Population genetic structure of black seabass (*Centropristis striata*) on the eastern U. S. coast, with an analysis of mixing between stocks north and south of Cape Hatteras, North Carolina.

Prepared by: Dr. Michael McCartney, University of North Carolina-Wilmington, Center for Marine Science, and Michael L. Burton, NMFS Beaufort Laboratory, SEFSC, 101Pivers Island Rd., Beaufort, NC 28516-9722

Disclaimer: This manuscript is a rough draft work in progress and is not to be cited without permission of the authors.

Introduction

Fishery managers have long recognized two distinct stocks of black seabass on the eastern U.S. seaboard, with Cape Hatteras recognized as the stock separation line. The northern stock migrates from Massachusetts, south and offshore, to deeper waters in the winter months, and then travels back to warmer inshore waters in the north again in the spring and summer (Musick and Mercer, 1977). Kendall and Mercer ((1978) stated that the southern stock did not appear to seasonally migrate, and Mercer (1978) and Shepherd (1991) considered the black seabass population from Cape Hatteras to Cape Canaveral to be a population distinct from the northern stock.

Genetic population structure in black seabass was examined by Bowen and Avise (1990) using mitochondrial DNA (mtDNA) techniques. They discovered strong differentiation between Gulf of Mexico and Atlantic populations, but no apparent differences between specimens from north and south of Cape Hatteras (sampled from Chesapeake Bay and Brunswick, GA). More extensive population sampling, coupled to more powerful multiple-locus DNA analysis, are needed to revisit this genetic assessment of stock structure; in particular, to address the extent of mixing between stocks. There has been anecdotal information from the North Carolina commercial fishing industry, recently, suggesting there may be a southward migration of black seabass across the Cape Hatteras boundary during the winter months. The evidence cited for this is the recent appearance in the landings of very large fish exhibiting different morphologies than usually seen (steep sloped foreheads, blue colored faces) (Tony Austin, pers. comm.)

Recently, the issue of population structure in black seabass was identified as a research priority by the Southeast Fisheries Science Center's SEDAR (Southeast Data, Assessment and Review) process in March 2005. Research recommendations from that stock assessment stated "*Tagging and genetic studies should be used to gain information on population structure*". Gary Shepherd at the Northeast Fisheries Science Center has been tagging black seabass. Additionally, SEFSC scientists have initiated a Cooperative Research Proposal (CRP) study to validate the observed morphological differences using otolith elemental analyses, and describe seasonal and annual migration histories of individual adult black seabass using otolith elemental analyses (by laser ablation inductively coupled plasma mass spectrometry). A study of population genetic structure of black seabass collected from different locales along the eastern U. S. seaboard was undertaken to address these stated SEDAR research recommendations

Material and Methods

Tissue sample collection—Black sea bass adults were collected by hook and line (headboat and commercial fishermen, fishery-dependent), trap sampling (fishery-independent), and by NOAA's Northeast Fisheries Science Center groundfish trawl surveys out of Woods Hole, MA (fishery-independent). Opportunistic sampling was used when necessary, but we controlled as carefully as possible the approximate size range of the fish selected and the season of collection. In both 2008 and 2009, we obtained fish between the months of June and October. These were designated summer/fall collections. An additional seasonal sample was obtained during the winter/spring season, February through April, from Onslow Bay. This sample was taken for the purpose of addressing the hypothesis of winter migration of Mid-Atlantic fish into Onslow Bay, which hadbeen reported by fishermen (Tony Austin, pers. comm.).

Fifty to 150 individuals were obtained from each of 9 populations (Fig. 1, Appendix 1), spanning the geographic range of *C. striata* from the northern Gulf of Mexico to Nantucket Sound, MA, with 5 Atlantic populations from north of Cape Hatteras [the Mid-Atlantic (Mid-Atl) stock or region], 3 Atlantic populations from south of Cape Hatteras [the South Atlantic Bight (SAB) stock or region]. In the Mid Atl region, one population (North Carolina, north of Hatteras) is best viewed as geographically transitional, as some fish captured here were taken either very close to or even slightly south of the Cape by the NOAA groundfish survey personnel. We use the term "stock" as a provisional category, which reflects the current management of these subpopulations as stocks separated at Cape Hatteras. All tissue samples (mostly gill) used for genomic DNA extraction were stored in salt saturated DMSO (Seutin *et al.* 1993) at 4°C. Individuals selected for DNA sequence analysis were chosen to represent a similar size range across populations. Mean TLs were similar, with a minimum of 181 mm in the Virginia population, and maximum of 327 mm in the NE Florida (Table 1). We were also careful to ensure that the winter collection from Onslow Bay included large fish, and the mean TL of fish from this collection exceeded the mean TL of fish from the summer Onslow Bay collection (Table 1).

DNA extraction, amplification and sequencing—Genomic DNA was extracted from gill tissue using a modification of the "Rapid Isolation of Mammalian DNA" protocol in Sambrook and Russell (Sambrook and Russell 2000), with DNA extracts typically given a final purification over QIAGEN QIAquick (Valencia, CA) PCR purification columns. Some DNAs were extracted using the QIAGEN DNAeasy kit. The full-length mitochondrial DNA (mtDNA) control region was amplified using universal primers L-Pro-F (5′-

AACTCTCACCCCTAGCTCCCAAAG-3′) and 12S-ARH (5′-ATAGTGGGGTATCTAATCCCAGTT-3′: (Palumbi 1996). For amplification, an initial denaturation for 1 min at 94 °C was followed by 35 cycles of 45 sec at 94 °C, 30 sec at 55 °C, 2 min at 72 °C, and a final extension step at 72 °C for 5 min. PCR products were purified over QIAquick minicolumns, and cycle-sequenced using C. striata-specific sequencing primers (available from the authors) and ABI Prism BigDye™ v 3.1 terminator sequencing kits (Applied Biosystems, Foster City CA). Raw sequence data was edited using Sequencher 4.10.1 (Gene Codes, Ann Arbor MI). Due to the fact that very few insertion-deletion mutations were found in this part of the control region, sequences were aligned by eye.

Sequence analysis—To obtain a model of molecular evolution that was appropriate for analysis of genetic differentiation by F-statistics, and for generating estimates of migration rates between populations, we used *Modeltest 3.7* (Posada and Crandall 1998). Based upon the Akaike Information Criterion, *Modeltest* selected a TVM + I molecular evolutionary model, with I = 0.775 for the proportion of invariant sites reflecting the relatively small number of variable sites in these black sea bass control region sequences. The hLRT criterion selected an HKY model with rates across sites gamma distributed ($\alpha = 0.0064$). The HKY model is similar to the Tamura 3-parameter model, which is designed for sequences showing high transition bias and G+C-content bias (Tamura 1992), as in the present case (transition:transversion ratio = 6.628, G+C = 0.393). This model is available in both *Arlequin* and *MEGA 4*, so it was adopted (and is denoted TM + G)

To construct the haplotype network, we used the method of median-joining (Bandelt *et al.* 1999). This method, according to comparisons of those available (Posada and Crandall 2001) is very rapid for generating large networks (such as this one) and appropriate for non-recombining segments of DNA (such as fish mtDNA). Median-joining networks, post-processed using parsimony (Polzin and Daneschmand 2003) were constructed using the software *Network 4.5.1.6* (http://www.fluxus-engineering.com). We estimated genetic distances with *MEGA 4* (Tamura *et al.* 2007). For estimating haplotype frequencies, estimates values F_{ST} between all pairs of populations, migration rates, and for conducting Analysis of Molecular Variance (AMOVA), we used *Arlequin 3.5* (Excoffier and Lischer 2009). F_{ST} was estimated using the method of Hudson et al. (Hudson *et al.* 1992), and migration rates were estimated as $M = Nm$ effective migrants per generation (where $N = N_e$ = the effective population size and m = the proportion of population A exchanging migrants with population B, per generation). This calculation is based upon the infinite island model (Hudson *et al.* 1992). Here we apply migration rate estimates to assess the amount of mixing between black sea bass populations, and adopt a benchmark value of $Nm = 1$, below which we consider migration to be substantially restricted (Slatkin 1985; Wright 1978), although we note that the change in genetic differentiation at $Nm = 1$ is not abrupt (Hudson et al. 1992; Slatkin 1981; Slatkin and Maddison 1989).

Results

The complete alignment included 645 base pairs of control region sequence in 280 fish total, collected from 9 populations in the summer and fall months (Table 1). This alignment was used for calculations of genetic distances, F_{ST} and migration estimates between populations, and AMOVA, but included some ambiguities in the 5′ and 3′ terminal regions of the sequenced fragment. Since these create issues for median-joining network construction (Bandelt *et al.* 1999), the termini were trimmed and 3 partial sequences were eliminated, leaving a 590 base pair alignment of 277 fish for haplotype network construction. An additional 48 fish collected from Onslow Bay in the winter months were used to assess the winter migration hypothesis (based on haplotype frequencies). This brought the total number of individuals characterized to 328, but these winter fish were excluded from all other analyses, since winter fish were absent from other populations surveyed (Table 1).

The haplotype network (Figs. 2) showed 3 major regional patterns. First, it showed that all Gulf of Mexico (GOM) haplotypes were separated from all Atlantic haplotypes by > 6 and usually > 8 mutations, and that no Gulf haplotypes were found in Atlantic fish (or the converse). Second, it showed that Atlantic haplotypes sort predominantly into two large clusters, one largely mid-Atl and the other largely restricted to SAB fish (Fig 2B). Each of these regional subnetworks is composed of a single very common haplotype (mid-Atl haplotype A in 39 fish, SAB haplotype A in 79 fish), surrounded by several uncommon or singleton haplotypes that are distinguished from the common haplotype by one mutation. Mid-Atl and SAB haplotype clusters are separated from each other by two mutations (Fig. 2B), at positions 364 and 391 in the control region alignment. Third, the haplotype network showed that the population just to north of Cape Hatteras was transitional, in that approximately half the fish from this population showed mid-Atl and half showed SAB haplotypes. This third pattern is most easily discerned in Fig. 2C.

The haplotype network allowed us to define 3 positions along the DNA sequence at which geographic differentiation in the frequency of base substitutions could be visualized on a map as “pie diagrams” (Fig. 3). Two of these positions are 364T and 391C, described above (391C = cytosine at position 391) in mid-Atl haplotype A and related haplotypes, and are 364C and 391T in SAB haplotype A and related haplotypes. The map (drawn only for the Atlantic populations) shows strong differentiation in the frequency of these DNA substitutions that coincides with Cape Hatteras—populations north of the Cape are dominated by 364T and 391C; populations to the south of the Cape are dominated by 364C and 391T. An exception to this is the population in North Carolina N of Cape Hatteras, in which 364T_391C and 364C_391T and nearly equally frequent. This transitional population lies in a narrow region between the Cape and the Virginia border.

The narrowness of this apparent zone of transition is clear in that the Virginia population, right over the state border off Virginia Beach, is already dominated by mid-Atl haplotypes (Fig 3).

This map also suggests that the winter population collected at Onslow Bay does show a slightly elevated frequency of mid-Atlantic haplotypes, consistent with the anecdotal information from the North Carolina commercial fishing industry, suggesting there may be a southward migration of black seabass across the Cape Hatteras boundary during the winter months. The apparent frequency of these vagrants was 3/45, and 9/48 fish, in the Onslow summer and winter samples, respectively, a slight and marginally not significant difference (G_{adj} (Williams' correction) = 3.024, $P > 0.05$). One final observation from this map concerns the Massachusetts population, in which fish captured in 2008 (Appendix) show substitutions at position 552 that distinguish them from the fish from any other Atlantic population. These odd haplotypes were not collected in 2009. Both the weak pattern of NC winter migration and the Massachusetts "endemic subpopulation" of black seabass may be worth later re-examination.

Analyses based upon genetic distances between haplotypes confirmed and extended these haplotype-frequency based findings. Based on TM + G corrected values, the mean pairwise distance was 0.31 and 0.43% within the mid-Atl and SAB regions, and 0.54% between these regions, reflecting the additional sequence differentiation across Cape Hatteras. Distances within the Gulf of Mexico (GOM) region were 0.93%, while between region distances were 2.09 between GOM and SAB and 2.28% between GOM and Mid-Atl. These comparisons showed the Gulf of Mexico to harbor greater genetic variation than any Atlantic population, and they also demonstrated that the Gulf/Atlantic differentiation is about 4 times the differentiation within the Atlantic, across Cape Hatteras.

Pairwise F_{ST} estimates showed several patterns (Table 2). First, the highest values separated GOM from Atlantic populations. Second, within the Atlantic, higher values of F_{ST} (i.e. greater differentiation) were found in comparisons across Cape Hatteras than in comparisons within mid-Atl or SAB regions. Twelve out of 15 cross-Cape comparisons showed $F_{ST} > 0.25$, the value Wright (Wright 1978) considered to indicate "very great" genetic differentiation. The 3 comparisons not exceeding this benchmark all involve the northern NC transitional population. In contrast, none of the 10 comparisons within the mid-Atl exceeded this benchmark, and while 7 of these are significant, each of these involves either the northern NC transitional population or the Massachusetts population. Similarly, none of the 3 comparisons within the SAB show $F_{ST} >$ 0.25.

Migration rate estimates (Table 3) parallel these same patterns, as is expected since they derive from F_{ST}, but this index allows some additional interpretation. Migration rate estimates can be used as indicators of long-term exchange of alleles (or in this case, of mtDNA haplotypes) between populations (Slatkin 1985). Values of $Nm < 1$ indicate that substantial genetic differentiation can accumulate between populations, and therefore that rates of adult migration between populations, and rates of exchange of pelagic larvae, or of mobile juveniles and subadults, should they exist, are fewer than the number needed to transfer one "vagrant" gene copy, per generation. Across Cape Hatteras (Table 3), only 5 of 15 population pairs were shown to exchange > 1 migrant per generation. Of the 5 with *Nm* > 1, three involve the northern NC population and 2 are marginally above 1. In contrast, *all* of the 13 population pairs within either the SAB or the mid-Atl regions exchange > 1 migrant per generation. Apparently, exchange of propagules and/or of adults between populations on the same side of Cape Hatteras is relatively free, but mixing is greatly restricted across this biogeographic barrier.

AMOVA analyses (Tables 4 and 5) provide a final measure of the contribution of Cape Hatteras towards population genetic differentiation in black seabass. Of the total genetic variation across the range of populations sampled, we found that 56.5% was due to differences among Mid Atlantic, South Atlantic Bight (SAB), and Gulf of Mexico (GOM) regions, while only 2.76% was due to differences among populations within these regions (Table 4). When this analysis was restricted to the Atlantic (hence eliminating the effect of GOM/Atlantic divergence), we found that of the total genetic variation, 31.0% was due to differences among mid-Atl and SAB regions, while only 5.1% was due to differences among populations within these regions. A fixation indices for differentiation among mid-Atl and SAB regions ($F_{CT} = 0.310$, $P < 0.01$), again indicated very great genetic differentiation across Cape Hatteras.

Discussion

Marine biogeographers have long recognized Cape Hatteras as a boundary between two faunal provinces, the Carolinian Province to the south and the Virginian province to the north (Briggs 1974; Engle and Summers 1999). This marks a line of transition between the geographic range limits of numerous species of benthic invertebrates (Engle and Summers 1999) and fishes (Schwartz 1989), perhaps set by a combination of dispersal barriers and by the abrupt change in sea surface temperature where waters originating from the Labrador current meet waters originating from the Gulf Stream. Indeed, in many months of the year, the coastal ocean of Cape Hatteras displays one of the sharpest thermal discontinuities in the world's oceans (see real-time SST satellite imagery at http://marine.rutgers.edu/cool/sat_data/?product=sst&region=capehat&nothumbs=0). It is striking, therefore, that with few exceptions, Cape Hatteras has not often been detected as a population genetic break between populations of marine species.

Marine species showing genetic differentiation across the Cape have so far been forms with restricted larval dispersal and sedentary or sessile adults. *Gammarus tigrinus*, an estuarine amphipod lacking larvae that survive marine salinities, shows phylogeographic structure suggesting a genetic break at Cape Hatteras (Kelly *et al.* 2006). So does the *Bugula neritina* bryozoan species complex

(McGovern and Hellberg 2003), a group with large non-feeding larvae with poor dispersal powers. Toadfish *Opsanus tau*, a species that lays large demersal eggs, shows separate mtDNA clades north and south of the Cape (Avise *et al.* 1987), and is the only finfish species with a published genetic break at the Cape. More mobile species, including weakfish (*Cynoscion regalis*), bluefish (*Pomatomus saltatrix*), menhaden (B*revortia tyrannus*), marine catfishes (Ariidiae), and summer flounder (*Paralichthys dentatus*) show no evidence for genetic separation at the Cape (Avise et al. 1987; Bowen and Avise 1990; Graves et al. 1992a; Graves et al. 1992b; Jones and Quattro 1999).

Our results with black seabass populations provide the first example of a finfish species with a Cape Hatteras population genetic break. This is true, despite the presence of a typical serranid larval form, capable of an approximately 3 week PLD , which should provide considerable dispersal potential. Moreover, our results showing that the population off Albemarle Sound NC is a mixture of adults from both mid Atlantic and south Atlantic stocks, coupled with the finding from MARMAP surveys (Berrien and Sibunka 1999) that this area shows very high concentrations of *C. striata* eggs, suggests the operation of strong reproductive isolating barriers that prevent genetic exchange between the stocks. It is important to emphasize that such a genetic separation between stocks, over the longer term (which must be true, given their phylogenetic distinctiveness) would allow for meaningful divergence in life history, behavioral, morphological and physiological characters relevant to the two separately managed fisheries, and to the performance of the two stocks in aquaculture. Life history differences, migratory and other behavioral differences, are thought to exist between mid-Atl and SAB populations, and the lack of gene flow between them should act to preserve these.

One question the reader may have asked concerns confidence in the migration estimates we have generated (Table 3). We can generate confidence limits around these estimates, for example, by coalescent simulations (Schneider et al. 2000; Slatkin and Maddison 1989). In ongoing analyses, we are doing so, and are focusing on more recent coalescent estimators of migration rates (Beerli and Felsenstein 1999; Beerli and Felsenstein 2001) available in the software package MIGRATE (http://popgen.sc.fsu.edu/Migrate/Migrate-n.html). MIGRATE has two important advantages over our present, more conventional analysis. First, it does not assume an equilibrium island model and hence seems more relevant to marine populations like this one in which star phylogenies (Fig. 2) and explicit analysis of population size changes (not shown) suggest expanding population sizes and non-equilibrium population structure as black seabass recolonized their Atlantic range. Second and more importantly in the present application, MIGRATE can provide asymmetric, directional migration estimates (e.g. we could assess a scenario in which migration of southern fish into the mid-Atlantic was more frequent than in the opposite direction). Results of these analyses are forthcoming.

In addition to the break at Cape Hatteras, our results also demonstrate that genetic separations between Atlantic and Gulf of Mexico populations are older, and that gene flow is even more restricted. While the sample size in the Gulf is small, we can also infer that this population has a very different population structure. Both Atlantic populations show star-like haplotype networks (Fig. 2), and examination of Tajima's D and Fu and Li's D* test statistic shows evidence that the Atlantic populations are colonizing populations that have undergone recent expansions in population size. This does not seem to be the case for the Gulf population, which may reflect a more stable history, such as would be expected if it served as a refugium during glacial periods (Avise 1992). Whatever the case, our results indicate that Gulf/Atlantic divergence substantially exceeds divergence across Cape Hatteras, and (with the caveat that the Gulf data set is relatively small), shows that two subpopulations are reciprocally monophyletic. This result would support the recognition of Gulf black seabass as a separate subspecies—*C. striata melana*—by some authors (Bortone 1977; Mercer 1989).

Management implications

Management implications of our results can be summarized as follows. Our work shows that black seabass mid-Atlantic and south Atlantic stocks, as currently managed, are well separated and have a long history of limited interbreeding. This suggests that any migration across Cape Hatteras, such as might occur during the suggested winter migration of mid-Atlantic fish, has not eliminated the strong genetic differentiation between stocks, so we would conclude that the long term effects have been minimal. However, we would emphasize that our method tracks genetically effective migration, which will generally underestimate migration rates of adults. For example, if mid-Atlantic fish enter the south Atlantic fishery in the winter, or as we have shown, that south Atlantic and mid-Atlantic fish coexist in roughly equal numbers off Albemarle Sound, then the two stocks interbreed very little in either case. Future research on the winter migration question could utilize multilocus DNA analysis and an "assignment" approach more explicitly designed to estimate interpopulation dispersal and mixing. Based on the current analysis, moreover, we would conclude that mixing of the adult populations appears mostly to be restricted to a narrow region between the VA border and Cape Hatteras. We emphasize that this finding and the region of apparent transition between the geographic range limits of the two stocks off Albemarle Sound is worthy of further study, using a combination of mtDNA markers developed here, multilocus nuclear DNA markers (e.g. microsatellites), and perhaps elemental analysis of otoliths. This future work could more precisely estimate the magnitude and geographic extent of mixing between mid-Atlantic and south Atlantic stocks of black seabass.

References

Avise, J. C., C. A. Reeb, and N. C. Saunders. 1987. Geographic population structure and species differences in mitochondrial DNA of mouthbrooding marine catfishes (Ariidae) and demersal spawning toadfishes (Batrachoididae). Evolution 41:991-1002.

Bandelt, H., P. Forster, and A. Rohl. 1999. Median-joining networks for inferring intraspecific phylogenies. Molecular Biology and Evolution 16:37-48.

Beerli, P., and J. Felsenstein. 1999. Maximum likelihood estimation of migration rates and effective population numbers in two populations. Genetics 152: 763-773.

Beerli, P., and J. Felsenstein. 2001. Maximum likelihood estimation of a migration matrix and effective population sizes in *N* subpopulations by using a coalescent approach. Proceedings of the National Academy of Sciences 98:4563-4568.

Berrien, P., and J. Sibunka. 1999. Distribution patterns of fish eggs in the U.S. northeast continental shelf ecosystem, 1977-1987. NOAA Technical Report NMFS 145.

Bortone, S. A. 1977. Osteological notes on the genus *Centropristis* (Pisces: Serranidae). Northeast Gulf Science 1:23-33.

Bowen, B. W., and J. C. Avise. 1990. Genetic structure of Atlantic and Gulf of Mexico populations of sea bass, menhaden, and sturgeon: Influence of zoogeographic factors and life-history patterns. Marine Biology 107:371-381.

Briggs, J. C. 1974. Marine zoogeography. McGraw-Hill, New York.

Engle, V. D., and J. K. Summers. 1999. Latitudinal gradients in benthic community composition in Western Atlantic estuaries. J. Biogeogr. 26:1007-1023.

Excoffier, L., and H. Lischer. 2009. Arlequin ver 3.5. Swiss Institute of Bioinformatics, Bern, Switzerland.

Graves, J. E., J. R. McDowell, and M. L. Jones. 1992a. A genetic analysis of weakfish, *Cynoscion regalis*, stock structure along the mid-Atlantic coast. Fisheries Bulletin 90:469-475.

Graves, J. E., J. R. McDowell, and M. L. Jones. 1992b. Stock structure of the bluefish *Pomatomus saltatrix* along the mid-Atlantic coast. Fisheries Bulletin 90:703-710.

Hudson, R. R., M. Slatkin, and W. P. Maddison. 1992. Estimation of levels of gene flow from DNA sequence data. Genetics 132:583-589.

Jones, W. J., and J. M. Quattro. 1999. Genetic structure of summer flounder (*Paralichthys dentatus*) populations north and south of Cape Hatteras. Marine Biology 133:129-135.

Kelly, D. W., H. J. MacIsaac, and D. D. Heath. 2006. Vicariance and dispersal effects on phylogeographic structure and speciation in a widespread estuarine invertebrate. Evolution 60:257-267.

Kendall, A.W. and L.P. Mercer. 1982. Black sea bass *Centropristis striata*. Pages 82-83 *in* M.D. Grosslein and T. R. Azarovitz, editors, Fish Distribution. New York Sea Grant Institute, MESA New York Bight Atlas Series, Monograph 15, Albany NY.

McGovern, T. M., and M. E. Hellberg. 2003. Cryptic species, cryptic endosymbionts, and geographical variation in chemical defences in the bryozoan *Bugula neritina*. Molecular Ecology 12:1207-1215.

Mercer, L. P. 1978. The reproductive biology and population dynamics of black seabass, Centropristis striata. Ph. D. thesis, Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, VA. 196 pp.

Mercer, L. P. 1989. Species profile: life histories and environmental requirements of coastal fishes and invertebrates (South Atlantic) black sea bass. Pp. 1-16. U.S. Fish and Wildlife

Musick, J.A. and L.P. Mercer. 1977. Seasonal distribution of black sea bass, *Centropristis striata*, in the Mid-Atlantic Bight with comments on the ecology and fisheries of the species. Trans. Am. Fish. Soc. **106**:12-25.

Palumbi, S. 1996. Nucleic acids II: the polymerase chain reaction. Pp. 205–247 *in* D. Hillis, C. Moritz and B. Mable, eds. Molecular Systematics. Sinauer & Associates, Inc., Sunderland, Massachusetts.

Polzin, T., and S. V. Daneschmand. 2003. On Steiner trees and minimum spanning trees in hypergraphs. Operations Research Letters 31:12-20.

Posada, D., and K. A. Crandall. 1998. Modeltest: Testing the model of DNA substitution. Bioinformatics 14:817-818.

Posada, D., and K. A. Crandall. 2001. Intraspecific gene genealogies: trees grafting into networks. Trends in Ecology and Evolution 16:37-45.

Sambrook, J., and D. W. Russell. 2000. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

Schneider, S., D. Roessli, and L. Excoffier. 2000. ARLEQUIN Version 2.000. Genetics and Biometry Laboratory, University of Geneva, Geneva, Switzerland.

Schwartz, F. J. 1989. Zoogeography and ecology of fishes inhabiting North Carolina's marine waters to depths of 600 meters. Pp. 335-374 *in* R. Y. George and A. W. Hulbert, eds. North Carolina Coastal Oceanography Symposium. U.S. Dept. of Commerce, National Oceanic and Atmospheric Administration, Office of Undersea Research, Rockville,Maryland.

Seutin, G., J. Brawn, R. E. Ricklefs, and E. Bermingham. 1993. Genetic divergence among populations of a tropical passerine, the Streaked Saltator (*Saltator albicollis*). Auk 110:117-126.

Shepherd, G. 1991. Meristic and morphometric variation in black sea bass north of Cape Hatteras, North Carolina. N. Am. J. Fish Mgmt. 11:139-148.

Slatkin, M. 1981. Estimating levels of gene flow in natural populations. Genetics 99:323-335.

Slatkin, M. 1985. Gene flow in natural populations. Annual Reviews of Ecology and Systematics 16:393-430.

Slatkin, M., and W. P. Maddison. 1989. A cladistic measure of gene flow inferred from the phylogenies of alleles. Genetics 123:603-613.

Tamura, K. 1992. Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G+C-content biases. Molecular Biology and Evolution 9:678-687.

Tamura, K., J. Dudley, M. Nei, and S. Kumar. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. Molecular Biology and Evolution 24:1596–1599.

Wright, S. 1978. Evolution And The Genetics Of Populations. Vol. 4: Variability Within And Among Natural Populations. University of Chicago Press, Chicago.

Table 1. Body size distribution of sequenced black sea bass. TL = total length.

Population	***N***	**TL range (mm)**	**TL mean**	**TL std. dev**
Massachusetts	28	59-390	256	99
New Jersey	26	132-326	220	58
Delaware	27	150-433	261	65
Virginia	32	128-287	181	44
NC-north of Hatteras	34	100-295	208	48
NC-Onslow Bay summer	45	176-342	235	41
NC-Onslow Bay Winter	48	172-365	287	43
South Carolina	31	160-321	237	49
East Florida	33	287-396	327	26
Gulf of Mexico	23	156-485	316	106

Table 2. F_{ST} between populations of *Centropristis striata*. Values are Φ_{ST}; significance was determined by permutation (1023 replicates), and in bold: $P < 0.001$, italics: $P < 0.01$, plain text: not significant. Note that the highest values exist between Gulf of Mexico and Atlantic populations (blue shaded cells). Also note the much higher values across Cape Hatteras (green shaded) compared to within the Mid Atlantic and South Atlantic regions (gray shaded). A negative value implies $F_{ST} = 0$.

	GOM	NE Florida	South Carolina	NC Onslow	N North Carolina	Virginia	Delaware	New Jersey
GOM								
NE Florida	**0.655**							
South Carolina	**0.735**	**0.064**						
NC Onslow	**0.701**	0.006	**0.061**					
N North Carolina	**0.699**	**0.094**	**0.211**	**0.119**				
Virginia	**0.762**	**0.307**	**0.509**	**0.345**	*0.079*			
Delaware	**0.772**	**0.390**	**0.613**	**0.425**	**0.157**	0.021		
New Jersey	**0.745**	**0.308**	**0.502**	**0.348**	*0.079*	-0.013	0.008	
Massachusetts	**0.743**	**0.349**	**0.532**	**0.396**	**0.176**	**0.154**	**0.156**	**0.123**

Table 3. Estimates of migration rates between populations of *Centropristis striata*. Values are *M* = *Nm*, or the genetically effective number of migrants between populations per generation, assuming an island migration model (Slatkin 1991). Values below 1 migrant per generation are sufficiently restricted that "meaningful" divergence can evolve in the island model (Slatkin 1991). Gulf of Mexico populations show highly restricted migration with all Atlantic populations (blue shaded cells). Migration across Cape Hatteras (green shaded) is restricted in 10/12 comparisons, but the transitional population in NE North Carolina shows moderate exchange with populations south of the Cape. Migration within Mid Atlantic and South Atlantic regions (gray shaded) is not restricted.

	GOM	NE Florida	South Carolina	NC Onslow	N North Carolina	Virginia	Delaware	New Jersey
GOM								
NE Florida	0.264							
South Carolina	0.180	7.307						
NC Onslow	0.213	79.654	7.763					
N North Carolina	0.215	4.803	1.865	3.712				
Virginia	0.156	1.129	0.483	0.949	5.774			
Delaware	0.148	0.781	0.316	0.675	2.692	22.793		
New Jersey	0.171	1.122	0.497	0.935	5.822	∞	63.358	
Massachusetts	0.173	0.933	0.440	0.763	2.338	2.748	2.696	3.563

Table 4. AMOVA Analysis: Gulf and Atlantic regions. Of the total genetic variation, 56.5% was due to differences among Mid Atlantic, South Atlantic Bight (SAB), and Gulf of Mexico (GOM) regions, while only 2.76% was due to differences among populations within these regions. Fixation indices: for differentiation among regions $F_{CT} = 0.565^{***}$, for among populations within regions $F_{SC} = 0.063^{***}$, and for both among and within drainages $F_{ST} = 0.592^{***}$, ***$P < 0.001$; *df* = degrees of freedom.

Source of variation	*df*	Sum of squares	Variance components	Per cent of variation
Among regions (Mid-Atlantic, SAB, GOM)	2	284.77	1.751	56.52
Among populations within regions	6	23.723	0.085	2.76
Within populations	271	341.85	1.261	40.72
Total	279	650.34	3.097	100

Table 5. AMOVA Analysis: Atlantic regions separated by Cape Hatteras. The AMOVA was repeated by eliminating the GOM population, in order to estimate differentiation across Cape Hatteras. Of the total genetic variation, 31.0% was due to differences among Mid Atlantic and South Atlantic Bight regions, while only 5.1% was due to differences among populations within these regions. Fixation indices: for differentiation among regions $F_{CT} = 0.310^{**}$, for among populations within regions $F_{SC} = 0.074^{***}$, and for both among and within regions $F_{ST} = 0.361^{***}$, $^{***}P < 0.001$, $^{*}P < 0.05$; *df* = degrees of freedom.

Source of variation	*df*	Sum of squares	Variance components	Per cent of variation
Among regions (Mid-Atlantic, SAB)	1	71.143	0.535	31.01
Among populations within regions	6	23.297	0.088	5.11
Within populations	248	273.49	1.103	63.87
Total	255	367.93	1.726	100

Table 6. mtDNA control region differentiation between populations of black seabass, in comparison to other well-studied marine finfish species. Comparisons are limited to studies of comparable effort that employed the mtDNA control region, and that focused on comparable biogeographic regions. The bluefin tuna results are provided for comparison across a wider geographic range in a more mobile, pelagic species.

*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, *ns* = not significant.

†pairwise Φ_{ST},mtDNA control region

$^{\lozenge}\Phi_{CT}$ from AMOVA, mtDNA control region

Species	Regions compared	Φ statistic	Reference
Bluefin tuna	Western Mediterranean/GOM	.0104*	Carlsson et al. 2007†
Gag	GOM/Atlantic	-.00002 *ns*	Cushman et al. 2009†
Black sea bass	GOM/Atlantic	.746***	This study$^{\lozenge}$
Summer flounder	North/South of Cape Hatteras	-.0016 *ns*	Jones and Quattro 1999$^{\lozenge}$
Black sea bass	North/South of Cape Hatteras	.301**	This study$^{\lozenge}$

FIGURE LEGENDS

Fig. 1 Sampling locations

Fig. 2 Median-joining haplotype network for black sea bass mtDNA control region sequences.

A. Complete network. Each colored ball represents a unique haplotype and the size of the ball is proportional to the number of individuals that share the haplotype (i.e. haplotype frequency). The color of the ball indicates geographic origin of the haplotype; for haplotypes common to multiple populations, color slices represent frequencies in each source population (e.g. copies of South Atlantic Bight haplotype B are ~ equally frequent in Onslow Bay, in South Carolina, and NE FL populations). Branches in the network interconnect haplotypes, and are scaled by the number of mutations between them (scale bar). Note the presence of three main subnetworks. The mid-Atlantic and South Atlantic Bight subnetworks are each dominated by a different, common haplotypes are embedded in a “star-like” configuration, where the common haplotype is surrounded by multiple haplotypes, one mutation different. The third subnetwork represents Gulf of Mexico haplotypes, which are separated from Atlantic haplotypes by multiple mutations.

B. Atlantic haplotypes: populations. This expanded image shows detail of relationships among Atlantic haplotypes. Haplotypes from populations in the mid-Atlantic mostly fall into a subnetwork that is separated from a subnetwork of haplotypes from South Atlantic Bight populations. These clusters (divided at Cape Hatteras) are distinguished by two mutations—at nucleotide positions 340 and 367 (indicated by curved arrows). Frequencies of some common haplotypes are given in the center of the ball (i.e. 79 fish showed haplotype A).

C. Atlantic haplotypes: regions. The same expanded image shows all haplotypes sorted into Mid-Atl and SAB regions of origin. The NC population north of Cape Hatteras is shown as a separate category to emphasize the fact that it carries roughly equal proportions of Mid-Atl and SAB haplotypes.

Fig. 3 Geographic differentiation of mtDNA—nucleotide site frequency “pie diagrams.”

Fig. 1

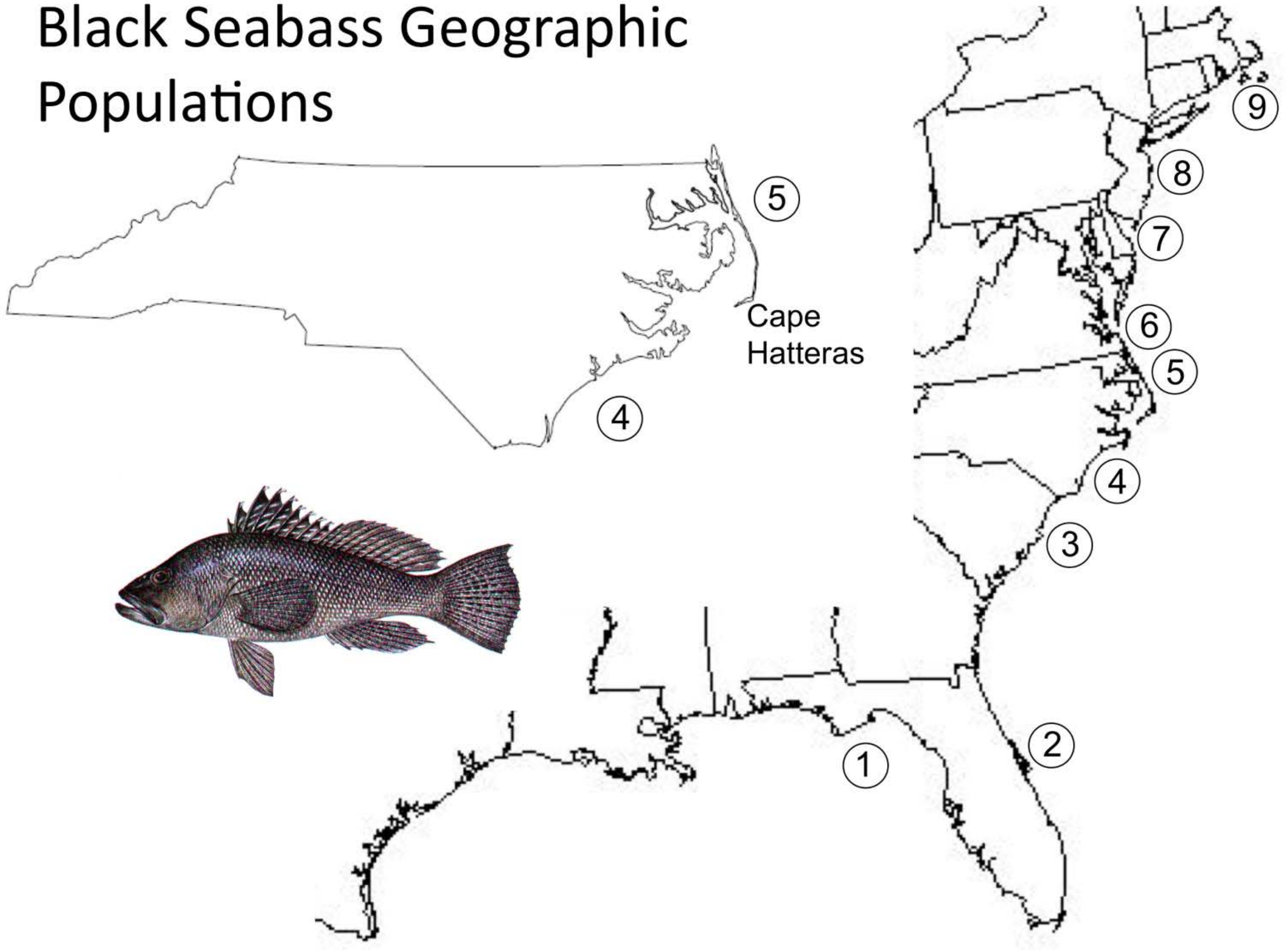

Black Seabass Geographic Populations
⑤
Cape Hatteras
④
⑨
⑧
⑦
⑥
⑤
④
③
②
①

Fig. 2A

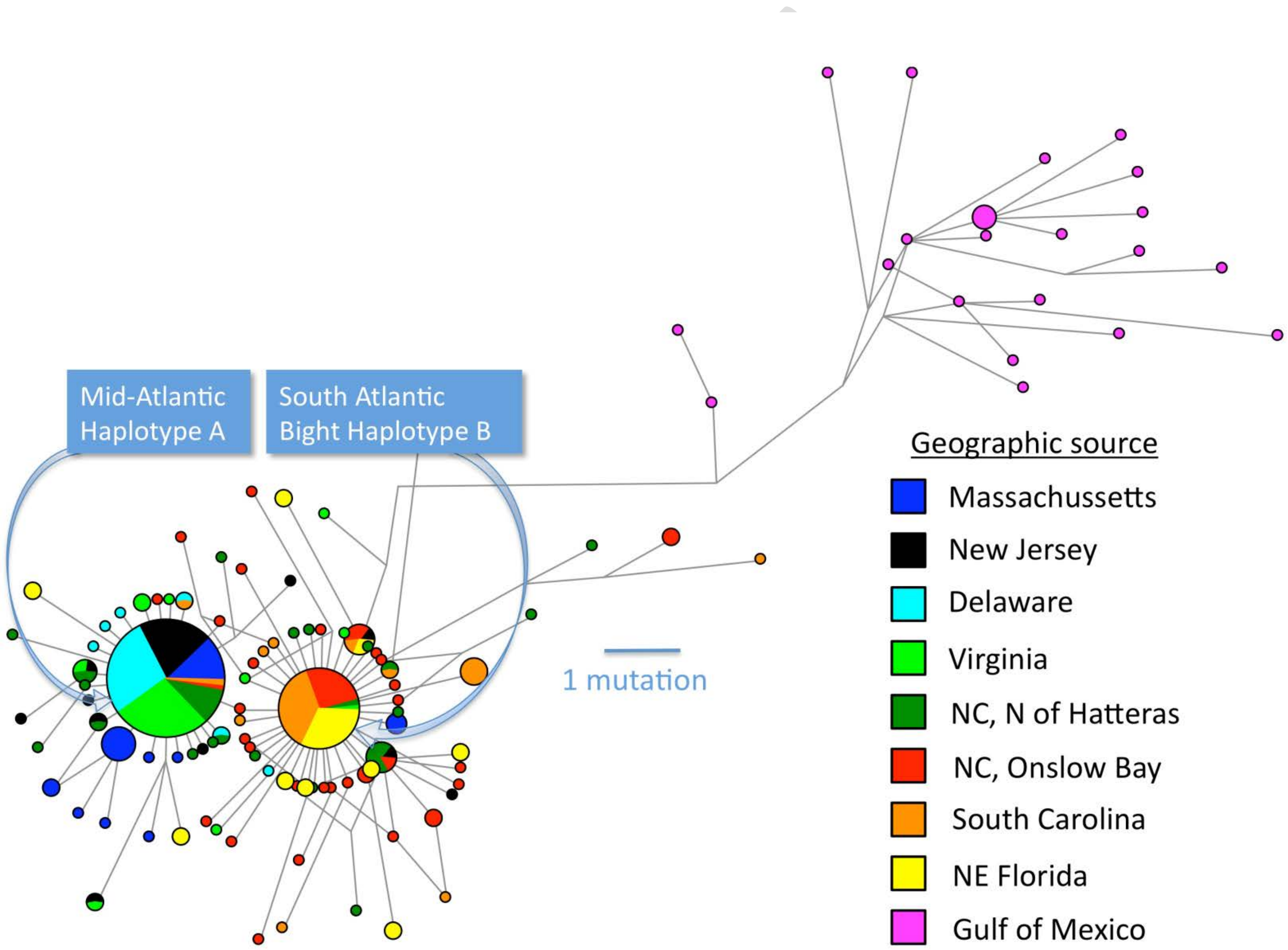

Mid-Atlantic Haplotype A
South Atlantic Bight Haplotype B
1 mutation
Geographic source
Massachussetts
New Jersey
Delaware
Virginia
NC, N of Hatteras
NC, Onslow Bay
South Carolina
NE Florida
Gulf of Mexico

Fig. 2B

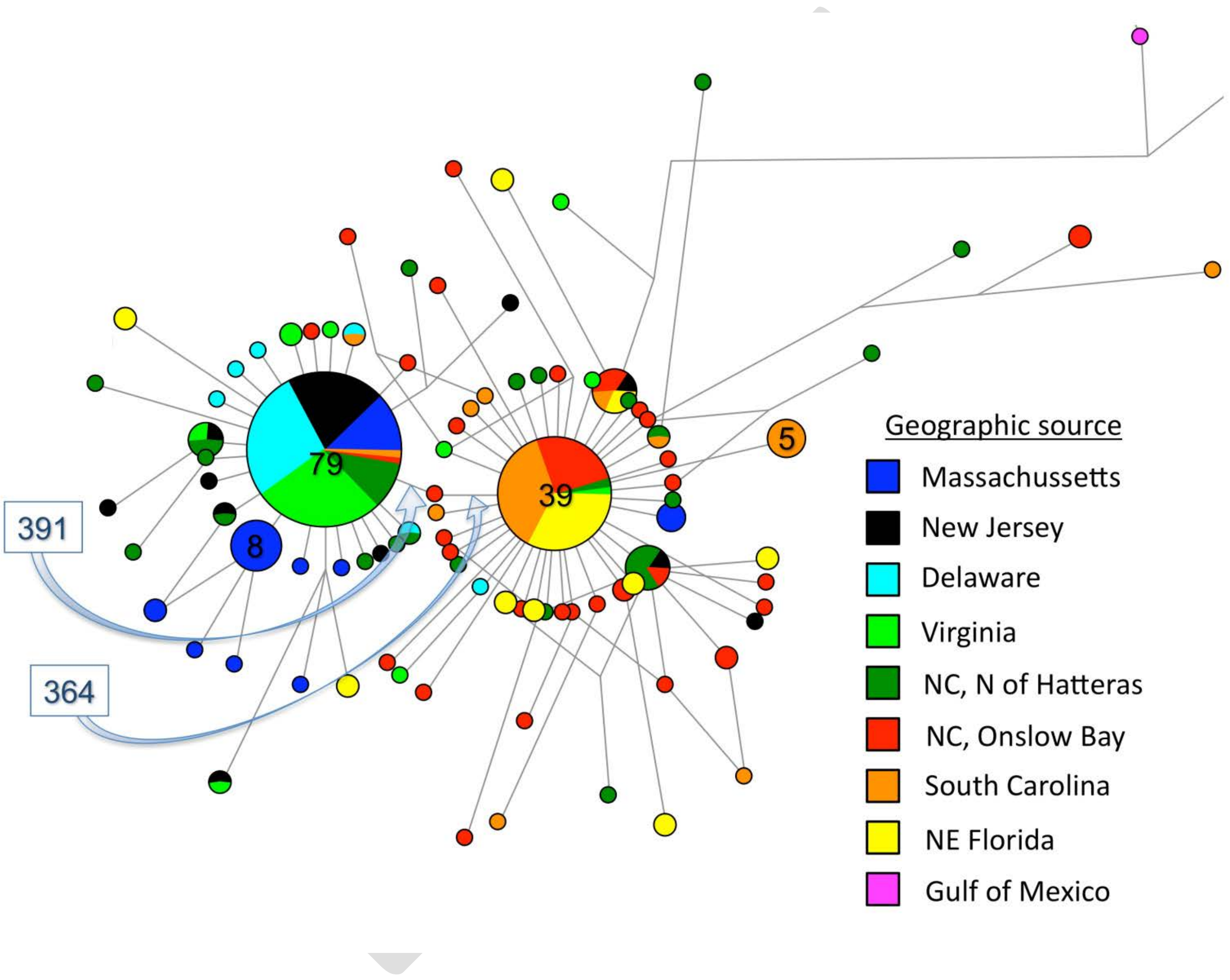

79
39
8
5
391
364
Geographic source
Massachussetts
New Jersey
Delaware
Virginia
NC, N of Hatteras
NC, Onslow Bay
South Carolina
NE Florida
Gulf of Mexico

Fig. 2C

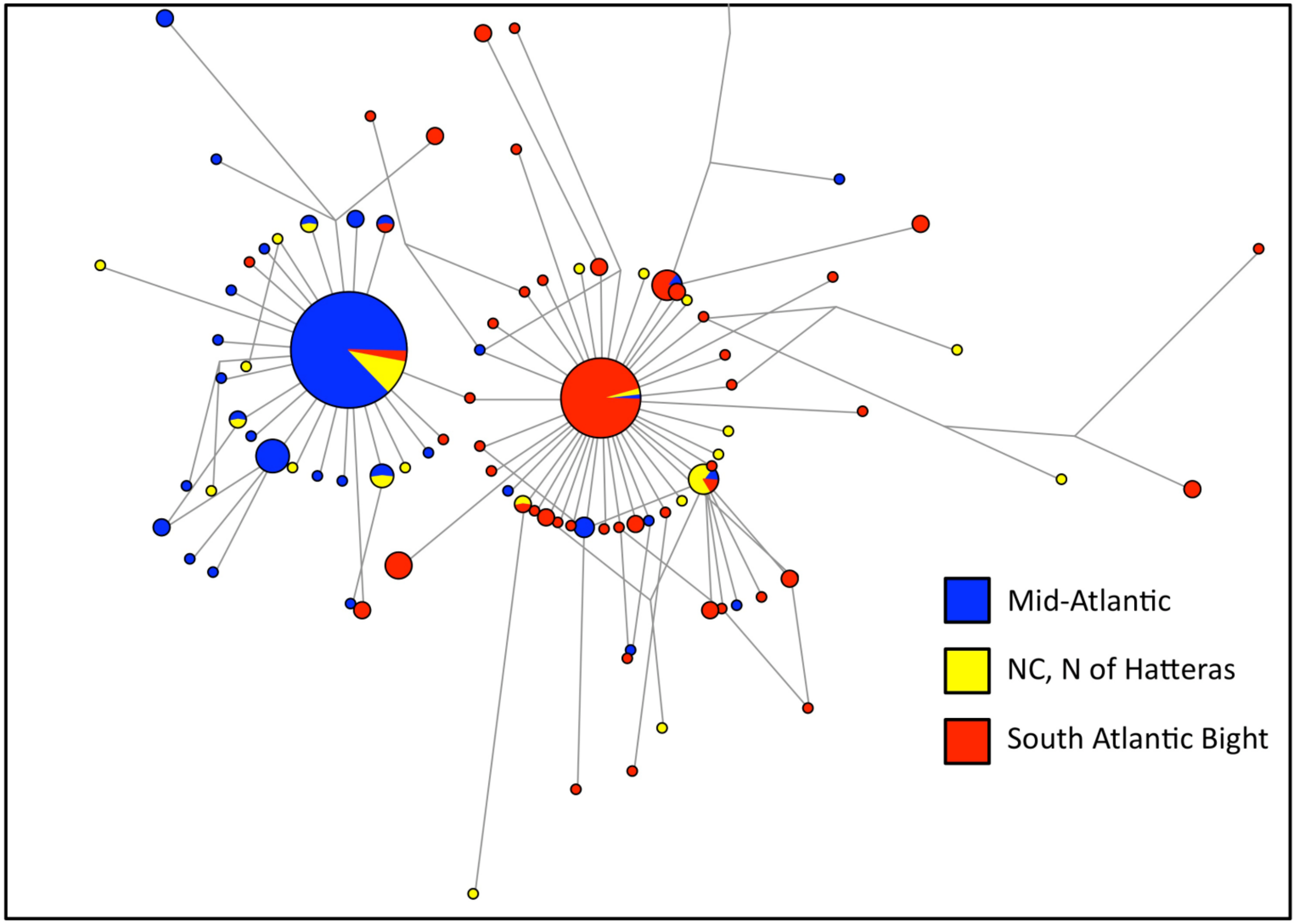
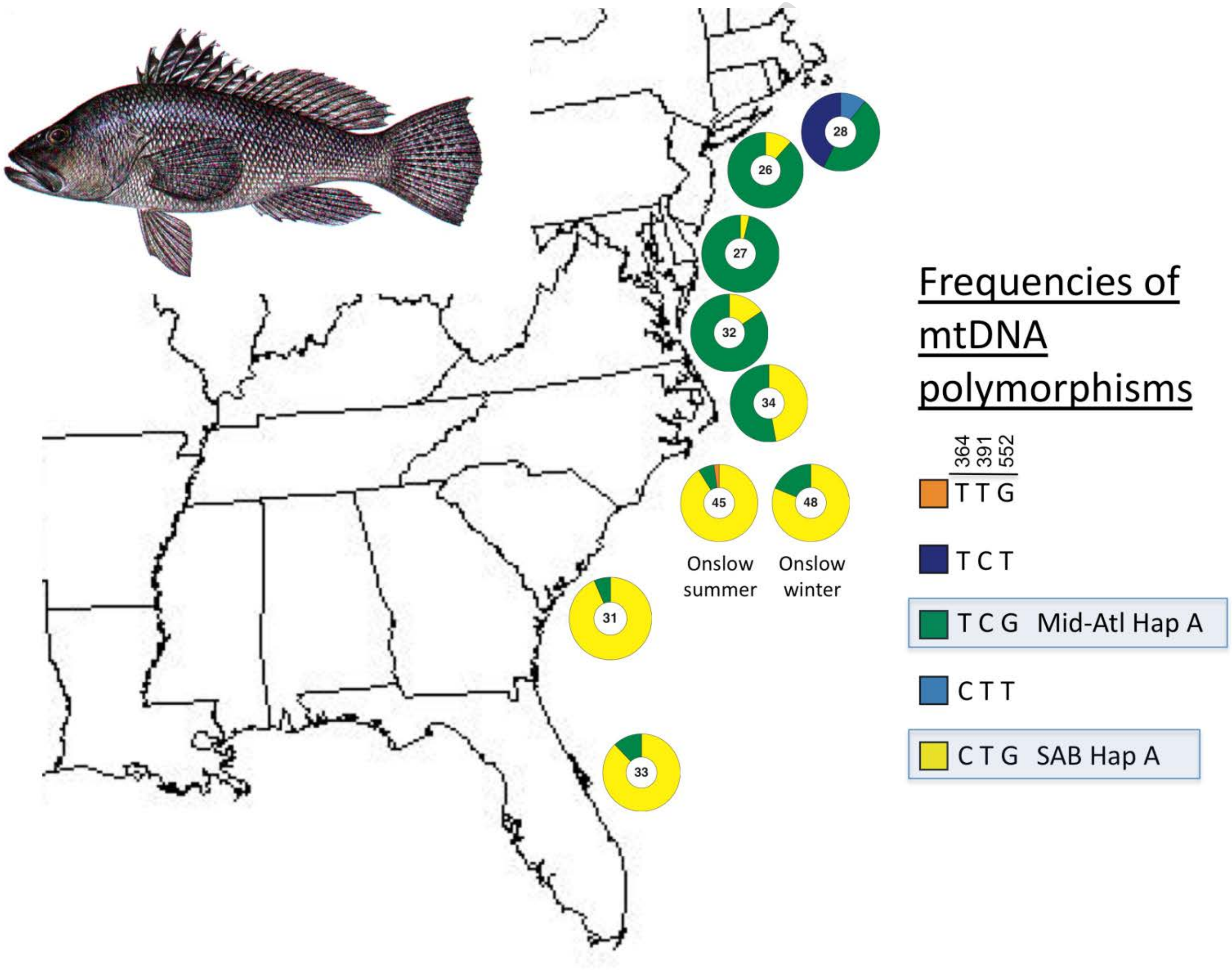
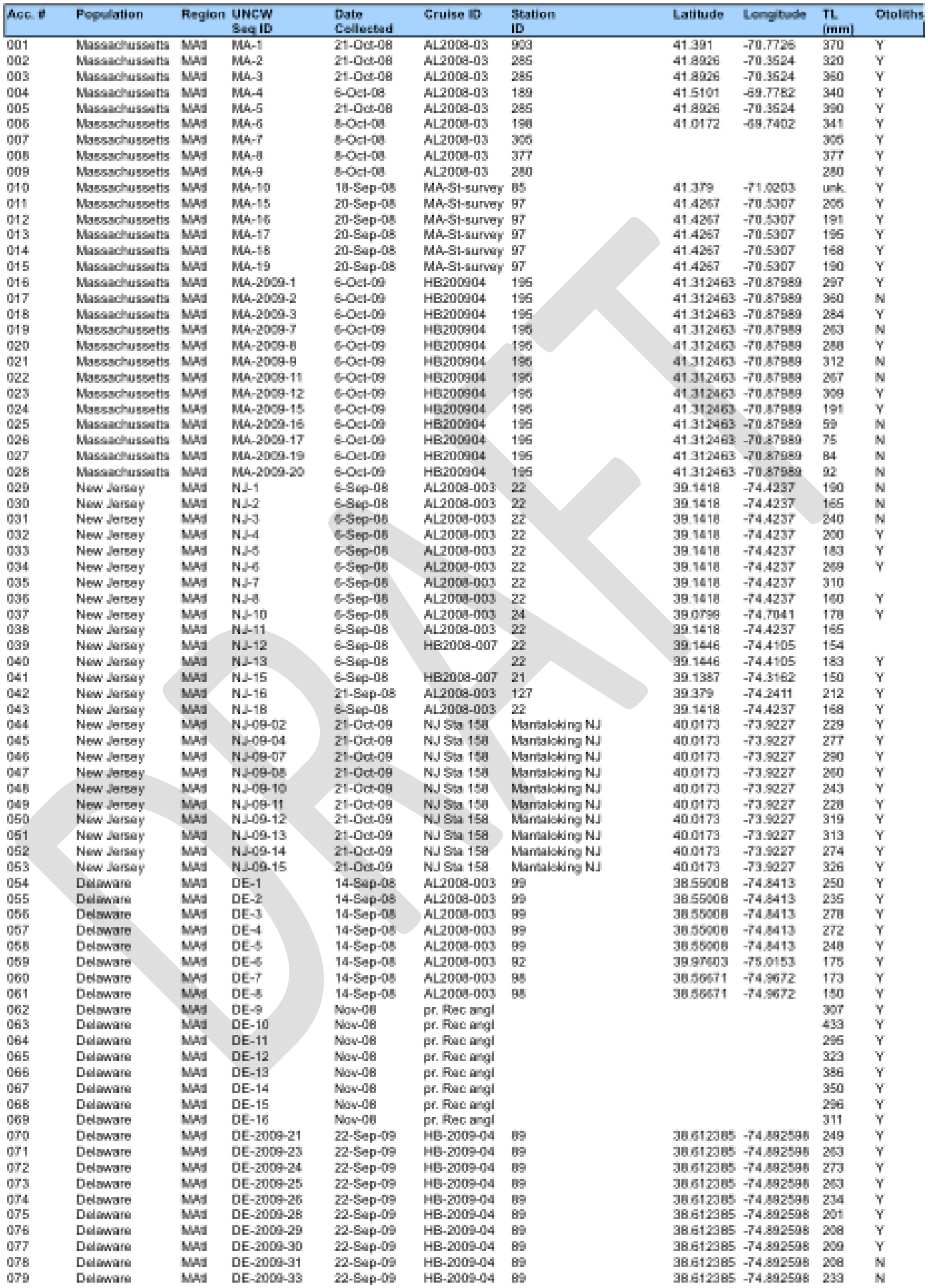


Fig. 3


28
26
27
32
34
45
48
Onslow summer
Onslow winter
31
33
Frequencies of mtDNA polymorphisms
364 391 552
🟧 T T G
🟦 T C T
🟩 T C G Mid-Atl Hap A
🟦 C T T
🟨 C T G SAB Hap A

Appendix



Acc. #	Population	Region	UNCW Seq ID	Date Collected	Cruise ID	Station ID	Latitude	Longitude	TL (mm)	Otoliths
001	Massachussetts	MAtl	MA-1	21-Oct-08	AL2008-03	903	41.391	-70.7726	370	Y
002	Massachussetts	MAtl	MA-2	21-Oct-08	AL2008-03	285	41.8926	-70.3524	320	Y
003	Massachussetts	MAtl	MA-3	21-Oct-08	AL2008-03	285	41.8926	-70.3524	360	Y
004	Massachussetts	MAtl	MA-4	6-Oct-08	AL2008-03	189	41.5101	-69.7782	340	Y
005	Massachussetts	MAtl	MA-5	21-Oct-08	AL2008-03	285	41.8926	-70.3524	390	Y
006	Massachussetts	MAtl	MA-6	8-Oct-08	AL2008-03	198	41.0172	-69.7402	341	Y
007	Massachussetts	MAtl	MA-7	8-Oct-08	AL2008-03	305			305	Y
008	Massachussetts	MAtl	MA-8	8-Oct-08	AL2008-03	377			377	Y
009	Massachussetts	MAtl	MA-9	8-Oct-08	AL2008-03	280			280	Y
010	Massachussetts	MAtl	MA-10	18-Sep-08	MA-St-survey	85	41.379	-71.0203	unk.	Y
011	Massachussetts	MAtl	MA-15	20-Sep-08	MA-St-survey	97	41.4267	-70.5307	205	Y
012	Massachussetts	MAtl	MA-16	20-Sep-08	MA-St-survey	97	41.4267	-70.5307	191	Y
013	Massachussetts	MAtl	MA-17	20-Sep-08	MA-St-survey	97	41.4267	-70.5307	195	Y
014	Massachussetts	MAtl	MA-18	20-Sep-08	MA-St-survey	97	41.4267	-70.5307	168	Y
015	Massachussetts	MAtl	MA-19	20-Sep-08	MA-St-survey	97	41.4267	-70.5307	190	Y
016	Massachussetts	MAtl	MA-2009-1	6-Oct-09	HB200904	195	41.312463	-70.87989	297	Y
017	Massachussetts	MAtl	MA-2009-2	6-Oct-09	HB200904	195	41.312463	-70.87989	360	N
018	Massachussetts	MAtl	MA-2009-3	6-Oct-09	HB200904	195	41.312463	-70.87989	284	Y
019	Massachussetts	MAtl	MA-2009-7	6-Oct-09	HB200904	195	41.312463	-70.87989	263	N
020	Massachussetts	MAtl	MA-2009-8	6-Oct-09	HB200904	195	41.312463	-70.87989	288	Y
021	Massachussetts	MAtl	MA-2009-9	6-Oct-09	HB200904	195	41.312463	-70.87989	312	N
022	Massachussetts	MAtl	MA-2009-11	6-Oct-09	HB200904	195	41.312463	-70.87989	267	N
023	Massachussetts	MAtl	MA-2009-12	6-Oct-09	HB200904	195	41.312463	-70.87989	309	Y
024	Massachussetts	MAtl	MA-2009-15	6-Oct-09	HB200904	195	41.312463	-70.87989	191	Y
025	Massachussetts	MAtl	MA-2009-16	6-Oct-09	HB200904	195	41.312463	-70.87989	59	N
026	Massachussetts	MAtl	MA-2009-17	6-Oct-09	HB200904	195	41.312463	-70.87989	75	N
027	Massachussetts	MAtl	MA-2009-19	6-Oct-09	HB200904	195	41.312463	-70.87989	84	N
028	Massachussetts	MAtl	MA-2009-20	6-Oct-09	HB200904	195	41.312463	-70.87989	92	N
029	New Jersey	MAtl	NJ-1	6-Sep-08	AL2008-003	22	39.1418	-74.4237	190	N
030	New Jersey	MAtl	NJ-2	6-Sep-08	AL2008-003	22	39.1418	-74.4237	165	N
031	New Jersey	MAtl	NJ-3	6-Sep-08	AL2008-003	22	39.1418	-74.4237	240	N
032	New Jersey	MAtl	NJ-4	6-Sep-08	AL2008-003	22	39.1418	-74.4237	200	Y
033	New Jersey	MAtl	NJ-5	6-Sep-08	AL2008-003	22	39.1418	-74.4237	183	Y
034	New Jersey	MAtl	NJ-6	6-Sep-08	AL2008-003	22	39.1418	-74.4237	269	Y
035	New Jersey	MAtl	NJ-7	6-Sep-08	AL2008-003	22	39.1418	-74.4237	310	
036	New Jersey	MAtl	NJ-8	6-Sep-08	AL2008-003	22	39.1418	-74.4237	160	Y
037	New Jersey	MAtl	NJ-10	6-Sep-08	AL2008-003	24	39.0799	-74.7041	178	Y
038	New Jersey	MAtl	NJ-11	6-Sep-08	AL2008-003	22	39.1418	-74.4237	165	
039	New Jersey	MAtl	NJ-12	6-Sep-08	HB2008-007	22	39.1446	-74.4105	154	
040	New Jersey	MAtl	NJ-13	6-Sep-08		22	39.1446	-74.4105	183	Y
041	New Jersey	MAtl	NJ-15	6-Sep-08	HB2008-007	21	39.1387	-74.3162	150	Y
042	New Jersey	MAtl	NJ-16	21-Sep-08	AL2008-003	127	39.379	-74.2411	212	Y
043	New Jersey	MAtl	NJ-18	6-Sep-08	AL2008-003	22	39.1418	-74.4237	168	Y
044	New Jersey	MAtl	NJ-09-02	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	229	Y
045	New Jersey	MAtl	NJ-09-04	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	277	Y
046	New Jersey	MAtl	NJ-09-07	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	290	Y
047	New Jersey	MAtl	NJ-09-08	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	260	Y
048	New Jersey	MAtl	NJ-09-10	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	243	Y
049	New Jersey	MAtl	NJ-09-11	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	228	Y
050	New Jersey	MAtl	NJ-09-12	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	319	Y
051	New Jersey	MAtl	NJ-09-13	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	313	Y
052	New Jersey	MAtl	NJ-09-14	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	274	Y
053	New Jersey	MAtl	NJ-09-15	21-Oct-09	NJ Sta 158	Mantaloking NJ	40.0173	-73.9227	326	Y
054	Delaware	MAtl	DE-1	14-Sep-08	AL2008-003	99	38.55008	-74.8413	250	Y
055	Delaware	MAtl	DE-2	14-Sep-08	AL2008-003	99	38.55008	-74.8413	235	Y
056	Delaware	MAtl	DE-3	14-Sep-08	AL2008-003	99	38.55008	-74.8413	278	Y
057	Delaware	MAtl	DE-4	14-Sep-08	AL2008-003	99	38.55008	-74.8413	272	Y
058	Delaware	MAtl	DE-5	14-Sep-08	AL2008-003	99	38.55008	-74.8413	248	Y
059	Delaware	MAtl	DE-6	14-Sep-08	AL2008-003	92	39.97603	-75.0153	175	Y
060	Delaware	MAtl	DE-7	14-Sep-08	AL2008-003	98	38.56671	-74.9672	173	Y
061	Delaware	MAtl	DE-8	14-Sep-08	AL2008-003	98	38.56671	-74.9672	150	Y
062	Delaware	MAtl	DE-9	Nov-08	pr. Rec angl				307	Y
063	Delaware	MAtl	DE-10	Nov-08	pr. Rec angl				433	Y
064	Delaware	MAtl	DE-11	Nov-08	pr. Rec angl				295	Y
065	Delaware	MAtl	DE-12	Nov-08	pr. Rec angl				323	Y
066	Delaware	MAtl	DE-13	Nov-08	pr. Rec angl				386	Y
067	Delaware	MAtl	DE-14	Nov-08	pr. Rec angl				350	Y
068	Delaware	MAtl	DE-15	Nov-08	pr. Rec angl				296	Y
069	Delaware	MAtl	DE-16	Nov-08	pr. Rec angl				311	Y
070	Delaware	MAtl	DE-2009-21	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	249	Y
071	Delaware	MAtl	DE-2009-23	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	263	Y
072	Delaware	MAtl	DE-2009-24	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	273	Y
073	Delaware	MAtl	DE-2009-25	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	263	Y
074	Delaware	MAtl	DE-2009-26	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	234	Y
075	Delaware	MAtl	DE-2009-28	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	201	Y
076	Delaware	MAtl	DE-2009-29	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	208	Y
077	Delaware	MAtl	DE-2009-30	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	209	Y
078	Delaware	MAtl	DE-2009-31	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	208	N
079	Delaware	MAtl	DE-2009-33	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	233	N

Acc. #	Population	Region	UNCW Seq ID	Date Collected	Cruise ID	Station ID	Latitude	Longitude	TL (mm)	Otoliths
080	Delaware	MAd	DE-2009-34	22-Sep-09	HB-2009-04	89	38.612385	-74.892598	212	N
081	Virginia	MAd	VA-1	11-Sep-08	HB2008-007	72	36.6386	-75.3025	143	Y
082	Virginia	MAd	VA-2	12-Sep-08	AL2008-003	79	37.0549	-75.4771	157	Y
083	Virginia	MAd	VA-3	12-Sep-08	AL2008-003	79	37.0549	-75.4771	144	Y
084	Virginia	MAd	VA-4	12-Sep-08	AL2008-003	79	37.0549	-75.4771	153	Y
085	Virginia	MAd	VA-5	13-Sep-08	AL2008-003	86	37.7293	-75.1406	166	Y
086	Virginia	MAd	VA-6	13-Sep-08	AL2008-003	87	37.6457	-75.3128	170	Y
087	Virginia	MAd	VA-7	12-Sep-08	AL2008-003	79	37.0549	-75.4771	154	Y
088	Virginia	MAd	VA-8	12-Sep-08	AL2008-003	79	37.0549	-75.4771	148	Y
089	Virginia	MAd	VA-11	13-Sep-08	AL2008-003	86	37.7293	-75.1406	136	Y
090	Virginia	MAd	VA-12	12-Sep-08	AL2008-003	79	37.0549	-75.4771	215	Y
091	Virginia	MAd	VA-14	12-Sep-08	AL2008-003	79	37.0549	-75.4771	130	Y
092	Virginia	MAd	VA-15	12-Sep-08	AL2008-003	79	37.0549	-75.4771	162	Y
093	Virginia	MAd	VA-16	?	?	?			205	Y
094	Virginia	MAd	VA-17	13-Sep-08	AL2008-003	86	37.7293	-75.1406	128	Y
095	Virginia	MAd	VA-18	?	?	?			151	Y
096	Virginia	MAd	VA-19	?	?	?			170	Y
097	Virginia	MAd	VA-2009-1	20-Sep-09	HB2009-04	70	36.766763	-75.68862	209	N
098	Virginia	MAd	VA-2009-2	20-Sep-09	HB2009-04	70	36.766763	-75.68862	192	N
099	Virginia	MAd	VA-2009-3	20-Sep-09	HB2009-04	70	36.766763	-75.68862	154	N
100	Virginia	MAd	VA-2009-4	20-Sep-09	HB2009-04	70	36.766763	-75.68862	160	N
101	Virginia	MAd	VA-2009-5	20-Sep-09	HB2009-04	73	36.903302	-75.651375	135	Y
102	Virginia	MAd	VA-2009-6	21-Sep-09	HB2009-04	80	37.885703	-74.664412	214	N
103	Virginia	MAd	VA-2009-7	21-Sep-09	HB2009-04	80	37.885703	-74.664412	212	N
104	Virginia	MAd	VA-2009-8	21-Sep-09	HB2009-04	80	37.885703	-74.664412	174	N
105	Virginia	MAd	VA-2009-9	16-Sep-09	HB2009-04	29	36.851003	-74.869195	242	N
106	Virginia	MAd	VA-2009-10	16-Sep-09	HB2009-04	28	36.853763	-74.804525	267	N
107	Virginia	MAd	VA-2009-11	16-Sep-09	HB2009-04	28	36.853763	-74.804525	276	N
108	Virginia	MAd	VA-2009-12	16-Sep-09	HB2009-04	28	36.853763	-74.804525	287	Y
109	Virginia	MAd	VA-2009-13	20-Sep-09	HB2009-04	79	37.810975	-74.911548	239	N
110	Virginia	MAd	VA-2009-14	20-Sep-09	HB2009-04	79	37.810975	-74.911548	179	N
111	Virginia	MAd	VA-2009-17	20-Sep-09	HB2009-04	79	37.810975	-74.911548	153	Y
112	Virginia	MAd	VA-2009-18	20-Sep-09	HB2009-04	71	36.720745	-75.465738	184	Y
113	Northeast NC	MAd	NNC-4	11-Sep-08	HB2008-007	71	36.3158	-75.2722	150	Y
114	Northeast NC	MAd	NNC-11	11-Sep-08	HB2008-007	71	36.3158	-75.2722	180	Y
115	Northeast NC	MAd	NNC-15	11-Sep-08	HB2008-007	66	35.9516	-75.5049	100	N
116	Northeast NC	MAd	NNC-16	11-Sep-08	HB2008-007	69	36.2586	-75.6951	120	Y
117	Northeast NC	MAd	NNC-17	10-Sep-08	HB2008-007	64	35.7916	-75.3132	?	Y
118	Northeast NC	MAd	NNC-18	9-Sep-08	HB2008-007	46	35.7688	-74.8583	150	Y
119	Northeast NC	MAd	NNC-09-1	15-Sep-09	N/A		35.7315	-75.4462	209	Y
120	Northeast NC	MAd	NNC-09-2	15-Sep-09	N/A		35.7315	-75.4462	183	Y
121	Northeast NC	MAd	NNC-09-3	15-Sep-09	N/A		35.7315	-75.4462	182	Y
122	Northeast NC	MAd	NNC-09-4	15-Sep-09	N/A		35.7315	-75.4462	197	Y
123	Northeast NC	MAd	NNC-09-5	15-Sep-09	N/A		35.7315	-75.4462	194	Y
124	Northeast NC	MAd	NNC-09-6	15-Sep-09	N/A		35.7315	-75.4462	265	Y
125	Northeast NC	MAd	NNC-09-7	15-Sep-09	N/A		35.7315	-75.4462	280	Y
126	Northeast NC	MAd	NNC-09-8	15-Sep-09	N/A		35.7315	-75.4462	253	Y
127	Northeast NC	MAd	NNC-09-9	15-Sep-09	N/A		35.7315	-75.4462	178	Y
128	Northeast NC	MAd	NNC-09-10	15-Sep-09	N/A		35.7315	-75.4462	197	Y
129	Northeast NC	MAd	NNC-09-11	15-Sep-09	N/A		35.7315	-75.4462	179	Y
130	Northeast NC	MAd	NNC-09-12	15-Sep-09	N/A		35.7315	-75.4462	197	Y
131	Northeast NC	MAd	NNC-09-13	15-Sep-09	N/A		35.7315	-75.4462	244	Y
132	Northeast NC	MAd	NNC-09-14	15-Sep-09	N/A		35.7315	-75.4462	254	Y
133	Northeast NC	MAd	NNC-09-15	15-Sep-09	N/A		35.7315	-75.4462	260	Y
134	Northeast NC	MAd	NNC-09-16	15-Sep-09	N/A		35.7315	-75.4462	203	Y
135	Northeast NC	MAd	NNC-09-19	15-Sep-09	N/A		35.7315	-75.4462	280	Y
136	Northeast NC	MAd	NNC-09-20	15-Sep-09	N/A		35.7315	-75.4462	200	Y
137	Northeast NC	MAd	NNC-09-21	15-Sep-09	N/A		35.7315	-75.4462	203	Y
138	Northeast NC	MAd	NNC-09-22	15-Sep-09	N/A		35.7315	-75.4462	172	Y
139	Northeast NC	MAd	NNC-09-23	15-Sep-09	N/A		35.7315	-75.4462	187	Y
140	Northeast NC	MAd	NNC-09-24	15-Sep-09	N/A		35.7315	-75.4462	197	Y
141	Northeast NC	MAd	NNC-09-25	15-Sep-09	N/A		35.7315	-75.4462	279	Y
142	Northeast NC	MAd	NNC-09-26	15-Sep-09	N/A		35.7315	-75.4462	170	Y
143	Northeast NC	MAd	NNC-09-27	15-Sep-09	N/A		35.7315	-75.4462	172	Y
144	Northeast NC	MAd	NNC-09-28	15-Sep-09	N/A		35.7315	-75.4462	196	Y
145	Northeast NC	MAd	NNC-09-30	15-Sep-09	N/A		35.7315	-75.4462	284	Y
146	Northeast NC	MAd	NNC-09-32	15-Sep-09	N/A		35.7315	-75.4462	245	Y
147	Northeast NC	MAd	NNC-09-33	18-Sep-09	HB2009-04	59	35.654	-74.8153	295	N
148	Onslow Bay NC	SAB	OS-1	6-Jun-08	CS-Tag	658	34.4	-77.43	303	Y
149	Onslow Bay NC	SAB	OS-2	6-Jun-08	CS-TAg	634	34.4	-77.43	190	Y
150	Onslow Bay NC	SAB	OS-3	6-Jun-08	CS-Tag	617	34.4	-77.43	205	Y
151	Onslow Bay NC	SAB	OS-4	6-Jun-08	CS-TAg	616	34.4	-77.43	185	Y
152	Onslow Bay NC	SAB	OS-5	6-Jun-08	CS-Tag	635	34.4	-77.43	167	Y
153	Onslow Bay NC	SAB	OS-6	6-Jun-08	CS-TAg	642	34.4	-77.43	310	Y
154	Onslow Bay NC	SAB	OS-7	6-Jun-08	CS-Tag	632	34.4	-77.43	342	Y
155	Onslow Bay NC	SAB	OS-8	6-Jun-08	CS-TAg	656	34.4	-77.43	234	Y
156	Onslow Bay NC	SAB	OS-9	6-Jun-08	CS-Tag	618	34.4	-77.43	255	Y
157	Onslow Bay NC	SAB	OS-10	6-Jun-08	CS-TAg	621	34.4	-77.43	247	Y
158	Onslow Bay NC	SAB	OS-11	6-Jun-08	CS-Tag	641	34.4	-77.43	180	Y

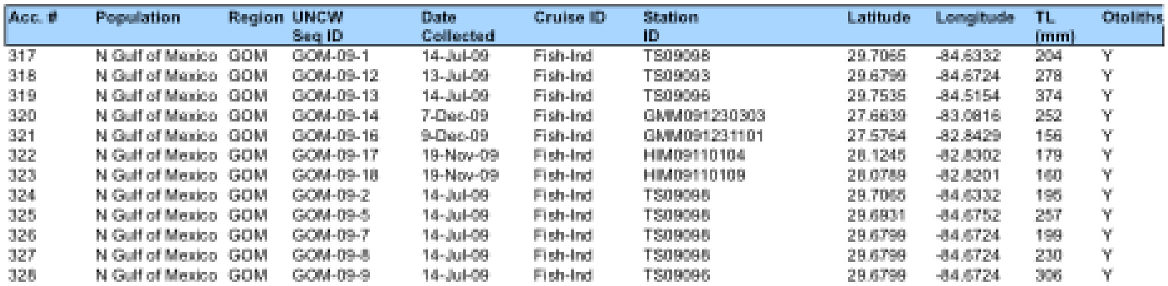
Acc. #	Population	Region	UNCW Seq ID	Date Collected	Cruise ID	Station ID	Latitude	Longitude	TL (mm)	Otoli
159	Onslow Bay NC	SAB	OS-12	6-Jun-08	CS-TAg		34.4	-77.43	187	Y
160	Onslow Bay NC	SAB	OS-13	6-Jun-08	CS-Tag	664	34.4	-77.43	264	Y
161	Onslow Bay NC	SAB	OS-14	6-Jun-08	CS-TAg	628	34.4	-77.43	270	Y
162	Onslow Bay NC	SAB	OS-15	6-Jun-08	CS-Tag	669	34.4	-77.43	265	Y
163	Onslow Bay NC	SAB	OS-16	6-Jun-08	CS-TAg	620	34.4	-77.43	265	Y
164	Onslow Bay NC	SAB	OS-17	6-Jun-08	CS-Tag	611	34.4	-77.43	291	Y
165	Onslow Bay NC	SAB	OS-18	6-Jun-08	CS-TAg	625	34.4	-77.43	240	Y
166	Onslow Bay NC	SAB	OS-19	6-Jun-08	CS-Tag	665	34.4	-77.43	253	Y
167	Onslow Bay NC	SAB	OS-20	6-Jun-08	CS-TAg	624	34.4	-77.43	246	Y
168	Onslow Bay NC	SAB	OS-21	6-Jun-08	CS-Tag	667	34.4	-77.43	323	Y
169	Onslow Bay NC	SAB	OS-23	6-Jun-08	CS-Tag	613	34.4	-77.43	238	Y
170	Onslow Bay NC	SAB	OS-24	6-Jun-08	CS-TAg	622	34.4	-77.43	233	Y
171	Onslow Bay NC	SAB	OS-26	6-Jun-08	CS-TAg	654	34.4	-77.43	288	Y
172	Onslow Bay NC	SAB	OS-27	6-Jun-08	CS-Tag	619	34.4	-77.43	205	Y
173	Onslow Bay NC	SAB	OS-28	6-Jun-08	CS-TAg	659	34.4	-77.43	291	Y
174	Onslow Bay NC	SAB	OS-30	6-Jun-08	CS-TAg		34.4	-77.43	205	Y
175	Onslow Bay NC	SAB	OS-31	6-Jun-08	CS-Tag	668	34.4	-77.43	238	Y
176	Onslow Bay NC	SAB	OS-32	6-Jun-08	CS-TAg	630	34.4	-77.43	233	Y
177	Onslow Bay NC	SAB	OS-33	6-Jun-08	CS-Tag	661	34.4	-77.43	209	Y
178	Onslow Bay NC	SAB	OS-34	6-Jun-08	CS-TAg	650	34.4	-77.43	193	Y
179	Onslow Bay NC	SAB	OS-35	6-Jun-08	CS-Tag	660	34.4	-77.43	228	Y
180	Onslow Bay NC	SAB	OS-36	6-Jun-08	CS-TAg	623	34.4	-77.43	202	Y
181	Onslow Bay NC	SAB	OS-37	6-Jun-08	CS-Tag	670	34.4	-77.43	212	Y
182	Onslow Bay NC	SAB	OS-39	6-Jun-08	CS-Tag	631	34.4	-77.43	192	Y
183	Onslow Bay NC	SAB	OS-40	6-Jun-08	CS-TAg	663	34.4	-77.43	271	Y
184	Onslow Bay NC	SAB	OS-41	6-Jun-08	CS-Tag	649	34.4	-77.43	263	Y
185	Onslow Bay NC	SAB	OS-42	6-Jun-08	CS-TAg	629	34.4	-77.43	224	Y
186	Onslow Bay NC	SAB	OS-43	6-Jun-08	CS-Tag		34.4	-77.43	176	Y
187	Onslow Bay NC	SAB	OS-44	6-Jun-08	CS-TAg	662	34.4	-77.43	215	Y
188	Onslow Bay NC	SAB	OS-45	6-Jun-08	CS-Tag	652	34.4	-77.43	226	Y
189	Onslow Bay NC	SAB	OS-46	6-Jun-08	CS-TAg	655	34.4	-77.43	197	Y
190	Onslow Bay NC	SAB	OS-47	6-Jun-08	CS-Tag	640	34.4	-77.43	240	Y
191	Onslow Bay NC	SAB	OS-48	6-Jun-08	CS-TAg	643	34.4	-77.43	212	Y
192	Onslow Bay NC	SAB	OS-49	6-Jun-08	CS-Tag	612	34.4	-77.43	209	Y
193	Onslow Bay NC	SAB	OS-50	6-Jun-08	CS-TAg	644	34.4	-77.43	201	Y
194	Onslow Bay NC*	SAB	OW0109	17-Feb-09			34.4	-77.43	279	Y
195	Onslow Bay NC*	SAB	OW0209	17-Feb-09			34.4	-77.43	266	Y
196	Onslow Bay NC*	SAB	OW0509	17-Feb-09			34.4	-77.43	251	Y
197	Onslow Bay NC*	SAB	OW0609	17-Feb-09			34.4	-77.43	290	Y
198	Onslow Bay NC*	SAB	OW0709	17-Feb-09			34.4	-77.43	331	Y
199	Onslow Bay NC*	SAB	OW0909	17-Feb-09			34.4	-77.43	262	Y
200	Onslow Bay NC*	SAB	OW1009	17-Feb-09			34.4	-77.43	259	Y
201	Onslow Bay NC*	SAB	OW1209	17-Feb-09			34.4	-77.43	268	Y
202	Onslow Bay NC*	SAB	OW1309	17-Feb-09			34.4	-77.43	265	Y
203	Onslow Bay NC*	SAB	OW1409	17-Feb-09			34.4	-77.43	264	Y
204	Onslow Bay NC*	SAB	OW1509	17-Feb-09			34.4	-77.43	253	Y
205	Onslow Bay NC*	SAB	OW1709	17-Feb-09			34.4	-77.43	302	Y
206	Onslow Bay NC*	SAB	OW1809	17-Feb-09			34.4	-77.43	256	Y
207	Onslow Bay NC*	SAB	OW1909	17-Feb-09			34.4	-77.43	249	Y
208	Onslow Bay NC*	SAB	OW2109	17-Feb-09			34.4	-77.43	275	Y
209	Onslow Bay NC*	SAB	OW2409	17-Feb-09			34.4	-77.43	307	Y
210	Onslow Bay NC*	SAB	OW8709	4-Apr-09			34.4	-77.43	310	N
211	Onslow Bay NC*	SAB	OW8809	4-Apr-09			34.4	-77.43	362	N
212	Onslow Bay NC*	SAB	OW8909	4-Apr-09			34.4	-77.43	291	N
213	Onslow Bay NC*	SAB	OW9009	4-Apr-09			34.4	-77.43	345	N
214	Onslow Bay NC*	SAB	OW9109	4-Apr-09			34.4	-77.43	244	N
215	Onslow Bay NC*	SAB	OW9209	4-Apr-09			34.4	-77.43	264	N
216	Onslow Bay NC*	SAB	OW9309	4-Apr-09			34.4	-77.43	283	N
217	Onslow Bay NC*	SAB	OW9409	4-Apr-09			34.4	-77.43	311	N
218	Onslow Bay NC*	SAB	OW9509	4-Apr-09			34.4	-77.43	311	N
219	Onslow Bay NC*	SAB	OW9609	4-Apr-09			34.4	-77.43	230	N
220	Onslow Bay NC*	SAB	OW9709	4-Apr-09			34.4	-77.43	280	N
221	Onslow Bay NC*	SAB	OW9809	4-Apr-09			34.4	-77.43	286	N
222	Onslow Bay NC*	SAB	OW9909	4-Apr-09			34.4	-77.43	181	N
223	Onslow Bay NC*	SAB	OW10009	4-Apr-09			34.4	-77.43	280	N
224	Onslow Bay NC*	SAB	OW10109	4-Apr-09			34.4	-77.43	305	N
225	Onslow Bay NC*	SAB	OW10309	4-Apr-09			34.4	-77.43	341	N
226	Onslow Bay NC*	SAB	OW10409	4-Apr-09			34.4	-77.43	350	N
227	Onslow Bay NC*	SAB	OW10509	4-Apr-09			34.4	-77.43	352	N
228	Onslow Bay NC*	SAB	OW10609	4-Apr-09			34.4	-77.43	332	N
229	Onslow Bay NC*	SAB	OW10809	4-Apr-09			34.4	-77.43	382	N
230	Onslow Bay NC*	SAB	OW10909	4-Apr-09			34.4	-77.43	278	N
231	Onslow Bay NC*	SAB	OW11009	4-Apr-09			34.4	-77.43		N
232	Onslow Bay NC*	SAB	OW11109	4-Apr-09			34.4	-77.43	304	N
233	Onslow Bay NC*	SAB	OW11209	4-Apr-09			34.4	-77.43	172	N
234	Onslow Bay NC*	SAB	OW11309	4-Apr-09			34.4	-77.43	304	N
235	Onslow Bay NC*	SAB	OW11409	4-Apr-09			34.4	-77.43	365	N
236	Onslow Bay NC*	SAB	OW11509	4-Apr-09			34.4	-77.43	299	N
237	Onslow Bay NC*	SAB	OW11609	4-Apr-09			34.4	-77.43	230	N

*

Winter Population, Onslow Bay NC

Acc. #	Population	Region	UNCW Seq ID	Date Collected	Cruise ID	Station ID	Latitude	Longitude	TL (mm)	Otoli
238	Onslow Bay NC*	SAB	OW11709	4-Apr-09			34.4	-77.43	279	N
239	Onslow Bay NC*	SAB	OW11809	4-Apr-09			34.4	-77.43	294	N
240	Onslow Bay NC*	SAB	OW12109	4-Apr-09			34.4	-77.43	221	N
241	Onslow Bay NC*	SAB	OW12209	4-Apr-09			34.4	-77.43	270	N
242	South Carolina	SAB	SC-09-1	1-Oct-09	MARMAP		33.2813	-78.4485	174	Y
243	South Carolina	SAB	SC-09-2	1-Oct-09	MARMAP		33.2813	-78.4485	199	Y
244	South Carolina	SAB	SC-09-3	1-Oct-09	MARMAP		33.2813	-78.4485	201	Y
245	South Carolina	SAB	SC-09-4	1-Oct-09	MARMAP		33.2813	-78.4485	316	Y
246	South Carolina	SAB	SC-09-5	1-Oct-09	MARMAP		33.2813	-78.4485	205	Y
247	South Carolina	SAB	SC-09-6	1-Oct-09	MARMAP		33.2813	-78.4485	310	Y
248	South Carolina	SAB	SC-09-7	1-Oct-09	MARMAP		33.2813	-78.4485	173	Y
249	South Carolina	SAB	SC-09-8	1-Oct-09	MARMAP		33.2813	-78.4485	268	Y
250	South Carolina	SAB	SC-09-9	1-Oct-09	MARMAP		33.2813	-78.4485	277	Y
251	South Carolina	SAB	SC-09-10	1-Oct-09	MARMAP		33.2813	-78.4485	179	Y
252	South Carolina	SAB	SC-09-11	1-Oct-09	MARMAP		33.2813	-78.4485	228	Y
253	South Carolina	SAB	SC-09-12	1-Oct-09	MARMAP		33.2813	-78.4485	160	Y
254	South Carolina	SAB	SC-09-14	1-Oct-09	MARMAP		33.2813	-78.4485	268	Y
255	South Carolina	SAB	SC-09-15	1-Oct-09	MARMAP		33.2813	-78.4485	231	Y
256	South Carolina	SAB	SC-09-16	1-Oct-09	MARMAP		33.2813	-78.4485	317	Y
257	South Carolina	SAB	SC-09-17	1-Oct-09	MARMAP		33.2813	-78.4485	273	Y
258	South Carolina	SAB	SC-09-18	1-Oct-09	MARMAP		33.2813	-78.4485	240	Y
259	South Carolina	SAB	SC-09-19	1-Oct-09	MARMAP		33.2813	-78.4485	301	Y
260	South Carolina	SAB	SC-09-24	1-Oct-09	MARMAP		33.2813	-78.4485	167	Y
261	South Carolina	SAB	SC-09-25	1-Oct-09	MARMAP		33.2813	-78.4485	227	Y
262	South Carolina	SAB	SC-09-26	1-Oct-09	MARMAP		33.2813	-78.4485	251	Y
263	South Carolina	SAB	SC-09-27	1-Oct-09	MARMAP		33.2813	-78.4485	240	Y
264	South Carolina	SAB	SC-09-28	1-Oct-09	MARMAP		33.2813	-78.4485	248	Y
265	South Carolina	SAB	SC-09-29	1-Oct-09	MARMAP		33.2813	-78.4485	178	Y
266	South Carolina	SAB	SC-09-30	1-Oct-09	MARMAP		33.2813	-78.4485	203	Y
267	South Carolina	SAB	SC-09-31	1-Oct-09	MARMAP		33.2813	-78.4485	251	Y
268	South Carolina	SAB	SC-09-32	1-Oct-09	MARMAP		33.2813	-78.4485	206	Y
269	South Carolina	SAB	SC-09-33	1-Oct-09	MARMAP		33.2813	-78.4485	321	Y
270	South Carolina	SAB	SC-09-34	1-Oct-09	MARMAP		33.2813	-78.4485	225	Y
271	South Carolina	SAB	SC-09-35	1-Oct-09	MARMAP		33.2813	-78.4485	310	Y
272	South Carolina	SAB	SC-09-36	1-Oct-09	MARMAP		33.2813	-78.4485	199	Y
273	NE Florida	SAB	EFL-1	4-Dec-2008	Headboat	Sea Spirit 2			396	Y
274	NE Florida	SAB	EFL-2	4-Dec-2008	Headboat	Sea Spirit 2			370	N
275	NE Florida	SAB	EFL-3	4-Dec-2008	Headboat	Sea Spirit 2			379	Y
276	NE Florida	SAB	EFL-4	4-Dec-2008	Headboat	Sea Spirit 2			318	Y
277	NE Florida	SAB	EFL-5	20-Nov-2008	Headboat	Miss Cape Canaveral			318	Y
278	NE Florida	SAB	EFL-6	20-Nov-2008	Headboat	Miss Cape Canaveral			316	Y
279	NE Florida	SAB	EFL-8	4-Dec-2008	Headboat	Sea Spirit 2			321	Y
280	NE Florida	SAB	EFL-9	4-Dec-2008	Headboat	Sea Spirit 2			317	Y
281	NE Florida	SAB	EFL-10	4-Dec-2008	Headboat	Sea Spirit 2			287	Y
282	NE Florida	SAB	EFL-11	4-Dec-2008	Headboat	Sea Spirit 2			365	Y
283	NE Florida	SAB	EFL-12	5-Dec-2008	Headboat	Super Critter 2			344	Y
284	NE Florida	SAB	EFL-13	5-Dec-2008	Headboat	Super Critter 2			343	Y
285	NE Florida	SAB	EFL-14	5-Dec-2008	Headboat	Super Critter 2			345	Y
286	NE Florida	SAB	EFL-15	5-Dec-2008	Headboat	Super Critter 2			365	Y
287	NE Florida	SAB	EFL-16	5-Dec-2008	Headboat	Super Critter 2			315	Y
288	NE Florida	SAB	NEF-2009-10	27-Aug-09	Headboat	v 73, Pt. Canaveral FL			288	Y
289	NE Florida	SAB	NEF-2009-11	27-Aug-09	Headboat	v 73, Pt. Canaveral FL			328	Y
290	NE Florida	SAB	NEF-2009-19	26-Aug-09	Headboat	v 59, Ponce Inlet FL			326	Y
291	NE Florida	SAB	NEF-2009-20	26-Aug-09	Headboat	v 59, Ponce Inlet FL			334	Y
292	NE Florida	SAB	NEF-2009-21	26-Aug-09	Headboat	v 59, Ponce Inlet FL			345	Y
293	NE Florida	SAB	NEF-2009-22	17-Aug-09	Headboat	v 73, Pt. Canaveral FL			318	Y
294	NE Florida	SAB	NEF-2009-23	17-Aug-09	Headboat	v 73, Pt. Canaveral FL			317	Y
295	NE Florida	SAB	NEF-2009-24	17-Aug-09	Headboat	v 73, Pt. Canaveral FL			291	Y
296	NE Florida	SAB	NEF-2009-25	17-Aug-09	Headboat	v 73, Pt. Canaveral FL			305	Y
297	NE Florida	SAB	NEF-2009-26	8-Aug-09	Headboat	v 376 Sebastian FL			340	Y
298	NE Florida	SAB	NEF-2009-27	8-Aug-09	Headboat	v 376 Sebastian FL			321	Y
299	NE Florida	SAB	NEF-2009-28	8-Aug-09	Headboat	v 376 Sebastian FL			322	Y
300	NE Florida	SAB	NEF-2009-29	23-Aug-09	Headboat	v 380 Mayport FL			310	Y
301	NE Florida	SAB	NEF-2009-30	23-Aug-09	Headboat	v 380 Mayport FL			307	Y
302	NE Florida	SAB	NEF-2009-31	23-Aug-09	Headboat	v 380 Mayport FL			322	Y
303	NE Florida	SAB	NEF-2009-32	23-Aug-09	Headboat	v 380 Mayport FL			296	Y
304	NE Florida	SAB	NEF-2009-33	23-Aug-09	Headboat	v 380 Mayport FL			317	Y
305	NE Florida	SAB	NEF-2009-34	6-Aug-09	Headboat	v 360 New Smyrna Bch FL			307	Y
306	N Gulf of Mexico	GOM	NGOM-2	12-Jun-08	Headboat	NA			362	Y
307	N Gulf of Mexico	GOM	NGOM-3	12-Jun-08	Headboat	NA			355	Y
308	N Gulf of Mexico	GOM	NGOM-5	12-Jun-08	Headboat	NA			375	Y
309	N Gulf of Mexico	GOM	NGOM-7	21-Jun-08	Headboat	NA			435	Y
310	N Gulf of Mexico	GOM	NGOM-8	21-Jun-08	Headboat	NA			375	Y
311	N Gulf of Mexico	GOM	NGOM-9	22-Jun-08	Headboat	NA			417	Y
312	N Gulf of Mexico	GOM	NGOM-10	22-Jun-08	Headboat	NA			465	Y
313	N Gulf of Mexico	GOM	NGOM-11	22-Jun-08	Headboat	NA			372	Y
314	N Gulf of Mexico	GOM	NGOM-12	28-Jun-08	Headboat	NA			475	Y
315	N Gulf of Mexico	GOM	NGOM-14	28-Jun-08	Headboat	NA			362	Y
316	N Gulf of Mexico	GOM	NGOM-15	1-Jul-08	Headboat	NA			485	Y

* Winter Population, Onslow Bay NC



Acc. #	Population	Region	UNCW Seq ID	Date Collected	Cruise ID	Station ID	Latitude	Longitude	TL (mm)	Otoliths
317	N Gulf of Mexico	GOM	GOM-09-1	14-Jul-09	Fish-Ind	TS09098	29.7065	-84.6332	204	Y
318	N Gulf of Mexico	GOM	GOM-09-12	13-Jul-09	Fish-Ind	TS09093	29.6799	-84.6724	278	Y
319	N Gulf of Mexico	GOM	GOM-09-13	14-Jul-09	Fish-Ind	TS09096	29.7535	-84.5154	374	Y
320	N Gulf of Mexico	GOM	GOM-09-14	7-Dec-09	Fish-Ind	GMM091230303	27.6639	-83.0816	252	Y
321	N Gulf of Mexico	GOM	GOM-09-16	9-Dec-09	Fish-Ind	GMM091231101	27.5764	-82.8429	156	Y
322	N Gulf of Mexico	GOM	GOM-09-17	19-Nov-09	Fish-Ind	HIM09110104	28.1245	-82.8302	179	Y
323	N Gulf of Mexico	GOM	GOM-09-18	19-Nov-09	Fish-Ind	HIM09110109	28.0789	-82.8201	160	Y
324	N Gulf of Mexico	GOM	GOM-09-2	14-Jul-09	Fish-Ind	TS09098	29.7065	-84.6332	195	Y
325	N Gulf of Mexico	GOM	GOM-09-5	14-Jul-09	Fish-Ind	TS09098	29.6831	-84.6752	257	Y
326	N Gulf of Mexico	GOM	GOM-09-7	14-Jul-09	Fish-Ind	TS09098	29.6799	-84.6724	199	Y
327	N Gulf of Mexico	GOM	GOM-09-8	14-Jul-09	Fish-Ind	TS09098	29.6799	-84.6724	230	Y
328	N Gulf of Mexico	GOM	GOM-09-9	14-Jul-09	Fish-Ind	TS09096	29.6799	-84.6724	306	Y