Evaluation of stocking success, age, and natural reproduction of striped bass *Morone saxatilis* in West Point Lake, GA: a comparison between genetic and OTC marking techniques

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Running title: assessing natural reproduction of striped bass

Abstract

Successful natural reproduction is critical for maintaining Gulf Coast striped bass populations. Unfortunately, the only evidence for natural reproduction of striped bass inhabiting Gulf Coast drainages is from the Apalachicola-Chattahoochee-Flint (ACF) river system and the occurrence and recruitment abundance of these events appears relatively low. Goals of this study were to evaluate the stocking success of age specific releases (i.e., phase I and phase II fish) in West Point Lake, GA and quantify the amount of natural reproduction of striped bass in a section of the Chattahoochee River where natural reproduction has been known to occur. To achieve this goal, all hatchery fish were marked prior to stocking with both an otolith oxytetracycline (OTC) mark and a molecular microsatellite tag. We also compared the efficiency and utility of marking techniques. Otolith analysis of 103 sampled individuals showed that 96% were from phase I stockings. The remainder (n = 4) were presumed to be of wild origin. Initial parentage analysis using eleven microsatellite markers indicated that only 47% (48 of 103) of the sampled progeny could be assigned to known brood stock whose progeny were stocked into West Point Lake; however, this discrepancy was the result of clerical errors during brood stock handling. Subsequent parentage analyses showed that 100% of the sampled fish were from hatchery stockings. There was complete age agreement (i.e., 103 of 103 aged correctly) between the estimation of age from parentage (via cohort assignment) and otolith aging techniques. Our data indicated that no natural reproduction was observed, survival of phase II was significantly less than expected, and that the OTC efficacy was 96%. We also showed that molecular tags were a reliable alternative to conventional marking techniques that estimate natural reproduction, age, and cohort contribution.

Introduction

The striped bass *Morone saxatilis* is a commercially and recreational important anadromous fish renowned among anglers for its large size and fighting ability when hooked. The native range of this species was Atlantic and Gulf Slope drainages from the St. Lawrence River (New Brunswick, Canada) to Lake Pontchartrain, LA (Page and Burr 1991); however striped bass have been widely introduced throughout North America and Europe (Ross 2001). Striped bass inhabiting Gulf Coast drainages were differentiated (both morphologically and genetically) from those in Atlantic rivers (Brown 1965; Wirgin et al. 1991), a pattern observed for numerous other freshwater and marine fishes (Avise 1992). However, hybridization and introgression of introduced Atlantic Coast striped bass with native Gulf Coast striped bass during the late 1960s through early 1970s has eroded this differentiation (Wirgin et al. 1997; Wirgin et al. 2005).

While striped bass are considered anadromous, populations inhabiting Gulf coastal drainages are often potamodromous, with individuals rarely venturing into coastal waters (Ross 2001). Spawning migrations occur during spring with males generally arriving on the spawning grounds before females. Striped bass are broadcast spawners having non-adhesive and semiboyant eggs that drift downstream; therefore, suitable habitats (shoal, gravel, and sand bars) and sufficient distances are needed to ensure that eggs and larvae hatch and develop (Boschung and Mayden 2004) Historical disturbances to Gulf Coast river systems (e.g., habitat destruction, impoundments, and water pollution) were arguably detrimental to a species with a reproductive strategy reliant on long river stretches of moderate water velocity and suitable habitat and probably contributed to the elimination of native stocks of striped bass along the Gulf Coast in the 1900s (Ross 2001; Boschung and Mayden 2004). Hence, hatchery augmentation was initiated.

The intensive hatchery stocking effort of approximately 120 million striped bass fingerlings over the course of five decades was a success in that it established (or reestablished) a recreational fishery throughout Gulf Coast drainages. Stocking first occurred with Atlantic Coast origin fish but by 1980 stocking consisted predominantly of Gulf origin fish (note that the extent of hybridization and introgression of these Gulf origin fish with Atlantic origin fish is unknown). Limited natural recruitment has resulted in primarily a put-grow-and-take fishery, not a self-sustaining one. Stocking of striped bass throughout the Gulf Coast consists of collecting and artificial spawning local brood stock and returning their progeny to the wild. Stocking is typically done by releasing either phase I (fry to fingerling stage, length ca. 25-60mm TL) or phase II (fish of lengths 80-250mm TL and under age-1) hatchery individuals into a river or reservoir. Phase I fish are often preferred for stock enhancement (Smith et al. 1990); however, differences in post stocking survival of phase-I and phase-II striped bass hybrids *(Morone saxatilis* x *M. chrysops)* suggest that survival of phase-II hybrids could be two orders of magnitude greater than that of phase-I hybrids (Yeager 1987).

Successful natural reproduction is critical for maintaining Gulf Coast striped bass populations; unfortunately, the only evidence for natural reproduction of striped bass inhabiting Gulf Coast drainages is from the Apalachicola-Chattahoochee-Flint (ACF) river system (GSMFC 2006). Assessing natural recruitment of Gulf Coast striped bass can entail the detection of striped bass eggs, young-of-year, and young age classes in the absence of stocking; however, this management strategy is often difficult to justify to recreational anglers. Thus, natural reproduction is often estimated by mass marking of hatchery reared striped bass with oxytetracycline (OTC) prior to release, sampling of juveniles in the wild, and assessing the number of juveniles without OTC marks (i.e., ones without marks are assumed to be natural recruits). The ability to detect an OTC mark is therefore crucial to the differentiation of hatchery

and wild striped bass; yet detection and retention rates of OTC marking can be much less that 100% (Reinert et al. 1998). Molecular markers can be a viable alternative to OTC tags (Schwartz et al. 2007) or if used in conjunction with physical tags can validate existing marking techniques.

By combining many highly variable independent microsatellite loci, molecular markers can provide a unique molecular tag or fingerprint for every individual in a population. This knowledge combined with genetic information regarding parents that produced these individuals allows for the matching of progeny to respective parents with high accuracy (termed parentage analysis; Jones and Ardren 2003). Thus if the genetic information of all brood stock that produced stocked progeny is known *a priori*, then when these progeny are sampled in the wild, parentage analysis can be conducted and individuals that are unassigned to brood stock would be considered of wild origin. This method also allows for determining the age of the organism, estimating cohort contribution if multiple years of stocking have occurred, and assisting in the validation of otolith or scale aging techniques (Logsdon et al. 2009).

Goals of this study were to evaluate the stocking success of phase I and phase II fish in West Point Lake, GA, determine hatchery cohort contributions, and quantify the amount of natural reproduction of striped bass in a section of the Chattahoochee River where natural reproduction has been known to occur. To achieve our goals, all phase I and II hatchery fish were marked prior to stocking with both an otolith oxytetracycline (OTC) mark and a molecular microsatellite tag. Thus, we assessed the efficacy and utility of these marking techniques and validated age estimates via otolith aging techniques.

Methods

Study site

The Chattahoochee and Flint rivers merge near the Georgia-Florida border to create the Apalachicola River, which flows into the Gulf of Mexico (Fig. 1). The ACF is the third largest river

system in the historic range of Gulf Coast striped bass encompassing about 1416 km in length (Bass and Cox 1985) and draining an area of 50,800 km^2 (Livingston 1992). The Chattahoochee River, which originates in north Georgia, is 690 km long and forms much of the border between Alabama and Georgia. There are a total of 13 dams on the Chattahoochee River (Fig. 1) for the purposes of flood control, navigation, hydropower, recreation, and/or water supply. The third and second most upstream dams are West Point Dam (impounding 12,000 ha and extending 53 km along the Chattahoochee River) and Morgan Falls Dam, respectively (Fig. 1). It is in this stretch of river, which is the focal point of our study, that three age-3 striped bass were collected in 1999 (Hess and Jennings 2000). Since no striped bass had been stocked in this portion of the system from 1992 through 2004, the presence of these fish indicated that some striped bass reproduction and recruitment occurred in the system as late as 1996 (Hess and Jennings 2000).

Over a three year period starting in 2007, striped bass brood stock were sampled annually from the ACF by various state and federal agencies and taken to one of three hatchery facilities (Marion Fish Hatchery, Alabama Department of Conservation and Natural Resources; Blackwater Fish Hatchery, Florida Fish and Wildlife Conservation Commission; Welaka National Fish Hatchery, U.S Fish and Wildlife Service) for artificial propagation. A tissue sample was taking from each brood stock individual (n = 372), preserved in 95% non-denatured ethyl alcohol, and archived at the United States Fish and Wildlife Service Conservation Genetics Lab in Warm Springs, GA. In 2007, 227,067 phase I and 31,104 phase II striped bass were stocked in West Point Lake (7 crosses of 7 females and 15 males). In 2008, 205,000 phase I and 25,316 Phase II striped bass were stocked (5 crosses from 5 females and 13 males). Finally, in 2009, 403,171 phase I and 23,150 phase II striped bass were stocked (8 crosses, 8 females and 21 males). Phase I stockings occurred in mid May whereas phase II fish were stocked in mid

October. All phase I fish were immersed in 350-400 mg/L buffered OTC solution for 6-8 h (Secor et al. 1991) prior to release, with a subset of marked fish held over for grow out to Phase II. Phase II fish were OTC marked again prior to stocking; thus providing a way to assess stocking success of the two phases (i.e., phase I fish should have single observed OTC mark and phase II a double OTC mark). Note that individuals designated as brood stock are used once for propagation upon which they are then tagged and released back to the wild.

Over a two year period from 2009-2010, we annually sampled West Point Lake for striped bass during the spawning season (March-April) by boat electrofishing. Total length (mm) and weight (g) of each sampled individual was recorded. In addition, a tissue sample was taken and placed in 95% non-denatured ethyl alcohol for genetic analysis and otoliths were removed to assess the OTC mark and determine the age of each sampled fish. Otoliths were stored in numbered vials in a darkened container until examination (Harrison and Heidinger 1996).

Otolith mark detection and aging

Otoliths were mounted on slides and cross-sectioned through the transverse plane with a low-speed diamond blade saw and if necessary sanded and polished to improve readability. Otoliths were examined for OTC marks with an epifluorescent compound microscope equipped with a blue excitation filter (450-490 nm; Reinert et al. 1998). OTC detection was determined by two independent readers with a third reader used to settle any discrepancies. For otoliths that lacked a detectable OTC mark, the corresponding otolith was cut and examined using the same procedure.

Annuli in striped bass otoliths have been verified to form at an annual rate (Heidinger and Clodfelter 1987; Secor et al. 1995a). Annuli were counted once for each fish under light microscopy (magnification 60x or 150x) by two independent readers without knowledge of the

158 estimate by the other reader. A third independent reader was used to resolve any
159 disagreements (i.e., majority rule).

160 *Parentage analysis and molecular tags*

161 DNA was extracted from a portion of the preserved fin clip using the DNeasy Blood and
162 Tissue kit (QIAGEN, Inc., Valencia, California) protocol. We used multiplex PCR reactions on a
163 suite of 11 microsatellite markers known to amplify in striped bass (Rexroad et al. 2006). The
164 three multiplex primer combinations were as follows: multiplex I consisted of primers *MSM*
165 1357, 1429, 1558; multiplex II consisted of primers *MSM* 1556, 1559, 1584, 1592; and multiplex
166 III contained primers *MSM* 1591, 1602, 1626, 1628. Multiplex PCR amplifications were
167 performed in 20 µL reactions using the following reaction components: 1 × *Taq* reaction buffer
168 (Applied Biosystems Inc., Foster City, California), 3.75 mM $MgCl_2$, 0.423 mM of each dNTP, 0.25
169 µM of each primer, and 0.08 U *Taq* polymerase (Applied Biosystems, Inc.). PCR conditions were
170 an initial denaturation at 94 °C (10 min), followed by a touchdown procedure involving 33 cycles
171 and consisting of denaturing (94 °C, 30 s), annealing (30 s), and extension (74 °C, 30 s) cycles,
172 where the initial annealing temperature was initiated at 56 °C and decreased by 0.2 °C per cycle.

173 Prior to electrophoresis, 2 µL of a 1:100 dilution of PCR product was mixed with a 8 µL
174 solution containing 97% formamide and 3% Genescan LIZ 500 size standard (Applied Biosystems,
175 Inc.). Microsatellite reactions were visualized with an ABI 3130 genetic analyzer (Applied
176 Biosystems, Inc.) using fluorescently labeled forward primers and analyzed using GeneMapper
177 software v3.7 (Applied Biosystems, Inc.). The program MICRO-CHECKER v2.2 (van Oosterhout
178 et al. 2004) was used to test for the occurrence of null alleles at each locus used for parentage
179 analysis. Hardy-Weinberg equilibrium and gametic disequilibrium was assessed using the
180 program GENEPOP v4.0.10 (Raymond and Rousset 1995).

Parentage analysis, which was initially performed on all West Point Lake brood stock and collected progeny simultaneously (i.e., all combined cohorts), was performed using the software PAPA v2.0 (Duchesne et al. 2002). Allocations were based on maximum-likelihood and were restricted by using the known structured mating history and a 2% non-uniform error model distributed on the next adjacent allele (Duchesne et al. 2002). A genotyping error rate of 2% was estimated by re-genotyping the brood stock for each locus, counting errors for each locus, and averaging these values for a global estimate. Allocation accuracy was assessed via simulations as implemented in PAPA. Simulations entailed the production of artificial offspring from sampled parents used in this study (i.e., brood stock whose progeny were stocked in West Point Lake). Simulated offspring were then allocated to known sampled parents and the percentage of correctly assigned individuals was assessed. Simulations were performed using 1000 iterations with 100 pseudo-offspring generated for each iteration (a value of 100 was used because it was close to the observed value of offspring collected throughout the study). The production and allocation of pseudo-replicated offspring used the error model implemented above.

Parentage analysis resulted in an allocation success rate that was significantly less than expected, which was an indication of missing parents (assuming that scoring errors are minimal; see below). To assess this discrepancy, we first performed parentage analysis (as above) but eliminated the brood stock mating history. Second, we included all known ACF brood stock crosses (2007, 19 crosses using 19 females and 31 males; 2008, 32 crosses of 28 females and 67 males; 2009, 23 crosses of 23 females and 53 males) that were performed at the hatcheries over the course of the study (i.e., not just the crosses whose progeny where stocked in West Point Lake, but crosses whose progeny were stocked throughout the ACF and the Gulf Coast). Next we removed the mating history for all ACF brood stock. Finally we included all striped bass

(2007, *n* = 109; 2008, *n* = 120; 2009, *n* = 143) that were held at the hatchery facilities over the course of our study (note that sometimes the hatchery will collect a brood stock individual only to realize that the fish is not needed for spawning purposes or is used to make *M. saxatilis* x *M. chrysops* hybrid striped bass).

Results

Age and OTC mark of striped bass otoliths

A total of 103 striped bass were sampled and their otoliths aged and checked for an OTC mark (Table 1). A mark was detected on 99 of 103 (96%) sampled otoliths. All OTC marked otoliths displayed a single mark indicating that they were stocked as phase I fish. Aging results indicated that the 2007 cohort comprised 69% of the sampled individuals with the 11% and 20% for the 2008 and 2009 cohorts (Table 1).

Parentage analysis

A total of 475 striped bass (372 individuals collected as brood stock and 103 putative offspring collected from West Point Lake) were analyzed using 11 microsatellite markers. Microsatellite marker *MSM* 1592 had a general excess of homozygotes for most allele size classes suggesting the existence of null alleles. This locus was removed from all subsequent analyses. For the 2007 brood stock, only two of ten loci conformed to Hardy-Weinberg expectations (*MSM* 1602 and *MSM* 1429). In 2008 and 2009, one (*MSM* 1357) and no loci, respectively, exhibited Hardy-Weinberg equilibrium. In contrast, seven of ten loci were in Hardy-Weinberg equilibrium for offspring collected in 2007 and 2009 from West Point Lake (in 2008 all loci conformed to expectations). A similar pattern was observed for gametic diequilibirum. For each year, all pairwise comparisons between loci (45 of 45 comparisons) from collected brood stock exhibited gametic disequilibrium (all $p > 0.03$). Pairwise comparisons

between loci from offspring of the 2007, 2008, and 2009 cohorts displayed gametic disequilibrium for 62%, 16%, and 13% of the loci.

Parentage simulation showed that the microsatellite markers could accurately assign pseudo-progeny to parents 99% of the time (assuming all parents are sampled and a 2% genotyping error rate) using greater than six loci (Fig. 2). In contrast, our initial parentage analysis based on observed data indicated that only 47% (48 of 103) of the sampled progeny could be assigned to known brood stock whose progeny were stocked into West Point Lake. This finding was in stark contrast to the expected value of 99% found via simulations and to that found via OTC analysis. We explored this discrepancy by first removing the mating history from the parentage analysis, but the results of were identical. Second, we included all known crosses that were performed at the hatcheries over the course of the spawning season, but again our findings were same – only 47% of the sampled progeny could be assigned to their respective parents. Third, we removed the mating history from all known brood stock collected in the ACF that were propagated in the hatcheries over the course of the study, and in doing so, we were able to match 100% (103 of 103) of sampled progeny to their respective parents.

There was disagreement between OTC and genetic marking techniques for 4% (n = 4) of the sampled individuals (USFWS # 4200, 4202, 4250, and 8560). In each case, the genetic mark indicated that the individual was of hatchery origin, but the lack of OTC mark for each fish indicated that the individual could be of wild origin, not marked, or that the mark was undetected. There was complete age agreement (i.e., 103 of 103 aged correctly) between the estimation of age from parentage (via cohort assignment) and otolith aging techniques.

Discussion

Mass marking of hatchery-produced striped bass with OTC has been shown to be an efficient and cost effective method (Secor et al. 1991); however, this method is not without

drawbacks. First, this technique is invasive such that the organism must be sacrificed for otolith removal. Second, the efficacy of this technique (i.e., the retention and detection of an OTC mark), while often greater than 95% for phase I striped bass and other organisms (Secor et al. 1991; Isermann et al. 2002; Mauk 2008), can be much less than 80% (Secor et al. 1991; Reinert et al. 1998). In fact, whole batches of OTC immersed striped bass can go unmarked especially for phase II striped bass (Secor et al. 1991). We found that effectiveness of OTC marking for our study was 96% (99 of 103 individuals displayed a mark) and similar to others. Yet, without and efficacy rate of 100% the evaluation of natural recruitment (in a system with limited recruitment) is arduous because of the ambiguity now associated with an unmarked fish (i.e., an unmarked fish could be of hatchery or wild origin).

Molecular marking techniques provide an alternative to conventional tags or can serve to validate conventional tagging techniques. Essentially, molecular markers can be used just like a conventional tag but are not subject to failure because of battery life, tissue regeneration, or loss of external/internal tag. Molecular markers also serve as a means to tag relatively small organisms and are a part of the fish until death-- a considerable problem for many conventional tags (Van Den Avyle and Wallin 2001). However, parentage analyses using molecular markers are not without problems. Collecting constraints, molecular marker consideration, null alleles, linked loci, mutations, genotype scoring errors, and relatedness among parents are potential technical and biological problems that can preclude individual identification (Jones and Ardren 2003; Jones et al. 2010)

Our initial parentage analysis was able to match 47% of the specimens from West Point Lake back to respective brood fish. This analysis would suggest that natural recruitment did occur in or above West Point Lake. It was only after results from independent otolith analyses did we realize that parentage analysis was grossly inaccurate. This finding was unexpected

because of our simulations indicated that the suite of microsatellite loci was powerful enough to match 99% of the progeny to brood stock. These simulations assumed that all brood stock were accounted for, there were no null alleles, the loci were not linked, and our average genotyping error rate was approximately 2%. Thus, the discrepancy between observed and expected allocation success was an indication that one (or more) of the parentage analysis assumptions had been violate.

The program PAPA produces one of three outcomes when an offspring is processed (either via simulation or with sampled data) – allocated, ambiguous, or null. A high degree of ambiguity is an indication of poor genetic information content (e.g., too few markers); conversely, a large percentage of null scores is suggestive of genotyping error or a substantial portion of missing parents. Initial PAPA results indicated a large proportion of null assignments (ca. 50%) suggesting that we either had gross genotyping error or there was a large portion of unaccounted brood stock. While we did observe that one microsatellite marker was suggestive of having a null allele(s), it was eliminated from subsequent parentage analyses; thus null alleles should not be inflating our genotyping error rate. We also found that the degree of genotyping error in our lab was similar to that of other studies (Bonin et al. 2004; Hoffman and Amos 2005), again suggesting that genotyping error was not influencing our results. Finally, while the striped bass microsatellite loci used in our study did show significant evidence of gametic disequilibrium (probably due to either genetic drift or population structure), gametic disequilibrium is expected to reduce the amount of genetic variation necessary for accurate parentage analysis (Amos et al. 1992; Jones and Ardren 2003). Therefore, we would expect a large portion of ambiguities (not nulls) if gametic disequilibrium was influencing our parentage results. A lack of evidence for violation of these assumptions suggests that our discrepancy in allocation success was caused by mismanagement of tissue samples or missing parents.

The high degree of null assignments was indicative of a mismanagement of the tissue samples (i.e., tissue placed in wrong tube) or data entry. Our analyses assumed that we knew the mating history of all brood stock without error and that all brood stock were sampled. Any mistake in data entry or misplacement of a tissue sample would ultimately lead to an incomplete mating history and produce null assignments. Yet, if all brood stock tissue samples were accounted for and the only mistake was the misplacement of the tissues sample(s) or a mistake in data entry, then by removing the assumption of a mating history in PAPA, the allocation success should match that of expected. Our results of including or excluding the mating history were identical indicating that the high degree of null assignments could not be explained by mismanagement of samples or data entry.

By process of elimination, the large discrepancy in allocation success appeared to be an artifact of missing brood stock in our analyses. Indeed, only when we removed the mating history from all known brood stock collected in the ACF that were propagated in the hatcheries over the course of the study, were we able to match 100% of sampled progeny to their respective parents. This analysis indicated two potential sources of error (which are not mutually exclusive) by hatchery personnel – either they inadvertently spawned the wrong brood stock or mistakenly recorded the mating history. Further evidence supporting this claim is that in any given year the error can be traced to one hatchery. For example, all assignment errors can be traced to a single hatchery in 2007. In this year, the hatchery spawned female 2086 with males 2096 and 2089 and progeny were destined to West Point Lake. The next recorded spawn occurring in the hatchery was for female 2080 and males 2071, 2076, and 2087 (note that progeny from this mating were not suppose to be stocked in West Point Lake). Parentage analyses indicated that female 2086 was spawned with male 2071 from the next recorded cross (a common mistake happening for three other crosses). Furthermore, we captured 38 progeny

from this cross (2068+2071), which alone contributed 70% (38 of 55) of the null assignments during parentage analyses. In similar regards, at the same hatchery, female 2061 was recorded to have been spawned with males 2085 and 2072; however, parentage analyses suggested that this female was actually never used for spawning. Instead female 2081 was found to have been spawned with 2085 -- again highlighting the potential clerical mistake of either writing 2061 instead of 2081 or actually spawning the wrong fish. Thus, the discrepancy in allocation success appeared to be caused by clerical error and highlights the potential pitfalls of molecular tags and the importance of accurate record keeping.

The main objective of this study was to assess natural reproduction of striped bass in West Point Lake. All sampled fish (n = 103) were of hatchery origin; thus providing no evidence of recruitment over the course of our study. Prior to spawning, striped bass inhabiting the ACF system typically migrate upstream to suitable spawning habitat. They are considers broadcast spawners, often spawning over rocky substrate of elevated flows (Boschung and Mayden 2004) . Eggs are non-adhesive, semi-buoyant, and depending on temperature conditions, take two to three days to hatch (Ross 2001). As such, striped bass require suitable spawning habitat a sufficient distance upstream from a reservoir river mouth and sufficient water flow to keep eggs suspended in the water column to assure that eggs and larvae have time to hatch, develop, and reach suitable nursery habitat (Ross 2001; Boschung and Mayden 2004). There are several non-mutually exclusive factors that could be impeding natural reproduction. A rocky shoal is located approximately 15 km above West Point Lake that appears to be suitable spawning habitat and we have collected adult striped bass of reproductive age at this site annually over the course of this study suggesting that spawning habitat is not a limiting factor. We would expect that if suitable nursery habitat was limiting recruitment then other fish species with similar juvenile life histories should also be experiencing the same problem. White bass *M. chyrsops* have a similar

life history to that of striped bass (Boschung and Mayden 2004) with post-larvae (7-12 mm SL) of both species preying upon larvae of other fish and invertebrates such as cladocerans and copepods (Ross 2001). Yet, we continually observe juvenile white bass in West Point Lake indicating that nursery habitat is not limiting in the system. The observation that white bass are annually recruiting in the system, but not striped bass is intriguing and may be answered by the one major difference in their life histories -- white bass eggs are adhesive and demersal (Webb and Moss 1968). This major difference draws considerable attention to the importance of both water flow and length of distance necessary for hatching to achieve successful recruitment. For example, while nursery and spawning habitat appeared available, the distance between them may be too long or short depending on annual water flow and reservoir discharge and could cause the eggs to settle out on silt or organic debris of the reservoir instead of the needed coarser substrates where there is not extensive siltation (Bayless 1968). Clearly, more information is needed to understand the ideal recruitment conditions for striped bass in West Point Lake and the ACF.

Most studies that have addressed the cost effectiveness of stocking larvae (5-13 day old fish), phase I, or phase II hatchery striped bass have found that stocking phase I fish is the most cost-effective strategy (Smith et al. 1990; Secor et al. 1995b); however, there are situations where stocking of phase II fish is preferred such as in coastal areas where predators may be more abundant (Yeager 1987). No phase II individuals were recaptured during our sampling efforts; yet, based on the number of stocked phase I fish in 2007 and the number recaptured, we would have expected the collection of at least five phase II fish during our sampling effort (assuming equal survivorship and catchability for phase I and II individuals). Our data, while not a cost/benefit analysis and limited in scope, indicated that survivorship of phase II fish was

significantly less than expected and that stocking of phase II striped bass was not a good management or conservation strategy for West Point Lake.

The basis or management strategy of stocking phase II fish is that by stocking fewer fish at a larger size there is a greater probability of survival when compared to stocking more fish at a smaller size. This premise appeared to be violated to a certain degree in this system. While the exact cause(s) of the violation is unknown and is out of the scope of our study, predation/stocking location and feed transition (phase II hatchery fish have converted to pellet feed) may be research avenues.

In conclusion, we found no evidence of natural recruitment in West Point Lake over the course of this study; however, we documented that molecular tags can provide a noninvasive alternative to OTC marking of striped bass assuming that the mating histories of the brood stock are known and correct. Therefore accurate records are imperative because without this information, molecular tags could produce unreliable and misleading results. We also showed that molecular tags can produce reliable estimates of age and assignment to cohort – a finding similar Logsdon et al (2009).

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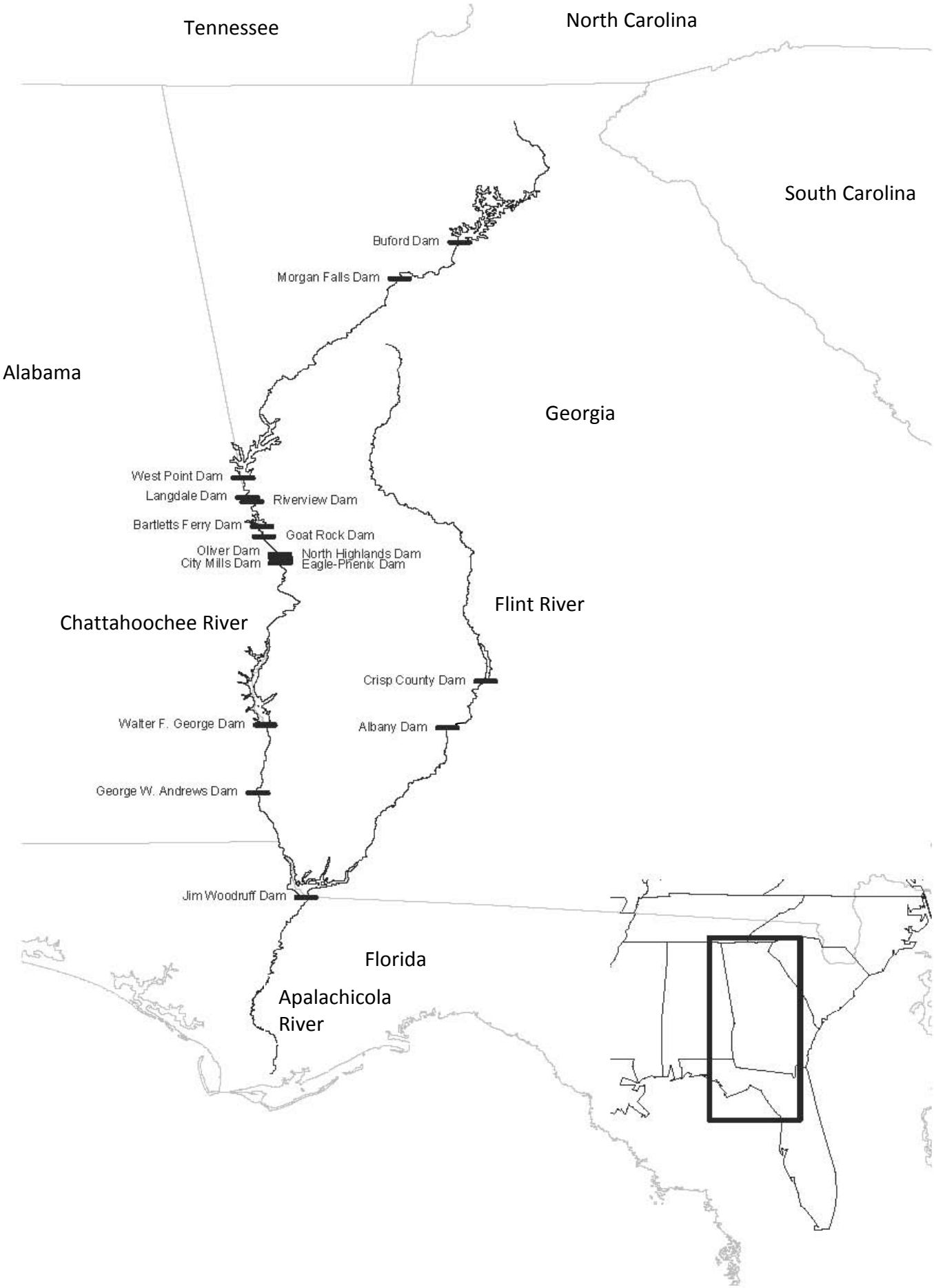
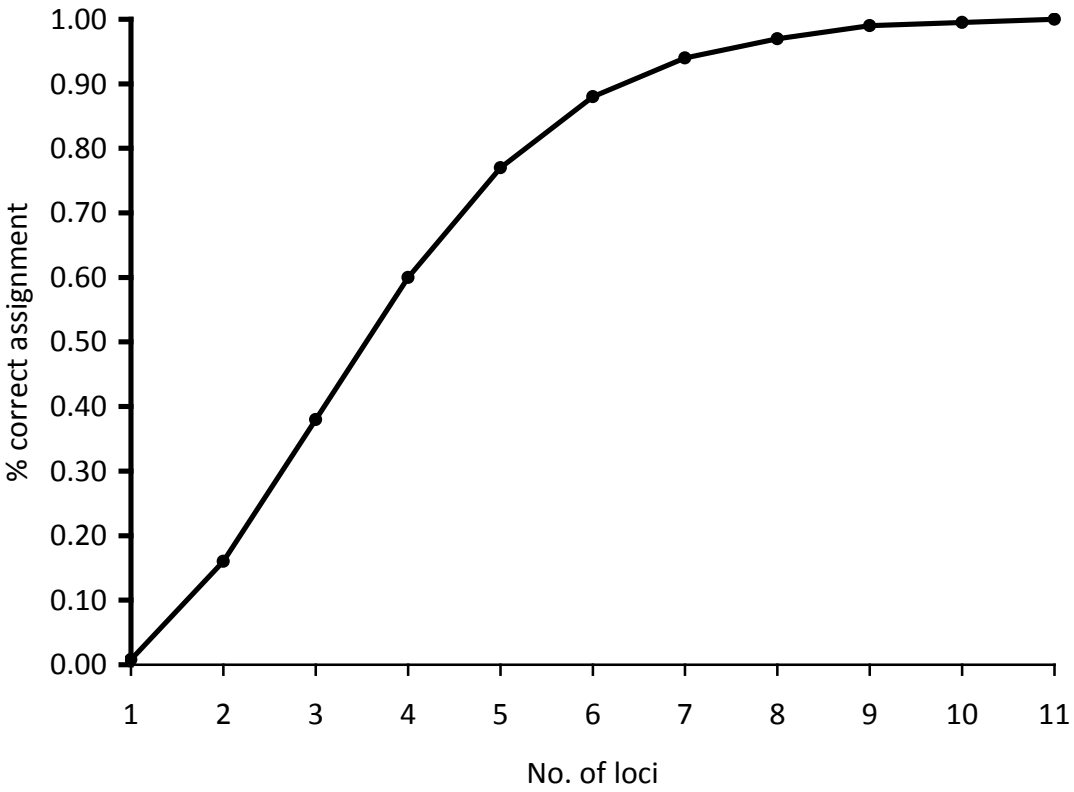
Table 1. Striped bass sampling information and otolith aging results. Brood stock and sampled progeny were collected from March through lat April of each collection year. In parenthesis is the number of females and males (F and M, respectively) used to produce progeny for stocking West Point Lake GA. Sampled progeny is the total number of collected each year and is categorized by cohort via aging of the otolith for each specimen.

Collection Year	Brood stock	Sampled progeny	2007 cohort	2008 cohort	2009 cohort
2007	22 (7F; 15M)				
2008	18 (5F; 13M)				
2009	29 (8F; 21M)	48	38	10	0
2010		55	33	1	21

Figure 1. Map of the Apalachicola, Chattahoochee, Flint river system with inclusion of water impoundments. Our study site focused on assessing natural recruitment of individuals between West Point and Morgan Falls dams.

Figure 2. Percent parentage assignment success vs. number of loci for simulated striped bass parents and progeny. Simulations entailed the production of artificial offspring from sampled parents used in this study (i.e., brood stock whose progeny were stocked in West Point Lake). Simulated offspring were then allocated to known sampled parents and the percentage of correctly assigned individuals was assessed. Simulations were performed using 1000 iterations with 100 pseudo-offspring generated for each iteration.


Tennessee
North Carolina
South Carolina
Alabama
Georgia
Buford Dam
Morgan Falls Dam
West Point Dam
Langdale Dam
Riverview Dam
Bartletts Ferry Dam
Goat Rock Dam
Oliver Dam
City Mills Dam
North Highlands Dam
Eagle-Phenix Dam
Chattahoochee River
Flint River
Crisp County Dam
Walter F. George Dam
Albany Dam
George W. Andrews Dam
Jim Woodruff Dam
Florida
Apalachicola River


1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
% correct assignment
1
2
3
4
5
6
7
8
9
10
11
No. of loci

513