse primers, and 0.05 µl of Taq polymerase (Roche Diagnostics Corporation, Indianapolis, IN). All forward primers were labeled with Well-Red dyes on their 5' end (Sigma Aldrich, St. Louis, MO). Cycling parameters were as follows: initial denaturation at 95°C for 5 min, followed by 69 cycles of denaturation at 95°C for 15 s, annealing at 56°C, 58°C, 62°C for 15 s, extension at 72°C for 30 s, and final extension at 72°C for 7 min.

Characterization of microsatellite genotypes were performed using a Beckman Coulter CEQ8000 capillary-based DNA sequencer (Beckman Coulter, Inc., Fullerton, CA). To make economical use of the sequencer, 0.5-4.5 µl of product from each of up to four PCR reactions were multi-pooled and loaded onto 96-well plates along with 0.5 µl of Beckman Coulter CEQ DNA Size Standard-400 and 36 µl of Sample Loading Solution (Beckman Coulter). All analyses were performed using the FRAG 1.

Statistical Analysis

Composite microsatellite genotypes at the eight loci were compiled for all Montauk and reference population specimens. Departures from Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium (LD) were assessed with GENEPOP version 4.1.0 (Rousset 2008) using default parameters. The program STRUCTURE version 2.3.4 (Pritchard et al. 2000) was used to evaluate population clusters with K = 1 – 11, where 11 was the total number of sampling locations. The web-based program StructureSelector (Li and Liu 2017) was used to visualize results. IBA tests implemented in GeneClass2 (Piry et al. 2004) were used to identify the population origin of each specimen collected from Montauk. IBA tests using multi-locus likelihood functions were used to determine the likelihood of each individual's genotype being found in the

Hudson, Delaware, Chesapeake, or Roanoke reference collections. MSA implemented in the ONCOR program (Kalinowski et al. 2008) was used to estimate the proportion of each reference population in the mixed sample of Montauk fish and to determine the probability of each individual's belonging to each of the reference collections. In contrast to IBA, MSA applies mixture modelling, taking into consideration the genotypes of individual fish across multiple loci, multilocus genotype distributions of the reference samples, and the multilocus genotype distribution in the mixture samples. Mixture proportions and their 95% confidence limits were determined based on 10,000 bootstraps. Tests to determine whether there were genetic differences by stock, Pearson's chi-square tests were performed in RStudio 1.4.1106.

Facilities

All the facilities and instrumentation needed to conduct these studies were available in Dr. Wirgin's lab and shared facilities in NYU's Department of Environmental Medicine. Equipment available in Dr. Wirgin's labs included many gel electrophoresis chambers, power supplies, three MJ Research thermal cyclers, and five microcentrifuges. Equipment available in the shared Molecular Support Core (Dr. Wirgin is Co-Director of the NIEHS Center Molecular Cell and Analytic Services Facility Core) included a Nanodrop ND-1000 Spectrometer and Beckman Coulter CEQ8000 automated DNA sequencer.

RESULTS

Genetic Diversity of Loci and Reference Populations

The number of alleles per locus in the reference collections ranged from 15 to 32, with MSM1598 having 15 alleles and MSM1556 having 32. The effective number of alleles, which state the number of alleles with the same frequencies, ranged from 7 to 14, with MSM1598, 1557, and SB108 having 7 and MSM1556 having 14. The fixation index (Fst) values show little genetic differentiation among populations for all loci. None of the loci showed significant departure from Hardy-Weinberg equilibrium.

Table 1. Allelic characteristics of polymorphic loci and genetic differentiation between reference populations

Locus	Number of Alleles	Effective Number of Alleles	Fst
MSM1598	15	7.1	0.018
MSM1584	19	8.9	0.004
MSM1357	18	8.0	0.009
SB108	22	7.1	0.006
MSM1626	30	11.9	0.006
MSM1556	32	14.6	0.005
MSM1592	25	10.3	0.007
MSM1557	20	7.3	0.020

F'st analysis showed highly significant differences among Hudson, Delaware, pooled Chesapeake, and Roanoke populations. F'st values were used instead of Fst since F'st corrects for Fst estimates for heterozygosity within populations. Hudson, pooled Chesapeake, and Roanoke populations were significantly different from each other ($p<0.005$), while the Delaware specimens could not be distinguished from the pooled Chesapeake collection, which included the Upper Bay, Choptank, Patuxent, Pocomoke, Nanticoke, Rappahannock, York, and Potomac specimens.

Table 2. P-values of F'st pairwise comparisons between reference populations; Populations were considered significantly distinct if their p-values were <0.05.

	Hudson	Delaware	Upper Bay	York	Rappahannock	Choptank
Hudson	--	0.001	0.001	0.001	0.001	0.001
Delaware	0.001	--	0.07	0.064	0.079	0.016
Upper Bay	0.001	0.07	--	0.039	0.022	0.001
York	0.001	0.064	0.039	--	0.183	0.001
Rappahannock	0.001	0.079	0.022	0.183	--	0.001
Choptank	0.001	0.016	0.001	0.001	0.001	--
Nanticoke	0.001	0.054	0.001	0.005	0.001	0.068
Potomac	0.001	0.072	0.161	0.23	0.293	0.001
Pocomoke	0.001	0.884	0.625	0.519	0.229	0.115
Patuxent	0.001	0.294	0.005	0.029	0.003	0.003
Roanoke	0.001	0.001	0.001	0.002	0.001	0.001

	Nanticoke	Potomac	Pocomoke	Patuxent	Roanoke
Potomac	0.001	--	0.087	0.02	0.001
Pocomoke	0.293	0.087	--	0.994	0.005
Patuxent	0.001	0.02	0.994	--	0.001
Roanoke	0.001	0.001	0.005	0.001	--

Population Clusters

STRUCTURE analysis showed three major distinct reference populations: Hudson, Chesapeake, and Roanoke. Delaware specimens were not genetically distinct from Chesapeake specimens. Separate analysis of only Chesapeake tributary populations showed two distinct populations, where Choptank and Nanticoke clustered moderately differently from the other populations.

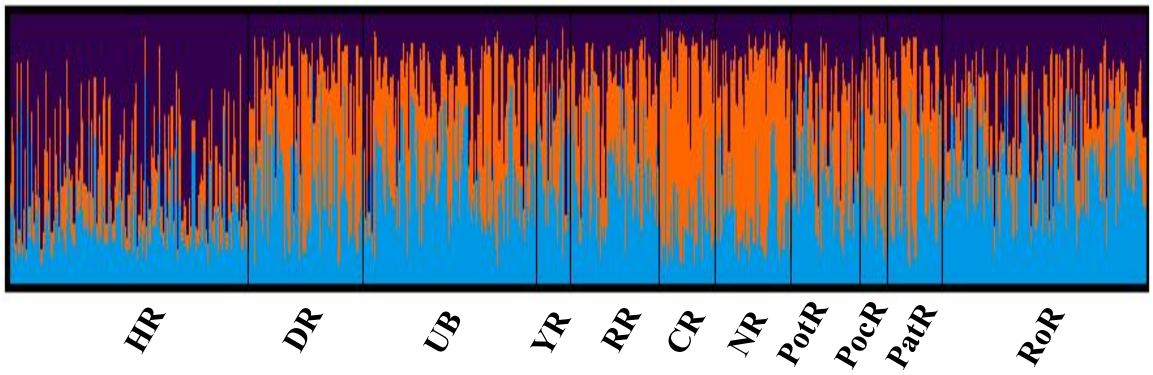

Figure 4. **Genetic clusters of reference populations based on eight microsatellite loci; HR = Hudson River, DR = Delaware River, UB = Upper Bay, YR = York River, RR = Rappahannock River, CR = Choptank River, NR = Nanticoke River, PotR = Potomac River, PocR = Pocomoke River, PatR = Patuxent River, RoR = Roanoke River**

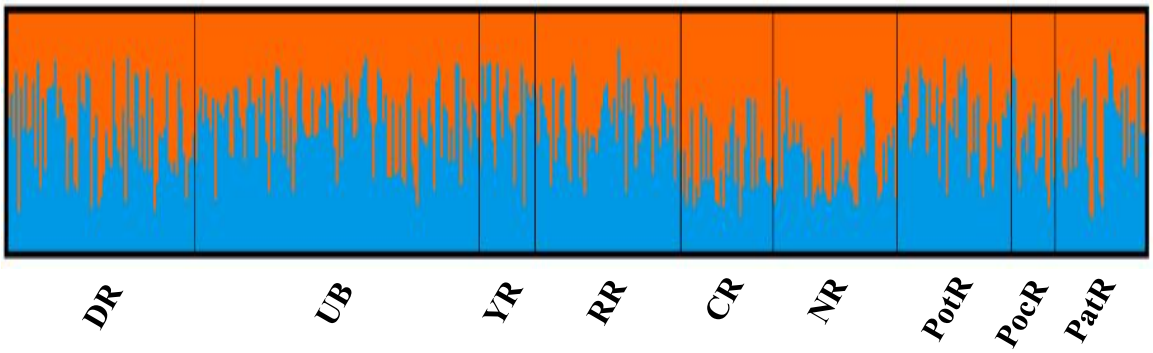

Figure 5. **Genetic clusters of reference individual Chesapeake populations based on eight microsatellite loci.**

Assignment Accuracy

Table 3. **Assignment accuracy of reference specimens with their respective 95% CIs.**

	Assignment Accuracy	95% CI
Hudson	0.9217	(0.8645, 0.9729)
Chesapeake	0.9638	(0.9118, 0.9984)
Roanoke	0.8128	(0.7251, 0.8858)

Using 100% simulations in ONCOR, the assignment accuracy of specimens to the three populations was tested. This step is required to measure how accurately specimens

are assigned back to their sampling location and indicates how useful the loci are at assigning a mixed stock fishery sample to reference populations. Assignment accuracy was highest for Chesapeake specimens with a value of 0.96, and lowest for Roanoke specimens with a value of 0.81.

Mixed Stock Analysis

MSA was performed with 10,000 bootstraps. The pooled Chesapeake population was the largest contributor to the Montauk mixed stock, followed by Hudson, then Roanoke as the smallest contributor.

Table 4. MSA performed with 10,000 bootstraps and 95% CIs.

	Population Estimate	**95% CI**
Hudson	0.0821	(0.044, 0.142)
Chesapeake	0.8839	(0.799, 0.920)
Roanoke	0.034	(0.010, 0.095)

Individual Based Assignment

IBA showed that the Montauk 2019 mixed stock was comprised of 77% Chesapeake, 14% Hudson, and 9% Roanoke specimens. Though the percentage of Chesapeake population is less in IBA than in MSA, and the Hudson and Roanoke populations are greater in IBA than in MSA, the results from both analyses are comparable since Chesapeake specimens are the predominant contributor, followed by Hudson, then Roanoke. IBA gives a confidence score of how likely an individual specimen is from a certain population. Specimens with a confidence score of 70% or greater were included.

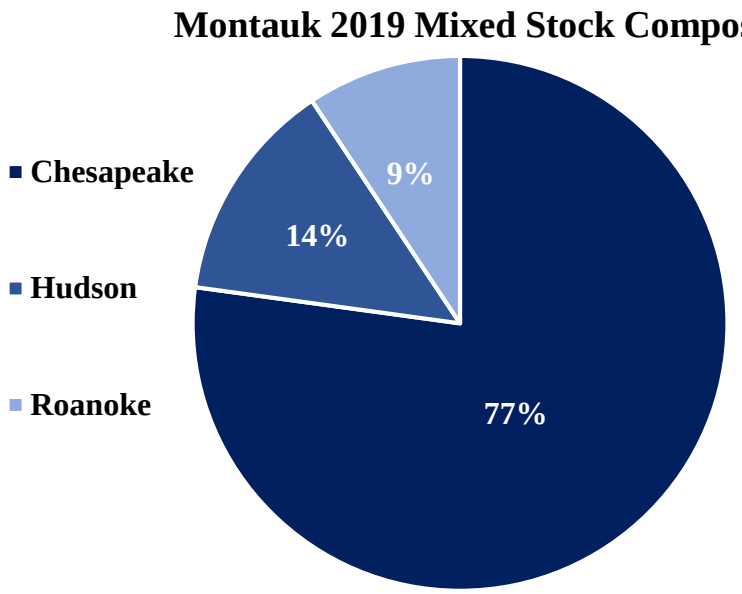

Figure 6. Percent composition of Montauk 2019 mixed stock based on IBA testing.

Genetic Differences by Collection Date and Total Length

To determine whether there were differences in stock composition by collection date or total length (cm), Montauk specimens were separated into quartiles, where the first quartile was comprised of fish caught earliest in the season or the smallest fish. IBA was done to find proportions of Chesapeake, Hudson, and Roanoke individuals per quartile. Pearson's chi-square tests were done to determine whether the stock and collection date or length were correlated. Chi-square tests did not show significant dependence between the two variables.

Table 5. Stock composition by collection date; $\chi^2 = 5.925$, p-value = 0.43

	Chesapeake (%)	Hudson (%)	Roanoke (%)
1st Quartile	76.6	13	10.4
2nd Quartile	82.8	9.4	7.8
3rd Quartile	80.0	12.0	8.0
Latest Group	69.9	19.2	11.0

Table 6. Stock composition by total length (cm); $\chi^2 = 3.715$, p-value = 0.72

	Chesapeake (%)	Hudson (%)	Roanoke (%)
1st Quartile	72.3	18.5	9.2
2nd Quartile	78.3	12.0	9.6
3rd Quartile	78.9	14.0	7.0
Largest Group	78.6	10.7	10.7

DISCUSSION

All loci used showed high numbers of alleles per locus and none significantly departed from Hardy-Weinberg equilibrium. All but one of the loci were four base-pair repeats, where SB108 was the only locus that was a two base-pair repeat. Preference for four base-pair repeats was due to how it was easier to score genotypes when there was more space between each allele. The MSA and assignment accuracy results from this study indicated that the eight loci used were reliable to differentiate populations in a mixed stock. There were an additional four loci that have been used in previous striped bass research (SB113, SB117D, SB91, and MSM1334) (Wirgin et al. 2020), though due to substantial failure in obtaining amplified PCR products, PCR specifications for these loci need to be reviewed. Although the eight loci used in this study were sufficient for achieving high assignment accuracy, more loci would increase the resolution.

Some loci were more difficult to genotype than others and there may have been errors in genotyping some alleles. Nevertheless, this issue was mostly relevant to SB108, a two base-pair repeat locus. As a result, more stutter peaks around the true allele made scoring more difficult than if the peaks were farther apart, as was true with four base-pair repeat loci. Nevertheless, most of the genotyping was done by one individual and methods were kept consistent to avoid recording false alleles.

Microsatellites have proven to be useful and reliable in distinguishing baseline populations from a mixed stock for fisheries management in commercially important species other than striped bass, including whiting (*Merlangius merlangus*), Atlantic salmon (*Salmo salar*), and Atlantic sturgeon (*Acipenser oxyrinchus*). Rico et al. (1997) found significant differences between northern and southern whiting of the North Sea using two loci. The authors found no significant differences among other sampled populations, indicating that there was high exchange of migrants. Bradbury et al. (2018) identified 26 reporting groups of Atlantic salmon in Labrador, Canada using a large panel of sequenced microsatellites. The authors achieved high levels of assignment accuracy, averaging between 88% to 91%. Wirgin et al. (2018) analyzed the mitochondrial DNA control region and microsatellite loci to determine the population of origin of subadult Atlantic sturgeon found in the Hudson River estuary north of the Battery in New York City. They found that the majority of subadult sturgeon assigned back to the Hudson River, but they also found small contributions from the Delaware River, Kennebec River, James River, and Ogeechee River with assignment accuracies above 80%. In sum, microsatellite analysis is capable of defining geographically fine-scale reporting groups from mixed stocks and resolution is improved upon addition of more loci.

This study's results are comparable to those of Berggren and Lieberman (1978), who found the Chesapeake population to be the major contributor by far to the coastal migratory stock of striped bass with Hudson and Roanoke populations being minor contributors. Berggren and Lieberman (1978) measured the number of lateral line scales, left and right pectoral rays, second dorsal rays, anal rays, upper-arm gill rakers, fork length, snout length, head length, and inter-nostril width to distinguish individuals and

used multivariate discriminant analyses to determine stock of origin. Similar population contributions were found by Kneebone et al. (2014), who determined striped bass population contribution to coastal Massachusetts waters using acoustic telemetry. The authors pooled the Roanoke and Chesapeake populations and kept the Delaware River stock separate from the Chesapeake. They also found the Chesapeake/Roanoke stock to be the largest contributor with lesser contributions from the Delaware and Hudson River stocks. Wirgin et al. (2020) recently used microsatellite DNA analysis to successfully define striped bass populations coastwide and to estimate the potential efficacy of microsatellite markers for mixed stock analysis. In their simulations, 93.2%, 96.5%, and 81.6% of the Hudson River, Chesapeake Bay-Delaware River, and Roanoke River specimens in individual collections were assigned to the correct baseline populations, respectively. Overall, the stock contributions to a mixed Atlantic stock from the present study are comparable to results reported by other studies.

Chesapeake Bay tributaries are the largest contributors to the Montauk mixed stock and the data indicates that the tributaries can be pooled into one management unit. Findings by Brown et al. (2005) also show little genetic differentiation among the Upper Bay, Choptank, Potomac, Nanticoke, Upper York, and Rappahannock tributaries when using microsatellite and mitochondrial marker estimates of population structure. Similarly, LeBlanc et al. (2018) pooled Delaware River specimens in with the Chesapeake stock and reported very low genetic differentiation among Upper Bay, Potomac River, Rappahannock River, and Delaware River specimens. The present study also showed that Choptank and Nanticoke specimens may be moderately differentiated

from collections from other Chesapeake tributaries since STRUCTURE analysis found an optimal K value of two across all sampled Chesapeake locations. LeBlanc et al. (2018) and Wirgin et al. (2020) reported similar results where Choptank and Nanticoke specimens showed heterogeneity from samples of western Chesapeake Bay tributaries. Fine-scale analyses of eastern tributary specimens are warranted.

There was a wide range of sample numbers per reference population among the Chesapeake tributaries in the present study; for instance, there were 117 specimens from the Upper Bay and only 18 from the Pocomoke River. Although previous research showed little genetic differentiation among striped bass from Chesapeake tributaries, more samples from each tributary would provide more fine-scale resolution of potential genetic dissimilarities among populations.

A recent study found that the majority of large striped bass tagged in Chesapeake Bay migrated to Massachusetts waters in the spring with a small group lingering for about 60 days in Long Island Sound, then stayed there again for about the same amount of time when they returned from Massachusetts in the fall (Secor et al. 2020). Montauk Point is a critical location in this migration corridor and any development that may interfere with movement in the area should be thoroughly evaluated.

Currently, there are plans for construction of more wind turbines at the Block Island Wind Farm off Rhode Island and connecting the cable ashore at East Hampton, NY. Construction will be in the migration route of striped bass and may impede steady movement. Interviews with recreational fishers who regularly fish around Block Island noticed seeing striped bass around the wind farm, perhaps due to wind farms creating artificial reefs that attract prey for striped bass (ten Brink and Dalton 2018); however,

construction noise from pile driving may deter striped bass, since some respondents noted seeing fewer individuals closer to turbine construction compared to other parts of the island. Threats to striped bass migration need to be considered when issuing permits for construction and more research should be done to determine how striped bass will react to wind farm expansion.

This study was the first to determine striped bass stock composition at Montauk Point, NY, over a whole fishing season from June to October, 2019. Using reference samples of baseline populations to compare with the mixed stock, the Chesapeake stock was shown to be the main contributor, with Hudson and Roanoke stocks being minor contributors. Hudson River striped bass are still recovering from overfishing and habitat loss and their reproductive success hit below the 25^{th} percentile in 2019. Recreational fishers and fisheries managers need to know whether the fish they are exploiting are sustainable; thus, knowing the main contributors to an important mixed stock with high landings is critical.

ACKNOWLEDGEMENTS

I would like to thank the Tibor T. Polgar Fellowship Committee and the Hudson River Foundation for the opportunity to complete and share this research with their continued support. I also thank my advisor Dr. Isaac Wirgin for his expert guidance and mentorship. Special thanks go out to Lorraine Maceda for her teachings and assistance, along with Dr. Nirmal Roy for his help in data analyses. This work would not have been possible without the efforts of Captain Burt Prince and the crew of the Susie E II for catching specimens. I would also like to thank Justin Prince for taking fin clips for DNA analysis.

REFERENCES

Abdul-Muneer, P.M. 2014. Application of microsatellite markers in conservation genetics and fisheries management: recent advances in population structure analysis and conservation strategies. Genetics Research International 2014:1–11.

Anderson, A.P., M.R. Denson, and T.L. Darden. 2014. Genetic structure of striped bass in the southeastern United States and effects from stock enhancement. North American Journal of Fisheries Management 34: 653–667.

Ashley, J.T.F., D.H. Secor, E. Zlokovitz, S.Q. Wales, and J.E. Baker. 2000. Linking habitat use of Hudson River striped bass to accumulation of polychlorinated biphenyl congeners. Environmental Science & Technology 34: 1023-1029.

Atlantic States Marine Fisheries Commission (ASMFC). 2016. Atlantic Striped Bass Stock Assessment Update. Final Report to the Atlantic States Marine Fisheries Commission. Arlington, VA.

Atlantic States Marine Fisheries Commission (ASMFC). 2019. Atlantic Striped Bass Benchmark Stock Assessment Finds Resource Overfished and Overfishing Occurring, Board Initiates Addendum to Reduce Total Fishing Mortality. Final Report to Atlantic States Marine Fisheries Commission. Arlington, VA.

Berggren, T.J., and J.T. Lieberman. 1978. Relative contribution of Hudson, Chesapeake, and Roanoke striped bass, *Morone saxatilis* stocks to the Atlantic coast fishery. Fishery Bulletin 76:335-345.

Bradbury, I.R., B.F. Wringe, B. Watson, I. Paterson, J. Horne, R. Beiko, S.J. Lehnert, M. Clément, E.C. Anderson, N.W. Jeffery, S. Duffy, E. Sylvester, M. Robertson, and P. Bentzen. 2018. Genotyping-by-sequencing of genome-wide microsatellite loci reveals fine-scale harvest composition in a coastal Atlantic salmon fishery. Evolutionary Applications 11: 918–930.

Brown, K.M., G.A. Baltazar, and M.B. Hamilton. 2005. Reconciling nuclear microsatellite and mitochondrial marker estimates of population structure: breeding population structure of Chesapeake Bay striped bass (*Morone Saxatilis*). Heredity 94: 606–615.

Callihan, J.L., J.E. Harris, and J.E. Hightower. 2015. Coastal Migration and Homing of Roanoke River Striped Bass. Marine and Coastal Fisheries: Dynamics, Management, and Ecosystem Science 7: 301-315.

Commonwealth of Virginia Marine Resources Commission. 2020. “Chapter: Pertaining to the taking of striped bass”, Virginia Marine Resources Commission. https://mrc.virginia.gov/regulations/fr252.shtm (accessed April 30, 2021).

Gallagher, B.K., M.C. Fabrizio, and T.D. Tuckey. 2018. Estimation of juvenile striped bass relative abundance in the Virginia portion of Chesapeake Bay. Annual Progress Report: 2017 – 2018, U.S. Fish and Wildlife Service Sport Fish Restoration Project F87R28. Final Report to the Virginia Marine Resources Commission. Department of Fisheries Science, Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, VA.

Gauthier, D.T., C.A. Audemard, J.E.L. Carlsson, T.L. Darden, M.R. Denson, K.S. Reece, and J. Carlsson. 2013. Genetic population structure of US Atlantic coastal striped bass (*Morone Saxatilis*). Journal of Heredity 104: 510–520.

Ingram, C.N. 2021. Proclamation. North Carolina Wildlife Resources Commission. Raleigh, NC.

Klawinski, G. and M.S. Greenberg. 2017. Proposed second five-year review report for Hudson River PCBs Superfund site. U.S. Environmental Protection Agency, Second Five-Year Review. New York.

Kalinowski, S.T., K.R. Manlove, and M.L. Taper. 2008. ONCOR: A computer program for genetic stock identification. Final Report to Montana State University. Bozeman, MT.

Kneebone, J., W.S. Hoffman, M.J. Dean, D.A. Fox, and M.P. Armstrong. 2014. Movement patterns and stock composition of adult striped bass tagged in Massachusetts coastal waters. Transactions of the American Fisheries Society 143: 1115–1129.

Kumar, M., A.P. Acharya, S. Kumar, J. Thakuria, G. Basumatary, and C.S. Chaturvedi. 2019. A review on microsatellite markers and their applications in fisheries and aquaculture. Journal of Experimental Zoology, India 22: 1311-1319.

LeBlanc, N.M., S.N. Andrews., T.S. Avery, G.N. Puncher, B.I. Gahagan, A.R. Whiteley, R.A. Curry, and S.A. Pavey. 2018. Evidence of a genetically distinct population of striped bass within the Saint John River, New Brunswick, Canada. North American Journal of Fisheries Management 38: 1339–1349.

Li, Y.L. and J.X. Liu. 2017. StructureSelector: A web-based software to select and visualize the optimal number of clusters using multiple methods. Molecular Ecology Resources 18: 176–177.

Limburg, K., K. Hattala, A. Kahnle, and J. Waldman. 2006. Fisheries of the Hudson River Estuary. Pages 189-204 in J. Levinton and J. Waldman, editors. The Hudson River Estuary. Cambridge University Press, Cambridge.

Morgan II, R.P., T.S.Y. Koo, and G.E. Krantz. 1973. Electrophoretic determination of populations of the striped bass, *Morone Saxatilis*, in the upper Chesapeake Bay. Transactions of the American Fisheries Society 102: 21–32.

New York State Department of Environmental Conservation (NYSDEC). 2020. "Striped Bass in the Hudson River", Department of Environmental Conservation. https://www.dec.ny.gov/animals/108092.html (accessed April 30, 2021).

Piry, S., A. Alapetite, J.M. Cornuet, D. Paetkau, L. Baudouin, and A. Estoup. 2004. GENECLASS2: A software for genetic assignment and first-generation migrant detection. Journal of Heredity 95:536-539.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155: 945–959.

Rexroad, C., R. Vallejo, I. Coulibaly, C. Couch, A. Garber, M. Westerman, and C. Sullivan. 2006. Identification and characterization of microsatellites for striped bass from repeat-enriched libraries. Conservation Genetics 7: 971–982.

Rico, C., K.M. Ibrahim, I. Rico, and G.M. Hewitt. 1997. Stock composition in North Atlantic populations of whiting using microsatellite markers. Journal of Fish Biology 51: 462–475.

Robinson, M., S. Courtenay, T. Benfey, L. Maceda, and I. Wirgin. 2004. Origin and movements of young-of-the-year striped bass in the southern Gulf of St. Lawrence, New Brunswick. Transactions of the American Fisheries Society 133:412–426.

Rousset, F. 2008. GENEPOP '007: a complete re-implementation of the GENEPOP software for Windows and Linux. Molecular Ecology Resources 8:103-106.

Roy, N.K., L. Maceda, and I.I. Wirgin. 2000. Isolation of microsatellites in striped bass *Morone Saxatilis* (Teleostei) and their preliminary use in population identification. Molecular Ecology 9:827–829.

Secor, D.H., M.H.B. O'Brien, B.I. Gahagan, J.C. Watterson, and D.A. Fox. 2020. Differential migration in Chesapeake Bay striped bass. PLOS ONE 15: 1–19.

Southwick Associates. 2019. The economic contributions of recreational and commercial striped bass fishing. Final Report to the McGraw Center for Conservation Leadership. Fernandina Beach, FL.

ten Brink, T.S. and T. Dalton. 2018. Perceptions of commercial and recreational fishers on the potential ecological impacts of the Block Island wind farm (US). Frontiers in Marine Science 5: 439.

Waldman, J.R., J. Grossfield, and I. Wirgin. 1988. Review of stock discrimination techniques for striped bass. North American Journal of Fisheries Management 8:410-425.

Waldman, J.R., R.A. Richards, W.B. Schill, I. Wirgin, and M.C. Fabrizio. 1997. An empirical comparison of stock identification techniques applied to striped bass. Transactions of the American Fisheries Society 126: 369–385.

Waldman, J.R. and I.I. Wirgin. 1994. Origin of the present Delaware River striped bass population as shown by analysis of mitochondrial DNA. Transactions of the American Fisheries Society 123: 15-21.

Wirgin, I., D. Currie, N. Roy, L. Maceda, and J.R. Waldman. 2005. Introgression of nuclear DNA (nDNA) alleles of stocked Atlantic coast striped bass with the last remaining native Gulf of Mexico population. North American Journal of Fisheries Management 25: 464–474.

Wirgin, I.I., C. Grunwald, S.J. Garte, and C. Mesing. 1991. Use of DNA fingerprinting in the identification and management of a striped bass population in the southeastern United States. Transactions of the American Fisheries Society 120: 273–282.

Wirgin, I.I., L. Maceda, M. Tozer, J. Stabile, and J. Waldman. 2020. Atlantic coastwide population structure of striped bass *Morone saxatilis* using microsatellite DNA analysis. Fisheries Research 226: 1–13.

Wirgin, I., L. Maceda, J.R. Waldman, and R.N. Crittenden. 1993. Use of mitochondrial DNA polymorphisms to estimate the relative contributions of the Hudson River and Chesapeake Bay striped bass stocks to the mixed fishery on the Atlantic Coast. Transactions of the American Fisheries Society 122: 669-684.

Wirgin, I., N.K. Roy, L. Maceda, and M.T. Mattson. 2018. DPS and population origin of subadult Atlantic sturgeon in the Hudson River. Fisheries Research 207: 165–170.

Wirgin, I.I., P. Silverstein, and J. Grossfield. 1990. Restriction endonuclease analysis of striped bass mitochondrial DNA: the Atlantic coastal migratory stock. American Fisheries Society Symposium 7:475-491.