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BRIEF COMMUNICATIONS

Genetic mixed-stock analysis of Atlantic sturgeon *Acipenser oxyrinchus oxyrinchus* in a heavily exploited marine habitat indicates the need for routine genetic monitoring

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Although a previous genetic mixed-stock analysis (gMSA) conducted in the early 1990s showed that marine-captured New York Bight Atlantic sturgeon *Acipenser oxyrinchus oxyrinchus* almost exclusively originated from the Hudson River, fish from southern U.S. rivers were well represented within this contemporary sample ($n = 364$ fish), at least during the autumn. Widely distributed spawning stocks are therefore exposed to heavy fishing activity and habitat degradation in this relatively small area, illustrating the need for spatial management across multiple management jurisdictions and routine gMSA to account for temporal change.

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One challenge of managing anadromous fishes is that they face threats during both the freshwater and marine stages of their life cycle. Although river-based threats primarily affect a single spawning stock due to natal homing, localized marine threats have the potential to affect many stocks due to mixing during this phase of the life cycle (Crozier *et al.*, 2004). Genetic mixed-stock analysis (gMSA) is frequently used to estimate the relative contribution of discrete spawning stocks to fishes under threat in a specific marine location. It is much less common for gMSA to be employed repeatedly over time in order to track how the contribution of different spawning stocks to fishes in a marine area changes (Gauthier-Ouellet *et al.*, 2009). A marked

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difference in the composition of two collections of Atlantic sturgeon *Acipenser oxyrinchus oxyrinchus* Mitchell 1815 from the New York Bight (NYB) that were made *c.* 15 years apart is demonstrated. Changes in the stock composition between autumn and spring seasons are also demonstrated. These temporal differences highlight the need to establish a time series of gMSA estimates for marine catches of exploited anadromous fishes. The composition of the sampling also has immediate implications for the management of this threatened species.

Acipenser o. oxyrinchus is a large, long-lived and late maturing anadromous fish found along the western Atlantic Ocean from the Gulf of St Lawrence to northern Florida (Smith & Clugston, 1997). A directed fishery for this species was developed in 1870 to supply an emerging caviar market (Smith & Clugston, 1997), producing record landings in 1890 that resulted in a fishery collapse in just over a decade (Smith & Clugston, 1997; Secor & Waldman, 1999). During the late 1980s, there was a brief reemergence of the *A. o. oxyrinchus* fishery in New York and New Jersey (Waldman *et al.*, 1996a; Bain *et al.*, 2000; Kahnle *et al.*, 2007). In 1990, the Atlantic States Marine Fisheries Commission (ASMFC) developed a fishery management plan outlining conservation and restoration measures to achieve population levels that support harvests at 10% of the historical peak landings (ASMFC, 1990). Despite this, continued population declines led to a 40 year moratorium to protect 20 year classes of female fish (ASMFC, 1998).

Acipenserids are particularly vulnerable to anthropogenic stressors given their complex life cycle and low intrinsic rates of population increase (Pikitch *et al.*, 2005). Genetic studies suggest that adult *A. o. oxyrinchus* return to spawn in their natal river (Ong *et al.*, 1996; Waldman *et al.*, 1996a, b; Wirgin *et al.*, 2000, 2002, 2007; King *et al.*, 2001; Grunwald *et al.*, 2008; Peterson *et al.*, 2008), which means that overfishing or habitat degradation within rivers can cause rapid, localized and lasting stock collapse. Analyses of mitochondrial DNA (mtDNA) sequences from early juveniles and spawning adults in 12 river systems along the east coast of North America indicate strong population structure with almost all riverine populations being genetically distinct [mean F_{ST} values 0.242 (Grunwald *et al.*, 2008)] confirming natal homing by spawning adults and early natal site-fidelity among juveniles (Wirgin *et al.*, 2000, 2007; Grunwald *et al.*, 2008). Incorporating both mitochondrial and nuclear marker data, the Atlantic Sturgeon Status Review Team (ASSRT, 2007) recommended that *A. o. oxyrinchus* be managed as five distinct population segments (DPS): (1) Gulf of Maine (Penobscot, Kennebec, Androscoggin, Sheepscot, Saco and Merrimack Rivers), (2) New York Bight (Taunton, Connecticut, Hudson and Delaware Rivers), (3) Chesapeake Bay (James, York, Rappahannock, Potomac, Susquehanna and Nanticoke Rivers), (4) Carolina [Albemarle (Roanoke River) and Pamlico Sound (Neuse and Tar Rivers), Cape Fear River, Santee-Cooper River and Winyah Bay (Waccamaw, Great Pee Dee, Black and Sampit Rivers)] and the (5) South Atlantic [ACE Basin (Ashepoo, Combahee and Edisto Rivers) Savannah, Ogeechee, Altamaha, Satilla, St Mary's and St John's Rivers]. Currently, the National Oceanic and Atmospheric Administration (NOAA) has proposed that all DPS's to be listed as either threatened (Gulf of Maine) or endangered (New York Bight, Chesapeake Bay, Carolina and South Atlantic) under the United States Endangered Species Act (Federal Register, 2010a, b).

Considerable research and management attention has been focused on *A. o. oxyrinchus* in rivers, while very little work has been done on the juvenile

marine migrant life stage. This requires rectification for at least two reasons: (1) this stage is vagile and encounters a wide variety of threats in the ocean (Dovel & Berggren, 1983) and (2) elasticity indices of acipenserids indicate that mortality of juveniles has a disproportionately large effect on population dynamics (Gross *et al.*, 2002). *Acipenser o. oxyrinchus* by-catch in marine trawl fisheries is estimated at 2000–7000 fish per year (ASMFC, 2007), equivalent to the mortality imposed by directed fisheries during the 1990s (ASMFC, 1998). Although direct mortality of by-catch *A. o. oxyrinchus* from trawls is rarely observed, mortality may be high due to delayed effects on individuals (Davis, 2002; Broadhurst *et al.*, 2006). Because *A. o. oxyrinchus* can only withstand very low levels of anthropogenic sources of mortality (ASMFC, 2007), inshore trawling is now considered the most significant marine threat to population recovery (Collins *et al.*, 1996; Stein *et al.*, 2004). By following shallow (<20 m) migration corridors (Dunton *et al.*, 2010), *A. o. oxyrinchus* gain *de facto* protection in states that restrict inshore trawling such as Maryland (1.61 km limit), Delaware (no trawling), New Jersey (3.22 km limit) and parts of New York (various no trawl zones in marine waters). There are large areas, particularly in the NYB, where no such closures exist and this species remains vulnerable to by-catch mortality.

Acipenser o. oxyrinchus aggregation areas in the NYB, off the coasts of NY and NJ, exhibit the highest abundance of *A. o. oxyrinchus* along the east coast of the U.S.A. and have been recommended as essential fish habitat, warranting either full time or seasonal closures (Dunton *et al.*, 2010). One such seasonal marine aggregation has been observed at the mouth of the Hudson River in an area that is heavily trawled (Dunton *et al.*, 2010). Most individuals within these aggregations are juvenile marine migrants (Dunton *et al.*, 2010). gMSA using restriction fragment length polymorphism of mtDNA conducted in this area prior to the closure of the directed fishery (1993) revealed that aggregating fish were almost always spawned in the Hudson River (97.2%) with a small contribution from southern rivers (2.8%) (Waldman *et al.*, 1996a). If this estimate is representative of the *A. o. oxyrinchus* exposed to inshore trawling today, it means that by-catch in this area greatly affects the Hudson River spawning stock. If fish from other spawning stocks are now present in greater numbers in the NYB, it is essential to assess their exposure to this incidental fishing mortality. The present objective was to revisit the natal origins of fish captured in this area by using gMSA c. 10–15 years after the study conducted by Waldman *et al.* (1996a).

Small tissue clips of either the barbel or anal fin of *A. o. oxyrinchus* [$n = 364$ fish, ranging in total length (L_T) from 54 to 215 cm, mean 107 cm] were collected in 2005–2009 off the coasts of NY and NJ in the NYB during the NJ Department of Environmental Protection's Finfish and the NY Bottom Trawl Surveys. Detailed descriptions of the surveys can be found in Dunton *et al.* (2010). All tissue samples were immediately stored in 95% ethanol until DNA extraction. DNA was isolated from 15 to 25 mg of tissue using DNeasy Tissue Kit (Qiagen Inc.; www.qiagen.com). A 580 bp section of the mitochondrial control region (mtCR) was amplified using *A. o. oxyrinchus* specific primers and amplification protocols previously identified by Wirgin *et al.* (2000). PCR products were purified by adding 0.25 μ l of exonuclease I, 0.50 μ l shrimp alkaline phosphatase and 2.0 μ l 10 \times buffer to 50 μ l of PCR product and incubated for 15 min at 37 $^\circ$ C followed by 15 min at 80 $^\circ$ C. Cleaned products were then sequenced in both the forward and reverse

directions using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems; www.appliedbiosystems.com). Sequencing reactions were precipitated with ethanol and 125 mM EDTA and run on an ABI 3730 capillary DNA analyser. Final mtDNA sequences were assigned haplotypes by comparing the present results to previously identified mtDNA haplotypes that were collected from the five DPSs among other studies (Waldman *et al.*, 1996a; Wirgin *et al.*, 2000; Grunwald *et al.*, 2008), using a known 205 bp region of the mtCR. Estimates of stock composition were made using a maximum likelihood approach implemented in the statistics programme for analyzing mixtures, SPAM v. 3.7b (www.cfadfg.state.ak.us). Baseline haplotype frequencies for riverine spawning stocks for the gMSA were obtained from Grunwald *et al.* (2008) and Wirgin *et al.* (2000) (Genbank accession numbers: AF162716, AF162717, AF162719, EU726274, AF162721, AF162753, EU726275, AF162722, AF162723, AF162724, AF162725, EU726276, EU726277, EU726278, AF162726, AF162728, AF162729, AF162749, AF162732, AF162733, AF162734, AF162735, AF162736, AF162737, AF162738, AF162741, AF162743, AF162744, AF162745, AF162746, EU726279, AF162748 and AF162751). To demonstrate the accuracy of the gMSA based on the haplotype frequencies observed in these DPS units, a sample of 100 fish drawn exclusively from each DPS unit with 1000 resamplings was simulated in SPAM v.3.7b. The simulation option was then used to estimate the contribution of each of the DPS units to the sample. After the simulation exercise proved that the U.S. DPS units were highly identifiable, the contribution of each DPS unit to the 364 juvenile *A. o. oxyrinchus* sampled was estimated. This was also carried out for the autumn and spring seasons on their own ($n = 150$ and 181). The summer ($n = 21$) and winter ($n = 12$) months did not contain enough samples to conduct separate analyses. To evaluate bias and variance in sampling error, the findings were also expressed in terms of the contribution of the five different DPSs to the NYB samples by calculating 90% symmetric C.I. for the contribution of each DPS using bootstrap resampling ($n = 1000$) of the baseline (*i.e.* DPS) and mixture (*i.e.* NYB marine) samples. Significance ($P < 0.001$) of seasonal differences in contributions of DPSs was made using $R \times C$ test of independence with William's correction for an $R \times C$ table.

In general, a population is considered highly identifiable based on gMSA when a simulated sample consisting of a 100% contribution from that population is estimated by the analysis to contribute $>90\%$ (Anderson *et al.*, 2008). The null hypothesis for the present study was that the fish sampled from the NYB were almost entirely spawned from NYB-DPS units, as found by Waldman *et al.* (1996a). Thus, the critical question was: Is the NYB-DPS highly identifiable? In the simulated sample consisting of 100% NYB-DPS fish, the estimated contribution was 89.1%, which is near the highly identifiable cut-off [Table I(a)]. Upon closer examination, almost all of the assignment error consisted of misassigning NYB-DPS fish to Canadian rivers, which is probably due to the ubiquity of the widespread haplotype A in this region. Few NYB-DPS were misassigned to any of the southern populations and the overall accuracy of the simulation increased to 90.9% when the Canadian populations were excluded [Table I(b)]. It was therefore concluded that the NYB-DPS unit was highly identifiable, especially relative to all of the other U.S. DPS units.

Overall, the haplotype distribution observed among fish sampled in the NYB is incompatible with these fish, nearly exclusively originating from the NYB-DPS, which is in contrast to the sample analysed by Waldman *et al.* (1996a). A total of 16 unique, previously identified (Wirgin *et al.*, 2000; Grunwald *et al.*, 2008),

TABLE I. SPAM v. 3.7b (www.cfadfg.state.ak.us) simulation results of a sample of 100 *Acipenser oxyrinchus oxyrinchus* drawn exclusively from Gulf of Maine (GOM) with (a) Canada (GOM-CAN) and (b) without Canada (GOM), New York Bight (NYB), Chesapeake Bay (CHE), Carolina (CAR) and South Atlantic (SOU) distinct population segments (DPS) with 1000 resamplings. Actual mean \pm s.d. values are shown for each DPS unit. Bold values indicate the simulation-estimated contribution when the sample is drawn exclusively from the specified source DPS

	GOM-CAN (100%)	NYB (100%)	CHE (100%)	CAR (100%)	SOU (100%)
(a) With Canada					
GOM/CAN (actual)	0.9965 \pm 0.0113	0.0490 \pm 0.0587	0.0317 \pm 0.0479	0.0903 \pm 0.1057	0.0624 \pm 0.0636
NYB (actual)	0.0000 \pm 0.0000	0.8912 \pm 0.0719	0.0000 \pm 0.0000	0.0002 \pm 0.0019	0.0000 \pm 0.0000
CHE (actual)	0.0000 \pm 0.0000	0.0309 \pm 0.0339	0.9519 \pm 0.5920	0.0102 \pm 0.3390	0.0230 \pm 0.0334
CAR (actual)	0.0001 \pm 0.0003	0.0010 \pm 0.0096	0.0161 \pm 0.0405	0.8738 \pm 0.1161	0.0035 \pm 0.0119
SOU (actual)	0.0002 \pm 0.0005	0.0194 \pm 0.0325	0.0002 \pm 0.0008	0.0117 \pm 0.0203	0.8982 \pm 0.0716
(b) Without Canada	GOM (100%)	NYB (100%)	CHE (100%)	CAR (100%)	SOU (100%)
GOM (actual)	0.9871 \pm 0.0345	0.0247 \pm 0.0452	0.0156 \pm 0.0356	0.0404 \pm 0.0756	0.0199 \pm 0.0431
NYB (actual)	0.0000 \pm 0.0002	0.9088 \pm 0.0665	0.0000 \pm 0.0001	0.0004 \pm 0.0058	0.0000 \pm 0.0000
CHE (actual)	0.0000 \pm 0.0000	0.0303 \pm 0.0340	0.9583 \pm 0.0581	0.0095 \pm 0.0328	0.0218 \pm 0.0324
CAR (actual)	0.0005 \pm 0.0009	0.0023 \pm 0.0132	0.0249 \pm 0.0498	0.9243 \pm 0.0891	0.0049 \pm 0.0149
SOU (actual)	0.0016 \pm 0.0134	0.0255 \pm 0.0402	0.0012 \pm 0.0086	0.1420 \pm 0.0284	0.9403 \pm 0.0563

TABLE II. Observed haplotype distribution from *Acipenser oxyrinchus oxyrinchus* within the New York Bight. Haplotypes were previously identified by Grunwald *et al.* (2008) and Wirgin *et al.* (2000) (Genbank accession numbers: AF162716, AF162717, AF162719, EU726274, AF162721, AF162753, EU726275, AF162722, AF162723, AF162724, AF162725, EU726276, EU726277, EU726278, AF162726, AF162728, AF162729, AF162749, AF162732, AF162733, AF162734, AF162735, AF162736, AF162737, AF162738, AF162741, AF162743, AF162744, AF162745, AF162746, EU726279, AF162748 and AF162751)

Season	Observed haplotypes															Total	
	A	A3	A5	B	B1	B2	C	C3	C4	C5	D	D2	N1	O	P7		S1
Spring	47	2	1	92	2	6	5	0	5	7	2	4	5	2	0	1	181
Autumn	39	1	1	51	3	7	8	1	6	8	5	8	6	2	1	3	150
Winter	1	1	0	6	0	0	0	0	2	2	0	0	0	0	0	0	12
Summer	5	0	0	4	0	0	0	1	2	0	2	2	1	2	1	1	21
Total	92	4	2	153	5	13	13	2	15	17	9	14	12	6	2	5	364

mtCR haplotypes were identified in the NYB collection (Table II). Haplotype B (the common endemic Hudson River haplotype, 42%) and haplotype A (the ubiquitous haplotype, 25%) occurred in the highest frequencies while all other haplotypes, all from populations south of the NYB, each occurred at much lower levels (<5%). gMSA analysis estimated that a majority of the *A. o. oxyrinchus* captured originated from the Hudson River (NY) (70.33%) followed by the Albemarle Sound (NC) (14.38%), James River (VA) (4.91%), Ogeechee River (GA) (3.55%), Savannah River (GA) (3.51%) and Delaware River (DE) (3.32%) (Table III and Fig. 1). Significant differences in the relative frequency of spawning stocks were found between the spring and autumn seasons ($\chi^2 = 18.47$, d.f. = 11, $P < 0.001$) with a higher per cent

TABLE III. Estimates (mean \pm s.d.) of stock composition of *Acipenser oxyrinchus oxyrinchus* using a maximum likelihood approach implemented in the statistics programme for analyzing mixtures, SPAM v. 3.7 (www.cfadfg.state.ak.us) for total samples collected ($n = 364$), autumn ($n = 150$) and spring ($n = 181$)

Population	Total	Autumn	Spring
	Mean \pm s.e.	Mean \pm s.e.	Mean \pm s.e.
Saint Lawrence	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000
Saint John	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000
Kennebec	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000
Hudson	0.7033 \pm 0.0327	0.6294 \pm 0.0516	0.7869 \pm 0.0477
Delaware	0.0332 \pm 0.0230	0.0336 \pm 0.0329	0.0441 \pm 0.0422
James	0.0491 \pm 0.0180	0.0768 \pm 0.0316	0.0464 \pm 0.0242
Albemarle	0.1438 \pm 0.0266	0.1899 \pm 0.0447	0.0893 \pm 0.0338
Edisto	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000
Combahee	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000
Savannah	0.0351 \pm 0.0167	0.0412 \pm 0.0278	0.0000 \pm 0.0000
Ogeechee	0.0355 \pm 0.0157	0.0291 \pm 0.0252	0.0332 \pm 0.0157
Altamaha	0.0000 \pm 0.0000	0.0000 \pm 0.0000	0.0000 \pm 0.0000

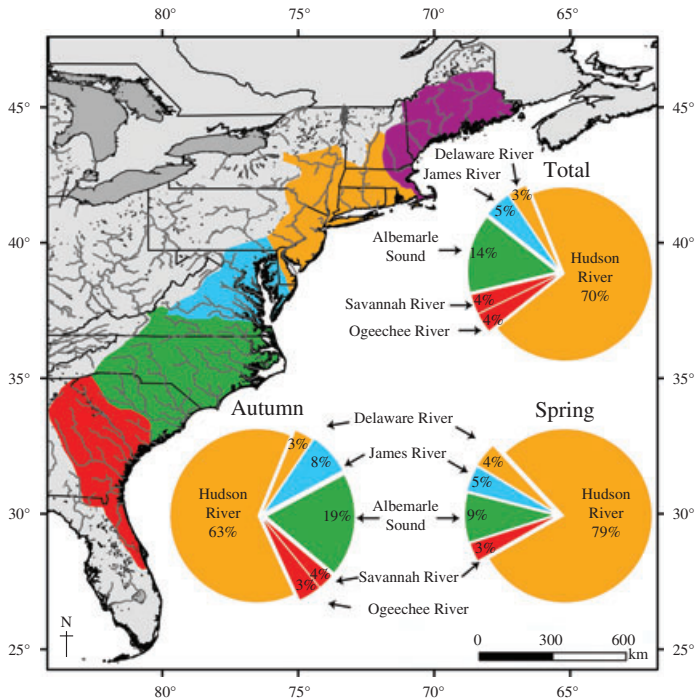


FIG. 1. Map of the U.S.A. showing the location of the five *Acipenser oxyrinchus oxyrinchus* distinct population segment (DPS) units: Gulf of Maine (■), New York Bight (■), Chesapeake Bay (■), Carolina (■) and the South Atlantic (■) as defined from the Atlantic Sturgeon Status Review Team (2007). Pie charts show the contribution of each river and DPS unit (colours of DPS units identified above) to the individuals sampled in this study from the New York Bight for spring ($n = 181$), autumn ($n = 150$) and overall ($n = 364$).

of fish originating from the Hudson River (NY) in the spring (78.69%) than in the autumn (62.94%) (Table IV and Fig. 1). Population estimates and bootstrap values for DPSs reveal that fish from the NYB-DPS contribute most to the *A. o. oxyrinchus* captured within the NYB (73.65%), followed by fish from Carolina DPS (14.38%), South Atlantic DPS (7.06%) and Chesapeake Bay DPS (4.91%) (Table IV). Mean estimates of 1000 bootstrap resampling yielded similar results with the exception of the appearance of an extremely small contribution ($<0.006\%$) of the Canadian and Maine spawning stock to account for a small fraction of the ubiquitous haplotype A (Table IV).

The gMSA indicates that the majority (70.33%) of *A. o. oxyrinchus* captured within the NYB originated from the NYB-DPS (probably the Hudson River) with a significant, but small, increase in the percentage of fish from that DPS present in the spring (78.69%) compared to the autumn (62.94%) (Table III and Fig. 1). A much larger contribution of southern stocks (26.35%) (Carolina > South Atlantic > Chesapeake) in the NYB (Table IV and Fig. 1) was found in this study than by Waldman *et al.* (1996a), who sampled NYB fisheries in 1993–1994. The findings of Waldman *et al.* (1996a) may differ from the present study because they primarily sampled during the spring ($n = 90$) with few samples obtained in the autumn

TABLE IV. Estimates (mean \pm s.e.) of stock composition of *Acipenser oxyrinchus oxyrinchus* using a maximum likelihood approach implemented in the statistics programme for analyzing mixtures SPAM v. 3.7 (www.cfadfig.state.ak.us) for total samples collected ($n = 364$), autumn ($n = 150$) and spring ($n = 181$) based on distinct population segments

	DPS unit	Expected		Bootstrap values	
		Mean \pm s.e.	90% C.I.	Mean \pm s.d.	90% C.I.
Total	Gulf of Maine and Canada	0.0000 \pm 0.0000	0.0000	0.0055 \pm 0.0168	0.0000–0.0434
	New York Bight	0.7365 \pm 0.0298	0.6880–0.7850	0.7287 \pm 0.0417	0.6561–0.7969
	Chesapeake Bay	0.0491 \pm 0.0180	0.0200–0.0790	0.0483 \pm 0.0238	0.0037–0.0873
Spring	Carolina	0.1438 \pm 0.0266	0.1000–0.1880	0.1263 \pm 0.0432	0.0414–0.1886
	South Atlantic	0.0706 \pm 0.0170	0.0430–0.0990	0.0749 \pm 0.0257	0.0405–0.1212
	Gulf of Maine and Canada	0.0000 \pm 0.0000	0.0000	0.0154 \pm 0.0289	0.0000–0.0840
Autumn	New York Bight	0.8310 \pm 0.0383	0.7680–0.8940	0.8149 \pm 0.0502	0.7295–0.8911
	Chesapeake Bay	0.0464 \pm 0.0242	0.0070–0.0860	0.0443 \pm 0.0258	0.0002–0.0887
	Carolina	0.0893 \pm 0.0338	0.0340–0.1450	0.0731 \pm 0.0417	0.0000–0.1420
Autumn	South Atlantic	0.0332 \pm 0.0157	0.0070–0.0590	0.0418 \pm 0.0235	0.0103–0.0905
	Gulf of Maine and Canada	0.0000 \pm 0.0000	0.0000	0.0080 \pm 0.0235	0.0000–0.0570
	New York Bight	0.6630 \pm 0.0489	0.5830–0.7430	0.6518 \pm 0.0589	0.5533–0.7447
Autumn	Chesapeake Bay	0.0768 \pm 0.0316	0.0250–0.1290	0.0783 \pm 0.0362	0.0151–0.1357
	Carolina	0.1899 \pm 0.0447	0.1160–0.2630	0.1659 \pm 0.0634	0.0470–0.2648
	South Atlantic	0.0703 \pm 0.0273	0.0250–0.1150	0.0745 \pm 0.0358	0.0283–0.1408

($n = 22$). That study also included larger individuals and adults ranging from 136 to 207 cm L_T , in contrast to the present study that included primarily juveniles (87.67%) ranging from 54 to 215 cm L_T (mean 107 cm) with 89% <136 cm. Under this scenario, Waldman *et al.* (1996a) may have primarily sampled Hudson-derived adults on their way to the river to spawn. The discrepancy between studies could also indicate a decline in the Hudson River spawning stock, an increase in the size of the southern river spawning stocks or both. Most populations had suffered major overfishing when Waldman *et al.* (1996a) obtained samples from the NYB fishery. At that time the NYB region accounted for 93% of total commercial landings (Smith & Clugston, 1997; Kahnle *et al.*, 2007) indicating that the Hudson River population was probably the largest at the time, although fisheries dependent data can contain significant spatio-temporal biases. As a result of intense fishing prior to the moratorium, the Hudson River population declined by *c.* 80% from 1977 to 1995 (Peterson *et al.*, 2000). While there have been slight signs of improvement in abundance of Hudson River pre-migrant juveniles since the mid 1990s, recruitment still remains at historic lows (Kahnle *et al.*, 2007). Although not captured within this study, some *A. o. oxyrinchus* populations, such as the Altamaha River, are in the beginning stages of recovery (Peterson *et al.*, 2008). Thus, the proportion of fish from DPSs aggregating in the NY region will vary depending on the abundance of each stock. Given the possible variation between seasons and years, the present study indicates that regular monitoring of the regional genetic composition of *A. o. oxyrinchus* in marine habitats is needed to track the species recovery and to assess the risks posed by localized marine threats to different spawning stocks. This is probably true for many, if not all, anadromous fishes that are captured in marine fisheries.

Currently, NOAA (Federal Register, 2010a, b) and the ASSRT recommends that *A. o. oxyrinchus* be managed as five DPS areas (ASSRT, 2007). This fairly rigid division of genetic structure, based on the freshwater portion of the species life history, does not translate into marine habitat where substantial mixing occurs and local factors far removed from natal rivers can affect populations. Further, improvements or protection in freshwater habitat may not achieve restoration targets while marine juveniles experience by-catch mortality in distant jurisdictions. There is an immediate need to limit by-catch of *A. o. oxyrinchus* in nearshore waters where aggregations commonly form (Dunton *et al.*, 2010). This need is highlighted by a recent extinction risk analysis indicating that three of the five DPS areas (New York Bight, Chesapeake and Carolina) have a >50% chance of becoming endangered within the next 20 years, while the Gulf Maine and South Atlantic are under a moderate risk (<50% chance) of becoming endangered (Patrick & Damon-Randall, 2008). Regular gMSA of incidental catches in marine fisheries is a crucial component of efforts to measure the effect of marine threats to *A. o. oxyrinchus* recovery as fisheries by-catch mortality within the marine environment far removed from the spawning stock of origin may have a significant, yet unrecognized, effect on individual DPSs recovery efforts. The present results also indicate that heavy inshore trawling in the NYB is a potential source of incidental by-catch mortality for fish spawned in rivers from the Hudson River to as far south as the Savannah River. Removing or minimizing this localized threat, perhaps by establishing closed areas similar to neighbouring states, is therefore likely to benefit this proposed threatened or endangered species across a large fraction of its range.

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