Characterization of Mitochondrial DNA Genotypes in Atlantic Sturgeon (*Acipenser oxyrinchus*) from the Hudson River: The Extent of Spatial and Temporal Heterogeneity

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Abstract

Atlantic sturgeon (*Acipenser oxyrinchus*) is a primitive anadromous chondrostean. Atlantic sturgeon supported substantial commercial fisheries in the past. However, their abundance today is severely reduced as a result of overfishing, pollution, construction of dams and the destruction of spawning habitat. Efforts have intensified to restore depleted populations of Atlantic sturgeon. While directed fisheries for Atlantic sturgeon have been banned in most spawning rivers, a growing coastal fishery has developed which targets sturgeon off the coasts of southern New Jersey and the south shore of Long Island, New York. If a means were available to identify the rivers of origin of fish taken in the intercept fisheries, it would provide a tool to evaluate the impact of this mixed fishery on the individual spawning stocks. This study was undertaken to systematically characterize mtDNA genotypes in Atlantic sturgeon from the Hudson River. Mitochondrial DNA was isolated from Atlantic sturgeon sampled from seven North American rivers, at multiple sites and at different times from the Hudson River, and off coastal New Jersey and Delaware Bay. Differences in mtDNA genotype frequencies permitted discrimination of the Hudson River from the Canadian and Georgian stocks. We tested whether the subadult Atlantic sturgeon stock in the Delaware River (no documented spawning) is genetically similar to the Hudson River stock (Restriction enzyme Eco RV: Hudson River: 39.13% A, 60.87% B; Delaware River: 63.16% A, 36.84% B). The frequencies of mtDNA genotypes in Atlantic sturgeon from the Hudson River were determined to be temporally and spatially stable from 1990 to 1993. The population of Hudson River Atlantic sturgeon revealed a relatively high percentage of B restriction enzyme haplotypes with the restriction enzyme Eco RV (60.87% B). A similar percentage of fish with these genotypes were present in the Atlantic sturgeon caught off the coast of New Jersey and Long Island. Therefore, a large proportion of these mixed fisheries sturgeon probably originated from the Hudson River. Analysis of the mtDNA genotypes can be a valuable tool in the management of exploited Atlantic sturgeon populations.

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Introduction

The Atlantic sturgeon (*Acipenser oxyrinchus*) is a large, long-lived anadromous chondrostean, the historical range of which extended along the Atlantic coast of North America from Labrador to northern Florida (Scott and Scott 1988). Many of the large rivers within this range supported substantial commercial fisheries for Atlantic sturgeon; however, their abundance today is severely reduced as a result of overfishing, pollution, construction of dams, and destruction of spawning habitat (ASMFC 1990). Spawning populations along the Atlantic coast of the United States may be restricted to several rivers in Georgia, two in South Carolina, and the Hudson River (Sutherland 1992). The Hudson River probably harbors the largest spawning population of Atlantic sturgeon in the United States (Sutherland 1992). Additionally, the St. John River, New Brunswick, and the St. Lawrence River, Quebec, are believed to support relatively large sturgeon spawning stocks (Scott and Scott 1988).

Concern has been expressed over these diminished Atlantic sturgeon stocks and efforts have intensified to enhance depleted populations. As a result, a management plan has been developed by the Atlantic States Marine Fisheries Commission to restore Atlantic sturgeon populations to fishable abundance, defined as approximately 10% of 1890 landing levels (7 million lbs.; ASMFC 1990). At present, landing levels are increasing slightly from the extreme decline that occurred around 1900 (Figure 1). This effort may include conservation of current natural populations, their enhancement by hatchery augmentation, and the restoration of extirpated populations. Maintenance of the genetic integrity of stocks is important because locally adapted stocks may outperform other non-native stocks. In recent years, techniques have been developed which allow for

Figure 1. Atlantic sturgeon commercial landings, 1880 to 1980.

Source: NMFS, Fishery Statistics Division, D. L. Sutherland (301-713-2328), 6/18/92.

hatchery propagation of white sturgeon (*Acipenser transmontanus*) (Doroshov et al. 1983) and it is believed that refinements will allow for their application to Atlantic sturgeon.

Restoration efforts may be thwarted by the recent increase in fishing mortalities in Atlantic sturgeon. Their longevity, delayed maturation, and slow growth exacerbates the long term effects of overharvesting. Ten Atlantic Coast State jurisdictions have totally closed their fisheries due to concern over low population levels. Within the United States, only the Hudson River and several rivers in Georgia still support commercial fisheries for adult Atlantic sturgeon. Only recently (1993) have seasonal restrictions as well as length restrictions been placed on commercial fisheries for Atlantic sturgeon in the Hudson River (Henneberger 1993). Additionally, fisheries for Atlantic sturgeon still exist in at least two rivers in Canada, including the St. John and St. Lawrence rivers. While directed fisheries for Atlantic sturgeon have been banned in most spawning rivers, a growing coastal fishery has developed which targets sturgeon off the coasts of southern New Jersey and the south shore of Long Island, New York (ASMFC 1990).

Commercial landings from these growing coastal fisheries are considerable and the number and poundage of fish far outweigh those taken within river systems. The National Marine Fisheries Services reports that 200,000 lbs. of sturgeon were landed in the New York and New Jersey coastal fisheries in 1991 compared to 58,000 lbs in 1987. As a result, although restrictions to reduce fishing mortalities within spawning rivers are stringent, these fish are vulnerable to harvest outside their natal systems, thus neutralizing the beneficial measures.

It is likely that fish targeted in the coastal fisheries are representative of several spawning stocks; however, evidence supporting this hypothesis is lacking. If a means were available to identify the rivers of origin of fish taken in

the intercept fisheries, it would provide a tool to evaluate the impact of this mixed fishery on the individual spawning stocks. This would provide a data base whereby managers could regulate the intercept fisheries in the interest of conserving threatened spawning stocks.

This problem could be addressed in two ways. A massive tagging program could be initiated which would track the migratory patterns of representatives of each of the individual unit stocks. Given the low numbers of fish in each stock, the costs incurred would be very high. An alternative and far more cost effective approach, is to develop genetic tags that can be used to identify representatives of the different stocks. A statistical comparison of the frequencies of genotypes in sturgeon from the intercept fisheries to those in fish from the reference spawning populations would allow for an estimation of the contribution of each stock to the mixed fishery. The success of this effort is predicted on the existence of genetic marks that can be used to distinguish among representatives of the different stocks. It is unreasonable to assume that fixed differences among representatives of different stocks will be detected. However, significant difference in the frequencies of informative genotypes is not an unreasonable expectation.

Mixed stock analysis has been successfully used to estimate the relative contribution of individual Pacific salmon stocks to oceanic fisheries. In this case, differences in the frequencies of protein variants (allozymes) among spawning stocks have been used to generate mixed stock models (Pella and Milner 1987). Unfortunately, levels of protein variation in anadromous fish species along the North American Atlantic coast are exceedingly low. Therefore, efforts have shifted in favor of DNA based approaches.

Results from other anadromous species, striped bass and American shad, suggest that highly significant differences in mitochondrial DNA genotype

frequencies can be expected when comparing different populations within this region. For example, (Wirgin et al. 1993) mtDNA frequency differences have been successfully used to estimate the relative contribution of the Hudson River striped bass stock to the Long Island coastal fishery.

In June, 1992, a workshop "Concerning the Culture and Stocking of Atlantic sturgeon" was conducted in Stony Brook, Long Island. A recurrent theme throughout the management report was the need to develop genetic approaches that could be used to determine the extent to which Atlantic sturgeon are genetically differentiated among rivers. This information could be used in management strategies to conserve existing healthy populations and in hatchery-based restoration programs planned for depleted stocks.

In this study, I used restriction endonuclease analysis (RFLP) of mtDNA to characterize the Hudson River stock. Ongoing studies in Dr. Wirgin's lab have demonstrated that sufficient geographically partitioned mtDNA diversity exists among several Gulf sturgeon (*Acipenser oxyrinchus desotoi*) populations to define population structure. For example, sturgeon from the Choctawhatchee River, Florida, are genetically distinct from sturgeon from all other Gulf rivers surveyed. Additionally, preliminary screenings of Atlantic sturgeon stock have identified restriction enzymes that identify mtDNA variants informative in defining populations, particularly the Hudson River stocks (Waldman et al. 1993).

In this regard, I addressed several questions:

1) Determine if spatial heterogeneity exists in mtDNA genotypes among Atlantic sturgeon in the Hudson River. Are there different sturgeon stocks in different spawning areas within the Hudson River?

2) Determine if mtDNA genotypes are temporally stable among different year classes of Atlantic sturgeon from the Hudson River.

3) Determine the genetic relatedness of juvenile Delaware River Atlantic sturgeon to adult Hudson River Atlantic sturgeon. No adult Atlantic sturgeon or signs of spawning have been seen in the Delaware River in the recent past. This suggests that these juveniles are migrants from another river system.

4) Determine the likely origin of fish caught off the coast of New Jersey.

One of the major prerequisites to the successful use of mixed stock analysis models is the characterization of reference stocks. The thoroughness with which we propose to describe the Hudson River stock will insure that its mtDNA genotype frequencies are accurately represented, that rare mtDNA genotypes are not missed, and that any spatial or temporal heterogeneity in genotype frequencies is taken into account. This analysis would permit a precise future estimation of the Hudson's contribution to the mixed intercept fishery.

During the summer of 1993, four specific tasks were completed:

1) Collect Atlantic sturgeon from the Hudson and the Delaware rivers and fish from coastal mixed fisheries.

2) Isolate mtDNA from liver tissue and barbels.

3) Characterize mtDNA genotypes with six informative restriction enzymes.

4) Compare the frequencies of mtDNA genotypes in Atlantic sturgeon for differences among collection sites and times.

Materials and Methods

Sample Collections

Samples were collected in the Hudson River, near Verplanck, New York, in May and June from commercial fishermen in conjunction with HRF sponsored projects. These fish were destined for sale, so both liver and blood samples were taken. Additionally, three separate fishing trips were made to the Hudson River during the summer of 1993. Atlantic sturgeon were captured by using two 600-foot gill nets with six inch mesh. These four feet high nets were placed at depths of forty to sixty feet during the slack tide. The nets remained in the water for approximately one hour before being retrieved. Once the nets were hauled onto the boat the fish were removed from the nets and placed in a floating net for live storage. From each sturgeon we removed one barbel and placed it in 100% ethanol for preservation. The live fish were then set free after all necessary data were taken (weight, total length, and tag number).

DNA Isolation

Mitochondrial DNA was isolated using a series of phenol/chloroform extractions followed by alcohol precipitations. A small piece of tissue (liver, barbel, or blood) was homogenized in a flask with 600 microliters of 1X C-Tab buffer (2X stock consisted of 50 ml 1M Tris, pH 8.0; 175 ml 4M NaCl; 20 ml 0.5M EDTA; 10 g hexadecyltrimethyammoniun bromide (Sigma); 1 ml B-mercapto-ethanol; and H_2O to a volume of 500 ml) (Wirgin et al. 1990) and 10 microliters of Proteinase K (20mg/ml). Once homogenized, samples were placed in 1.5 ml Eppendorf tubes and incubated at 65° C. After one hour, the samples were removed from the water bath and 600 microliters of chloroform: isoamyl alcohol (24:1 ratio) were added. The samples were then agitated for 10 minutes and placed in a centrifuge at 2,500-3,000 RPM (Table top centrifuge 1EC HN-S II). After 10 minutes of spinning, the supernate was transferred to new tubes containing 600 microliters of pH equilibrated phenol. The samples were again agitated and centrifuged for 10 minutes but this time the supernate was placed in a new tube containing 300 microliters of phenol. The samples were then agitated for 5 minutes and 300 microliters of chloroform: isoamyl alcohol (24:1) was added. After 5 minutes of agitating the samples were again centrifuged for 10

minutes. The supernate was then transferred to yet another new tube containing 600 microliters chloroform: isoamyl alcohol (24:1). The samples were again agitated, centrifuged and the supernate was transferred to 600 microliters of isopropanol. The samples were then stored at -80° C for approximately 15-20 minutes. Samples were then centrifuged at full speed (15,000 x G) in a microfuge for 18 minutes. The isopropanol was discarded and 1 ml of 70% EtOH was added to each pellet. The samples were again stored at -80° C for 15-20 minutes and were then spun for 18 minutes in the centrifuge at 15,000 x G. To complete the mtDNA isolation procedure, the 70% EtOH was poured off, and the pellets were allowed to air dry. After approximately 1-2 hours, the pellets were resuspended in 150 microliters of sterile 1X TE buffer (10 mM Tris base, pH 8.0, 1 mM EDTA).

Each sample was then digested with those restriction enzymes that had already revealed polymorphisms among sturgeon populations, including Bgl I, Eco RV, Hinc II, Hinf I, Msp I, and Rsa I. All mtDNA fragments were separated electrophoretically in horizontal agarose gels made in 1X TBE buffer (10X TBE: 4 liters double distilled H_2O, 432g Tris base, 220g Boric acid, 4.6g EDTA free acid and pH 8.3 with NaOH) and run overnight. DNA was then transferred to Zetabind membranes by Southern blotting (Southern 1975) and DNA was fixed to the membranes by baking in a vacuum oven for two hours at 80° C or by UV irradiation in a Stratalinker.

The membranes were hybridized to ^{32}P radiolabeled (Rigby et al. 1977) sturgeon mtDNA probes as described by Wahl et al. (1979) at 65° C using dried milk as a blocking agent. Final wash stringencies were 0.1X SSC/0.1% SDS at 65° C for 30 minutes. Membranes were subjected to autoradiography for 1-3 days at -70°C. These autoradiographs were analyzed and interpreted for all variant

genotypes and restriction site polymorphisms as compared to molecular weight standards of known Atlantic sturgeon mtDNA genotypes.

Genotypes for each individual fish were determined for each restriction enzyme used. Composite mtDNA genotypes based on individual enzyme digests were compiled for each fish. Genotypic frequencies for individual year classes, collection years, or different Hudson River collection sites were compared for significance of differences using the Monte Carlo simulation approach developed by Roff and Bentzen (1989). Additionally, the mtDNA genotype frequency in the composite Hudson River sample was compared with that of subadult sturgeon collected from the Delaware River. A significant difference in the mtDNA genotype frequencies would suggest that these juvenile fish are not migrants from the Hudson River. Genotypes in Atlantic sturgeon caught off the coast of New Jersey were compared to the composite Hudson River sample. This analysis will permit a precise future estimation of the Hudson's contribution to the mixed intercept fishery.

Results

Mitochondrial DNA isolated from Atlantic sturgeon from the Hudson River was screened for polymorphisms with six different restriction enzymes. The mtDNA genotype frequencies were compared with those detected in earlier studies from Atlantic sturgeon collected from other North American Atlantic coast river systems and a coastal region off southern New Jersey.

The frequencies of mtDNA genotypes in the various populations are depicted in Table 1. Atlantic sturgeon from the Hudson River revealed two mtDNA genotypes, A and B, for the restriction enzyme Eco RV whereas three genotypes (A, B, C) were observed in Atlantic sturgeon from the four rivers in Georgia (Altamaha, Ogeechee, Satilla and Savannah) (86.27% A, 11.76% B, 1.96%

Table 1. Frequencies of mitochondrial DNA RFLP genotypes of Atlantic sturgeon from Atlantic coast rivers and coastal New Jersey

	Restriction enzyme Genotypes								
	Eco RV			Hinc II		Hinf I		Msp I	
Collection Sites	A	B	C	A	B	A	B	A	B
ST. LAWRENCE	57	0	0	56	0	0	54	57	0
ST. JOHN	66	0	0	53	0	1	49	46	0
HUDSON RIVER	27	42	0	62	0	2	56	70	1
SAVANNAH	2	0	0	2	0	1	1	1	1
OGEECHEE	8	1	0	10	0	4	4	5	3
ALTAMAHA	30	5	1	36	0	3	32	33	3
SATILLA	4	0	0	3	1	3	1	1	3
DELAWARE RIVER	27	14	0	38	0	0	2	28	0
NEW JERSEY COAST	27	42	0	72	1	0	68	71	0

C). The Hudson River spawning population consists of a relatively high frequency of the B genotype (60.87%). The B mtDNA genotype was not detected in mtDNA from Atlantic sturgeon from the two Canadian rivers. Among the four Georgian rivers, the Altamaha was the only river which both B and C length genotypes were detected.

The genetic distinctiveness of these Atlantic sturgeon populations was evaluated based on frequency differences in these mtDNA genotypes (Table 1). Significant heterogeneic differences exist between genotypic frequencies from the Hudson River and the four rivers in Georgia for restriction enzymes Eco RV, Hinf I, and Msp I (Georgia: Eco RV $X^2=30.05$, $P<0.001$; Hinf I $X^2=8.98$, $P<0.001$; Msp I $X^2=12.27$, $P<0.001$).

The frequencies of mtDNA genotypes for the Hudson River and the Canadian rivers are depicted in Table 1. The Atlantic sturgeon from the Hudson River were determined to have significant heterogeneic differences from the St. John and St. Lawrence stocks. Genotype frequencies revealed with the restriction enzyme Eco RV were compared and it was determined that there where significant heterogeneic differences between the Atlantic sturgeon of the Hudson River and the Atlantic sturgeon of the St. John River and St. Lawrence River (Canada: $X^2=95.83$, $P<0.001$).

The Hudson and the Delaware are two mid-Atlantic river systems that expressed both A and B Atlantic sturgeon genotypes for the restriction enzyme Eco RV and only genotype B for Hinc II (Table 2). Data for restriction enzyme Eco RV was analyzed and it was determined that geographic heterogeneity in mtDNA genotype frequencies does exist between the Hudson River and Delaware River Atlantic sturgeon populations (Delaware: $X^2=5.67$, $P<0.05$).

Table 2. Frequencies of mtDNA genotypes in Atlantic sturgeon using restriction enzymes Eco RV and Hinc II

	Eco RV		Hinc II	
Genotype	A	B	A	B
Hudson River	27	42	62	0
Delaware River	24	14	38	0

The temporal comparison of the mtDNA RFLP genotypes of Hudson River Atlantic sturgeon was from the years 1990-1993. This four year study includes the analysis of mtDNA digested with the following restriction enzymes: Bgl I, Eco RV, Hinc II, Hinf I, Msp I (Table 3). The mtDNA genotype frequencies were determined to be temporally stable for Atlantic sturgeon for these four years (Eco RV: X^2=4.23; P=0.236).

Table 3. A comparison of the mitochondrial DNA RFLP genotypes of Atlantic sturgeon collected from the Hudson River in the years 1990-1993

	Restriction enzyme Genotypes									
	Bgl I		Eco RV		Hinc II		Hinf I		Msp I	
Years collected	A	B	A	B	A	B	A	B	A	B
1990	22	0	12	11	16	0	2	20	20	1
1991	08	0	01	06	07	0	0	05	09	0
1992	20	0	06	14	20	0	0	20	20	0
1993	17	0	08	11	19	0	0	11	20	0

Samples of Hudson River Atlantic sturgeon were caught in two different areas of the river, and the geographically specific mtDNA RFLP genotypes are depicted in Table 4. Genotype frequencies for restriction enzymes Bgl I, Eco RV, Hinc II, Hinf I and Msp I were homogenous (Hudson Spatial: Eco RV X^2=0.10, P=0.602).

Table 4. A comparison of the frequencies of mitochondrial DNA RFLP genotypes of Atlantic sturgeon from different areas of the Hudson River.

	Bgl I		Eco RV		Hinc II		Hinf I		Msp I	
Region	A	B	A	B	A	B	A	B	A	B
Catskill, N.Y. (UPRIVER)	50	0	19	31	43	0	2	45	49	1
Verplanck, N.Y. (DOWNRIVER)	17	0	08	11	19	0	0	11	20	0

The final comparison made was for the genotypic frequencies of mtDNA digested with Eco RV for the Hudson River and the New Jersey coast (Table 5). Atlantic sturgeon from the Hudson River and the New Jersey coast exhibited similar frequencies of mtDNA genotypes and could not be distinguished. The A and B mtDNA genotypes commonly seen in Hudson River Atlantic sturgeon are found in a relatively high frequency (37.5% A and 62.5% B). The Atlantic sturgeon from the offshore fisheries produced similar frequencies of 39.13% A and 60.87% B.

Table 5. Frequencies of mtDNA Eco RV genotypes in Atlantic sturgeon from the Hudson River and coastal New Jersey.

	Genotypes		
	A	B	C
HUDSON RIVER	27	42	0
NEW JERSEY COAST	27	42	0

Discussion

The decline of Atlantic sturgeon along the North American eastern seaboard has prompted concern and the development of a management plan. The objective of this plan is the restoration of this once abundant fish. The identification of the population structure of Atlantic sturgeon throughout its Atlantic coast distribution is critical to this effort. How many different unit stocks is the species divided into, and what are the contributions of these individual units to mixed fisheries? We have used RFLP analysis of mtDNA to address these questions.

The populations of Atlantic sturgeon along the Atlantic coast can be distinguished by comparing the mtDNA genotype frequencies, particularly for restriction enzyme Eco RV. The Hudson River is a mid-Atlantic estuary and its stocks of Atlantic sturgeon were differentiated from both northern and southern stocks. Canadian stocks in the St. John River and St. Lawrence River did not exhibit any individual with the variant Eco RV genotype B . Sturgeon stocks from the four rivers in Georgia only exhibited an Eco RV genotype B frequency of 11.76%. The mtDNA genotype frequency of 39.13% genotype A and 60.87%

genotype B, distinguished the Hudson River population of Atlantic sturgeon from the stocks of Georgia and Canada.

Significant differences between the Hudson and Canadian stocks are only present for the restriction enzyme Eco RV. The Hudson River stock of Atlantic sturgeon differs from those in the Georgian rivers on a broader basis. Thus, this one restriction enzyme proved powerful in distinguishing sturgeon stocks along the Atlantic coast. The restriction enzymes Hinf I and Msp I, as well as Eco RV, reveal variant mtDNA genotypes and distinguish the sturgeon of Georgia from the stocks in the Hudson.

From these results we can conclude that Atlantic sturgeon stocks fall into at least three broad geographic groupings; Canadian stocks, Hudson River stock, and southern stocks. However, we have yet to examine Atlantic sturgeon populations from lower mid-Atlantic spawning rivers, such as those in North Carolina and South Carolina. Though these fish are migratory, it seems that they spawn only in their natal river systems. If sturgeon randomly spawned in any river system, mtDNA genotype frequencies would be similar for all stocks of Atlantic sturgeon. Mitochondrial DNA genotype frequencies of these populations of Atlantic sturgeon were significantly different, evidence that Atlantic sturgeon actively home in on their natal river system to spawn.

The stocks of Hudson River Atlantic sturgeon were sampled over a four year period (1990-1993). During this period mtDNA genotypes were characterized for each fish using six restriction enzymes. No differences were seen in mtDNA genotype frequencies among sturgeon sampled in those different years, and we conclude that mtDNA genotype frequencies are temporally stable over a short period of time. It would be informative to obtain age data from these fish to determine for how many different year classes these genotypes frequencies are stable. The Atlantic sturgeon of the Hudson River were also

analyzed for spatial heterogeneity of mtDNA genotype frequencies to determine if one or more stocks exist in the Hudson River. No differences in the mtDNA genotype frequencies were seen in fish from spatially distant collection sites in the Hudson River, and we concluded that genotype frequencies for Hudson sturgeon also spatially stable. The Hudson's population is homogenous; this is a solid foundation with which to compare mtDNA genotype frequencies in the single Hudson River stock to the Delaware River and the off-shore fisheries.

Juvenile Atlantic sturgeon were caught in late summer from the Delaware River and mtDNA genotype frequencies were compared with those in the spawning Hudson River stock. The sturgeon mtDNA genotype frequencies for sturgeon from the Hudson River and Delaware River populations were significantly different, suggesting that these two populations are genetically heterogenous. Frequencies of mtDNA genotypes were also different between the Delaware River and all other spawning stocks. Two hypotheses may be advanced to explain these findings. 1) Although no mature adult Atlantic sturgeon and/or evidence of very young life stages have been seen in the Delaware River in the recent past, it is possible that a remnant population may exist. 2) Atlantic sturgeon caught in the Delaware River might also be migrants from a mix of other systems such as the Hudson River and other major rivers found along the east coast of North America. The Hudson River has the largest thriving population of Atlantic sturgeon in the United States and geographically the Hudson River estuary is the closest system from which these juveniles could emigrate. Furthermore, the frequency of Eco RV genotype A (63.16%) is much higher in the Delaware River than in all other stocks,
confirming a Hudson River contribution to the Delaware River sub adult stocks.

This study attempted to differentiate stocks of Atlantic sturgeon found in seven major rivers along the east coast of North America. Once genetic tags were

identified that could be used to differentiate among sturgeon, the origin of an Atlantic sturgeon outside their natal river systems could be determined. It has been established that Hudson River Atlantic sturgeon have a mtDNA genotype frequency of 39.13% A, 60.87% B for restriction enzyme Eco RV. The Atlantic sturgeon caught off the coast of New Jersey exhibited similar mtDNA genotype frequencies (39.13% genotype A, 60.87% genotype B). This analysis suggests that a large proportion of sturgeon caught off the New Jersey coast likely originated from the Hudson River. Further statistical analysis on a larger coastal sample should permit a robust estimate of the relative contribution of the Hudson River stock to this coastal fishery. This will provide a tool that managers of this valuable resource can use in the future to preserve current abundance levels of Hudson River sturgeon.

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