

# FISHERIES INVESTIGATIONS IN LAKES AND STREAMS



## ANNUAL PROGRESS REPORT

F-63

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## TABLE OF CONTENTS

STATEWIDE FISHERIES RESEARCH .....		1
Distribution of Striped Bass in J. Strom Thurmond Reservoir, South Carolina-Georgia, in Relation to Pump Storage Operation and Hypolimnetic Oxygenation .....		
1		
Table 1.	Date of implantation, transmitter ID, Total Length (mm), location of implantation, fate, number of detections with receivers and while manual tracking, and the number of days tracked post implantation for transmitter implanted striped bass in Thurmond Reservoir, SC-GA through August 2013. Fate codes are; Alive (A), Dead (D), Transmitter Expired (E), Reported Harvested (H), Assumed Harvested (H?), Missing (M), Tagging Mortality (TM), and Unknown (U). .....	5
Table 2.	Date of implantation, transmitter ID, Total Length (mm), location of implantation, fate, number of detections with receivers and while manual tracking, and the number of days tracked post implantation for transmitter implanted hybrid striped bass in Thurmond Reservoir, SC-GA through August 2013. Fate codes are; Alive (A), Dead (D), Transmitter Expired (E), Reported Harvested (H), Missing (M), and Tagging Mortality (TM). .....	9
Figure 1.	Acoustic receiver locations in J. Strom Thurmond Reservoir SC-GA, during 2010 -2013. ....	10
Table 3.	Fate of striped bass implanted during 2010 – 2013 in J. Strom Thurmond Reservoir, SC-GA. Fish of “unknown” fate were transmitted and released before the receiver system was deployed, and their location history could not be used to successfully place them in another category.....	11
Figure 2.	Number of striped bass, based on mean monthly August position in each section of Thurmond Reservoir during August 2010 - 2013.....	12
Condition of Stocked Striped Bass .....		
15		
Figure 1.	Relative condition factor, using dry weights, of striped bass juveniles from stocked in May of 2012 from 27 distinct batches. ....	18
Figure 2.	Relative condition factor, using wet weights, of striped bass juveniles from stocked in May of 2012 from 27 distinct batches. ....	18

Figure 3.	Variation and change in relative condition factor of striped bass juveniles from stocked from May 7 through May 29, 2012.....	19
Figure 4.	Average relative condition in 2012 of 8 distinct genetic families of hatchery-produced juvenile striped bass, using both wet and dry weights. ....	19
Figure 5.	Variation in dry weight, relative condition factor among unique rearing ponds used to produce in the hatchery striped bass juveniles from 4 distinct genetic families.....	20
Pee Dee River Striped Bass.....		23
Striped Bass Fecundity - Santee-Cooper.....		27
Figure 1.	Logistic regression analysis of the maturity schedule of female striped bass from Lakes Marion and Moultrie, South Carolina. ....	29
Developing Sediment Management Guidelines to Enhance Habitat and Aquatic Resources in the Broad River Basin, South Carolina.....		31
Table 1.	Sample sites for habitat and fish assemblage monitoring in the Broad River basin. ....	33
Table 2.	Environmental, habitat and sediment variables used in NMS ordination to investigate relationships among fish assemblage structure, habitat and sediment characteristics in tributaries of the Broad River, 2012-2013.....	35
Table 3.	Fish species collected at 10 tributary monitoring sites in the Broad River basin, 2013. Presence and abundance data are totals including both spring (7) and fall (10) samples. Sites are listed in Table 1 in Methods. ....	39
Figure 1.	NMS ordination plot of 17 Broad River tributary samples. Sample labels show the first four letters of the site followed by the year (13) and season (S = spring; F = fall). Species are shown as three-letter codes (refer to Table 3). Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%. ....	40
Table 4.	Correlations among environmental, habitat and sediment variables and fish assemblage structure with all 17 tributary samples included. Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%. Variables are defined in Table 2. ....	41

Table 5.	Correlations among environmental, habitat and sediment variables and fish assemblage structure for 15 tributary samples (Enoree and Tyger excluded). Axis 1 represented the majority of variation in fish assemblage structure (56%), Axis 3 about 21% and Axis 2 about 18%. Variables are defined in Table 2. ....	42
Table 6.	Preliminary results for fish egg and larva collections at study sites in the Broad River basin. Confirmation of fish origin and taxonomic identification are pending.....	43
Table 7.	Species abundance by sample for sites upstream versus downstream of an active sand mine on the North Pacolet River, Fall 2012 and Fall 2013. ....	44
South Carolina Stream Assessment .....		46
South Carolina Stream Conservation Planning Tool .....		47
Figure 1.	SC Stream Assessment sample locations apportioned among major river basins and EPA level IV ecoregions.....	50
Figure 2.	NHDPlus flowlines and associated local catchments. The NFHAP database additionally attributes flowlines with network catchment spatial data. ....	53
Table 1.	NFHAP database spatial predictor variables included in random forests models. ....	54
Figure 3a.	Depicts a random forests variable importance plot.....	56
Figure 3b.	Depicts a random forests partial dependence plot. ....	57
Fish Community Response to Dam Removal in Twelvemile Creek, Pickens County, South Carolina.....		64
Figure 1.	Twelvemile Creek drainage shaded in gray. Inset (a) shows sample locations (black circles), locations of two former mainstem dams (Woodside I and Woodside II), and the location of a remaining third dam (Easley-Central Dam). Inset (b) shows watershed location in SC.....	67
Table 1.	Fish metric definitions. ....	68

Figure 2.	Total density, cyprinid invertivore density, benthic invertivore density, round bodied catostomid density, native centrarchid density, and non-native species density through time at Twelvemile Creek sample sites immediately upstream and downstream of the Woodside I and Woodside II Dams. The left-most vertical dashed line represents the complete removal of Woodside I Dam, and the right-most vertical dashed line represents the complete removal of Woodside II Dam. ....	69
Figure 3.	Non-metric multidimensional scaling of fish species by site. Points closer to one another in the ordination are more similar in species composition. Species names in gray refer to species that correlate strongly on each axis, whether positively or negatively. Environmental variables in red are parameters that were strongly correlated with each axis. Species correlations are inherent weights (i.e. the ordination is based on the species) whereas environmental correlations are post-hoc. Inferred groups are indicated with black circles. ....	73
Assessing introgressive hybridization within and habitat requirements of native South Carolina redeye bass.....		77
Table 1.	Genetic identifications of black bass collected from Savannah basin streams in 2009 and 2010; redeye bass (REB), largemouth bass (LMB), Alabama bass (ASB), smallmouth bass (SMB), hybrid (HYB). Streams are grouped by the reservoir they are associated with, or as a direct tributary to the Savannah River. ....	81
Figure 1.	Spatial distribution of Savannah Basin tributary black bass collections from 2004 – 2010. Circles mark collection sites where only genetically pure redeye were collected. Crosses mark those sites where congeneric hybrids with redeye were collected. The lower most site depicted is the Augusta Shoals area of the Savannah River which produced smallmouth bass and their hybrids with redeye. All other hybrid collections were Alabama x redeye bass.....	82
Figure 2.	Neighbor-joining tree relating ND2 sequences collected from Saffron Shiners ( <i>Notropis rubricroceus</i> ). ....	84
Figure 3.	Neighbor-joining tree relating ND2 sequences collected from Warpaint Shiners ( <i>Luxilus coccogenis</i> ). ....	85
Figure 4.	Neighbor-joining tree relating Calmodulin sequences collected from Saffron Shiners ( <i>Notropis rubricroceus</i> ). ....	86

Figure 5.	Neighbor-joining tree relating Calmodulin sequences collected from Warpaint Shiners ( <i>Luxilus coccogenis</i> ).....	87
Table 2.	Estimates of population differentiation based on allelic diversity at the mitochondrial ND2 and Calmodulin loci in two species of minnow. Differentiation is based on an Analysis of Molecular Variance that partitions genetic variation to components within versus between river drainages. Significant values (*) are indicated (P < 0.05). .....	88
Redbreast Stocking Evaluation – Edisto River .....		92
Table 1.	Age 1+ redbreast collected by river segment from the Edisto River in Fall of 2011. N collected is for 1 hour of electrofishing in each segment. ....	94
Figure 1.	Marked and unmarked 2010 year class redbreast sunfish collected by boat electrofishing from the Edisto River at age 1+. Number collected is presented by 8 contiguous 1-mile river segments (2 upstream of the stocking zone, 4 within the stocking zone, and 2 downstream of the stocking zone). Catch represents 60 minutes of standardized pedal time in each river segment. ....	95
Table 2.	Mean total length (tl) and relative weight (Wr) of marked and unmarked age 1+ redbreast collected from the Edisto River Fall of 2011.....	95
Performance Comparison of Largemouth Bass Strains in Farm Ponds .....		99
Robust Redhorse Annual and Seasonal Movements within the Upper Santee River System .....		102
Figure 1.	Receiver locations (VR2 and VR2W) in the upper Santee River system during 2009 – 2013. ....	104
Table 1.	Date of transmitter implantation, transmitter ID, total length (TL,mm), tagging location, fate, days tracked, and total number of detections for robust redhorse implanted with transmitters and tracked in the Santee-Cooper system during 2009 – 2013. Fate codes are; TE (tag expired), TM (tagging mortality/transmitter expulsion), A (alive), and D (died). ....	107
Figure 2.	Number of Robust Redhorse that used each section of the upper Santee River system for 12 fish that were tracked for at least one year during 2009 -2013. ....	108

Figure 3.	Number of transmitter-implanted Robust Redhorse in the Wateree Dam Tailrace by date during spring of each study year 2010 - 2013. “N” denotes the number of transmitter implanted Robust Redhorse alive each year.....	110
Assessment of condition, growth, contribution to fish community, and diet of striped bass, white perch, and American shad young-of-the-year in the Santee-Cooper lakes, South Carolina.....		
Table 1.	Number of transects sampled on each date and electrofishing effort (h) during nighttime electrofishing at two sites on Lake Marion, SC during 2012. ....	114
Figure 1.	Relative abundance of young-of-the-year American shad (AMS), threadfin shad (TFS), striped bass (STB), gizzard shad (GZS), white perch (WTP), and blueback herring (BBH) collected from littoral areas at the Big Water (BW) and Indian Bluff (IB) sites, Lake Marion, South Carolina, during 2009-2012 (top panel). Overall relative abundance is given for each year (bottom panel).....	115
Figure 2.	Proportion numerically (top panel) and by weight (bottom panel) of major prey items in the diets of young-of-the-year American shad (AMS), striped bass (STB), and white perch (WTP) collected from littoral areas of Lake Marion, South Carolina, during 2009. ....	117
Table 2.	Prey taxa encountered and frequency of occurrence (percent) of prey taxa in the stomachs of threadfin shad collected from Lake Marion, South Carolina during 2011. ....	119
Trophic Resources for Larval Fish in Lake Marion .....		
Figure 1.	Upper region of Lake Marion. The Santee River flows along a defined channel through the uppermost part of Lake Marion, which is mainly forested swamp. At the lower end of this zone, the river submerges, and open water predominates. The map was derived from the National Hydrography Dataset for the Edisto-Santee Subregion (USGS, 2007). Filled circles show water quality stations. ....	122
Table 1.	Variables used in model of algal population dynamics. ....	123
Figure 2.	Mean discharge Congaree and Wateree rivers into Upper Lake Marion, 2001-2012. Means for April-October of 2003, an exceptionally wet year, and 2009 and 2010, the years of our benthic samples, are marked by arrows. ....	128

Figure 3.	Chlorophyll a in Upper Lake Marion, 2001-2012. Monthly values are summarized for three stations; n of years for each station and month is 4-11. ....	129
Figure 4.	Chlorophyll a at station SC-010 in Upper Lake Marion, 2001-2012, as function of combined discharge from the Congaree and Wateree rivers. Discharge value was lagged by 3 days from the sampling date for chlorophyll a to account for travel time from the gages to the lake. ....	130
Table 2.	Modeled spring and summer algal productivity.....	131
Figure 5.	Phytoplankton productivity required to maintain algal populations in Upper Lake Marion, based on consumption by <i>Corbicula</i> population. ....	132

**Study Title:** STATEWIDE FISHERIES RESEARCH

**Job Title:** Distribution of Striped Bass in J. Strom Thurmond Reservoir, South Carolina-Georgia, in Relation to Pump Storage Operation and Hypolimnetic Oxygenation

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

During FY13 thirty-nine (39) striped bass *Morone saxatilis* and 14 hybrid striped bass *Morone saxatilis x Morone chrysops* collected from four tributaries to Thurmond Reservoir were implanted with acoustic transmitters. One hundred thirty-seven (137) striped bass have been successfully implanted since the study began in FY10. Implanted striped bass were detected by 64 different receivers stationed throughout the reservoir and were manually tracked on 25 dates. Thirty-one percent (31%) of implanted striped bass appeared to be alive at the end of FY13, 10% of fish have expired transmitters, 47% have been harvested or assumed harvested, and the remaining fish have either died (7%) or are missing (4%). The Russell Tailrace and the oxygenated area of the lower reservoir were important habitats for striped bass during August 2010 - 2013 with all fish occupying one of those habitats during August of each year.

### **Introduction**

J. Strom Thurmond (Thurmond) Reservoir supports a popular recreational striped bass fishery. Striped bass production at Thurmond is largely due to suitable habitat provided by artificially oxygenated, hypolimnetic releases from Richard B. Russell (Russell) Dam, that provide cool well oxygenated water in the tailrace and upper portions of Thurmond Reservoir.

During 2011 Russell Dam commenced expanded pump-storage operations which could result in warmer tailrace temperatures below Russell Dam, possibly reducing suitable habitat for some

species of fish. Given the unsuitable striped bass habitat throughout most of the reservoir during the summer the loss of the refuge in the Russell tailrace and upper Thurmond could have a negative impact on the striped bass fishery. To mitigate for the potential loss of striped bass habitat in the Russell tailrace and upper Thurmond, the USACOE installed an oxygen injection system in the lower portion of Thurmond near Modoc, SC to provide striped bass habitat.

It is unknown how striped bass will utilize the expected reduction of habitat in the Russell tailrace and upper Thurmond or the new artificially oxygenated area in the lower reservoir. Considerable expense has been expended in the development and installation of the new oxygen injection system and it is important to document the extent of striped bass use of the newly-created habitat. Information on the seasonal distribution of striped bass after project implementation will be important for successful management of the striped bass fishery in Thurmond Reservoir.

### **Materials and Methods**

The study will monitor the seasonal movement of adult striped bass in Thurmond Reservoir. Specifically monitoring their seasonal use of the current refuge area in the upper reaches of Thurmond and the Russell Tailrace as well as the enhanced area below Modoc, SC. In spring of 2010, 2011, 2012, and 2013 striped bass were collected from the Russell tailrace and at least two major tributaries (e.g., Little River, GA and Little River, SC) and surgically implanted with individually coded temperature sensing acoustic transmitters. During spring 2013 hybrid striped bass were also collected and implanted with transmitters. Two different transmitters manufactured by Sonotronics were used based on fish length. A high powered long-range transmitter (Model CHP-87-L) expected to last 18 months was implanted in striped bass > 575 mm TL and a less powerful transmitter (Model CTT-83-3) expected to last 36 months was implanted in striped bass > 480 mm

TL. To facilitate the return of transmitters from harvested fish external reward tags (Hallprint Pty Ltd., Victor Harbor, South Australia) were inserted into most striped bass implanted during 2013.

An array of remote acoustic receivers (SUR-3BT, Sonotronics Inc.) was used to collect movement data from transmitter implanted fish. Receivers were positioned throughout the mainstem reservoir with expanded arrays in the tailrace and oxygen injected area to achieve continuous coverage of the Savannah River channel in those areas. Additional location data was collected with a hand held ultrasonic receiver (USR-08, Sonotronics Inc.) to identify other potential refuges and locate missing fish. Temperature and oxygen profiles at 1-m depth intervals were collected monthly during the summer study period at a series of fixed stations throughout the monitored area.

We considered four possible fates for transmitter implanted fish in J. Strom Thurmond Reservoir. Striped bass could be, alive in the fishery until the conclusion of the study (or transmitter expiration), harvested, missing, or die of natural causes. During 2013 we posted signs at major access points, and issued press releases to inform anglers of the ongoing telemetry study. Signs and press releases advised anglers that a \$50.00 reward would be given for returning transmitters from harvested fish. Fish were determined to be harvested when an angler returned a transmitter from a captured fish, or were assumed harvested when a fish went missing from an area with overlapping receiver coverage, and were not detected in subsequent manual searches. Fish lost from the fishery were either confirmed as dead by lack of movement during manual searches or simply classified as missing when they were no longer located at automated receiver stations or during manual searches. Due to the extensive receiver network it was unlikely that fish classified as missing were at large and simply undetected so ultimately they were lost from the fishery by harvest or natural mortality.

## **Results**

Thirty-nine (39) striped bass (mean TL = 825 mm; range 627 – 1155 mm TL) collected from four tributaries to Thurmond Reservoir were implanted with acoustic transmitters between 1 March 2013 and 18 March 2013 (Table 1). Thirty-five (35) of those fish also received an external reward tag. Since April 2010 a total of 151 striped bass collected from Thurmond Reservoir and its tributaries have been implanted with transmitters. Fourteen (14) hybrid striped bass (mean TL = 560 mm; range 500 – 622 mm TL) collected from three tributaries to Thurmond Reservoir were implanted with transmitters between 1 March 2013 and 10 April 2013 (Table 2).

Submersible acoustic receivers at up to 64 different sites were used to collect striped bass movement information during FY10 - 13 (Figure 1). Striped bass and hybrid striped bass implanted with transmitters were manually tracked on 25 dates during FY13.

There have been roughly 5.9 million detections at the 64 receiver locations. The average number of detections at receiver locations for fish known to survive transmitter implantation was 42,782 (Range; 0 - 234,067) through August 2013. During manual tracking events 106 different striped bass were located at least once (Table 1). At the conclusion of FY 13, 31% of successfully implanted striped bass were assumed to be alive, 47% were harvested or assumed to have been harvested, 7% of fish had died and the remaining fish either had expired transmitters or were missing (Table 3). Of the 14 hybrid striped bass implanted with transmitters, three fish were assumed to have expired due tagging, five fish are currently alive, five fish are missing, and one fish was reported as harvested.

Table 1. Date of implantation, transmitter ID, Total Length (mm), location of implantation, fate, number of detections with receivers and while manual tracking, and the number of days tracked post implantation for transmitter implanted striped bass in Thurmond Reservoir, SC-GA through August 2013. Fate codes are; Alive (A), Dead (D), Transmitter Expired (E), Reported Harvested (H), Assumed Harvested (H?), Missing (M), Tagging Mortality (TM), and Unknown (U).

Date	ID	TL	Location	Fate	Receiver	Manual	Days Tracked
4/16/2010	3	665	Little River, SC	U	0	0	0
4/16/2010	6	650	Long Cane Creek, SC	D	6,090	6	0
4/16/2010	10	730	Long Cane Creek, SC	U	26	2	68
4/16/2010	19	655	Little River, SC	E	38,481	5	623
4/16/2010	20	820	Little River, SC	H?	72,493	1	242
4/20/2010	2	1200	Broad River, GA	H	43,035	4	304
4/20/2010	9	693	Thurmond	U	0	1	0
4/28/2010	18	690	Little River, GA	H?	0	2	64
4/28/2010	21	632	Little River, GA	E	93,626	5	712
4/28/2010	22	565	Little River, GA	H?	21,103	4	432
5/4/2010	4	1400	Broad River, GA	D	47,032	8	345
5/4/2010	5	800	Broad River, GA	M	0	5	50
5/4/2010	7	1200	Broad River, GA	H	0	2	91
5/4/2010	8	930	Broad River, GA	E	146,372	12	1,160
5/4/2010	11	863	Broad River, GA	A	92,684	7	1,242
5/4/2010	17	950	Broad River, GA	H?	0	3	56
5/4/2010	23	722	Broad River, GA	U	0	0	0
5/4/2010	38	650	Russell Tailrace	E	66,304	3	772
8/18/2010	49	549	Russell Tailrace	H	74,988	3	912
8/18/2010	53	622	Russell Tailrace	H?	26,683	3	301
8/18/2010	54	547	Russell Tailrace	H?	52,570	6	499
8/18/2010	56	605	Russell Tailrace	H	27,525	2	306
8/18/2010	24	1040	Russell Tailrace	E	48,191	0	894
8/24/2010	25	582	Russell Tailrace	H	28,525	3	98
8/24/2010	33	604	Russell Tailrace	H?	7,563	1	59
8/24/2010	35	635	Russell Tailrace	H?	58,125	1	401
8/24/2010	37	573	Russell Tailrace	A	140,734	6	868
8/24/2010	39	708	Russell Tailrace	E	184,780	6	852
8/24/2010	47	616	Russell Tailrace	H	143,756	6	524
8/24/2010	50	530	Russell Tailrace	A	172,334	6	1,109
8/24/2010	51	480	Russell Tailrace	D	153,952	7	493
8/24/2010	52	510	Russell Tailrace	H?	2,207	2	41
8/24/2010	32	613	Russell Tailrace	TM	677	0	37
8/25/2010	34	970	Russell Tailrace	D	62,353	1	47
8/25/2010	36	588	Russell Tailrace	H?	8,341	0	28

Table 1. Continued

Date	ID	TL	Location	Fate	Receiver	Manual	Days Tracked
8/25/2010	40	645	Russell Tailrace	E	70,479	9	614
8/25/2010	41	934	Russell Tailrace	E	234,067	3	932
8/25/2010	48	593	Russell Tailrace	E	64,279	8	821
8/25/2010	62	680	Long Cane Creek, SC	H?	13,417	2	139
3/24/2011	63	702	Long Cane Creek, SC	H?	58,531	4	465
3/24/2011	64	600	Little River, SC	TM	21,389	1	3
3/24/2011	65	670	Long Cane Creek, SC	H?	93,707	3	192
3/24/2011	67	682	Long Cane Creek, SC	H?	6,496	1	113
3/24/2011	68	723	Long Cane Creek, SC	H	4,177	0	28
3/24/2011	71	705	Long Cane Creek, SC	H?	11,779	1	153
3/24/2011	82	862	Little River, SC	A	82,213	5	881
3/24/2011	86	925	Little River, SC	A	46,066	7	885
3/24/2011	96	620	Long Cane Creek, SC	H	1,882	0	78
3/24/2011	100	630	Long Cane Creek, SC	H	3,575	0	46
3/24/2011	113	810	Long Cane Creek, SC	H?	14,078	0	215
3/24/2011	66	652	Broad River, GA	H?	97,179	5	503
4/5/2011	69	780	Broad River, GA	A	165,283	2	909
4/5/2011	70	680	Little River, GA	H?	1,327	0	85
4/5/2011	77	590	Broad River, GA	H?	6,502	1	118
4/5/2011	78	690	Broad River, GA	E	50,043	4	665
4/5/2011	79	735	Broad River, GA	E	85,921	5	801
4/5/2011	80	690	Little River, GA	H?	8,890	1	97
4/5/2011	81	765	Broad River, GA	D	3,940	1	44
4/5/2011	83	550	Broad River, GA	H?	3,322	2	102
4/5/2011	84	785	Little River, GA	A	67,908	6	907
4/5/2011	112	620	Little River, GA	TM	0	0	0
4/5/2011	93	670	Little River, GA	H?	6,154	0	87
4/8/2011	101	650	Little River, GA	E	31,653	5	542
4/8/2011	94	1300	Little River, GA	E	26,409	1	596
4/18/2011	97	705	Little River, GA	M	56,516	2	265
4/18/2011	98	1200	Little River, GA	E	31,903	6	815
4/18/2011	85	702	Russell Tailrace	TM	2,351	6	11
5/25/2011	92	695	Russell Tailrace	H?	51,935	3	135
5/25/2011	95	638	Russell Tailrace	H?	45,461	2	339
5/25/2011	108	622	Russell Tailrace	TM	5,819	1	19
5/25/2011	114	574	Russell Tailrace	H?	932	0	4
5/25/2011	115	675	Russell Tailrace	A	98,850	5	701
5/25/2011	100.1	643	Russell Tailrace	H?	56,720	2	325
5/25/2011	68.1	990	Russell Tailrace	D	66,732	3	220
5/25/2011	125	890	Little River, GA	D	44,689	3	263

Table 1. Continued

Date	ID	TL	Location	Fate	Receiver	Manual	Days Tracked
3/15/2012	130	930	Little River, GA	H?	1,817	0	71
3/15/2012	143	630	Little River, GA	H?	12,392	0	111
3/15/2012	169	595	Little River, GA	TM	0	0	0
3/15/2012	153	740	Little River, SC	H?	51,281	1	184
3/20/2012	167	610	Little River, SC	H?	210	1	4
3/20/2012	124	800	Broad River, GA	A	80,623	2	539
3/22/2012	129	715	Little River, GA	TM	3	0	0
3/22/2012	157	793	Broad River, GA	A	80,252	5	558
3/22/2012	160	640	Broad River, GA	M	454	0	10
3/22/2012	170	605	Broad River, GA	H?	45,361	1	283
3/22/2012	175	567	Broad River, GA	A	62,457	0	537
3/22/2012	176	590	Broad River, GA	H?	2,818	0	61
3/22/2012	127	810	Little River, SC	A	42,830	1	553
3/26/2012	139	1025	Little River, GA	H?	2,124	0	19
3/26/2012	140	785	Little River, SC	A	54,216	1	555
3/26/2012	141	796	Little River, SC	A	70,464	1	553
3/26/2012	142	798	Little River, SC	H?	27,565	2	185
3/26/2012	145	760	Little River, SC	H?	51,775	1	445
3/26/2012	154	735	Little River, SC	H?	1,354	0	26
3/26/2012	156	622	Little River, SC	H	29,066	1	369
3/26/2012	161	795	Little River, SC	D?	118,651	2	277
3/26/2012	168	705	Little River, SC	D	9,360	1	67
3/26/2012	172	600	Little River, SC	D?	23,148	1	332
3/26/2012	173	600	Little River, SC	H	7,560	1	158
3/26/2012	138	738	Big Creek, GA	A	79,338	4	549
3/28/2012	144	950	Little River, GA	H?	2,432	0	81
3/28/2012	174	647	Little River, GA	A	107,921	3	549
3/28/2012	122	855	Russell Tailrace	A	79,340	1	487
5/30/2012	126	554	Russell Tailrace	M	13,515		98
5/30/2012	128	745	Russell Tailrace	TM	903	0	0
5/30/2012	131	837	Russell Tailrace	A	53,946	2	486
5/30/2012	137	607	Russell Tailrace	TM	162	0	3
5/30/2012	146	668	Russell Tailrace	H?	33,266	2	366
5/30/2012	152	655	Russell Tailrace	A	167,824	4	485
5/30/2012	155	920	Russell Tailrace	A	148,240	3	442
5/30/2012	158	560	Russell Tailrace	A	65,940	1	464
5/30/2012	171	487	Russell Tailrace	H	58,640	1	419

Table 1. Continued

Date	ID	TL	Location	Fate	Receiver	Manual	Days Tracked
3/1/2013	109	707	Little River, SC	H	4,016		
3/1/2013	200	857	Little River, SC	A	27,563	0	212
3/1/2013	212	862	Little River, SC	A	37,966	2	213
3/1/2013	215	755	Little River, SC	TM	2,437	0	8
3/1/2013	218	915	Little River, SC	A	34,488	0	214
3/1/2013	230	910	Little River, SC	A	39,875	0	212
3/1/2013	248	735	Little River, SC	H?	18,999	1	148
3/1/2013	259	808	Little River, SC	A	12,966	0	213
3/1/2013	263	822	Little River, SC	A	14,954	0	195
3/6/2013	227	865	Little River, GA	A	9,510	1	208
3/6/2013	229	730	Little River, GA	H	30,958	0	206
3/6/2013	231	784	Little River, GA	A	22,999	1	208
3/6/2013	232	784	Little River, GA	A	29,805	1	208
3/6/2013	233	1067	Little River, GA	A	23,658	1	209
3/6/2013	234	755	Little River, GA	H	1,364	0	48
3/6/2013	235	822	Little River, GA	A	33,536	1	208
3/6/2013	242	710	Little River, GA	A	39,773	1	206
3/6/2013	244	690	Little River, GA	A	24,841	3	208
3/6/2013	246	1020	Little River, GA	H	28,242	0	155
3/6/2013	247	798	Little River, GA	A	19,481	1	208
3/6/2013	249	1155	Little River, GA	A	44,444	0	209
3/7/2013	206	883	Broad River, GA	A	37,394	1	208
3/7/2013	217	930	Broad River, GA	H?	1,529	0	96
3/7/2013	219	1050	Broad River, GA	H	17,823	1	180
3/7/2013	221	690	Broad River, GA	H	0	0	11
3/7/2013	243	842	Broad River, GA	A	46,911	1	206
3/18/2013	188	915	Broad River, GA	A	8,212	0	195
3/18/2013	190	834	Long Cane Creek, SC	H	10,903	0	144
3/18/2013	204	628	Long Cane Creek, SC	H	11,176	1	75
3/18/2013	213	960	Broad River, GA	H	11,600	0	152
3/18/2013	214	925	Broad River, GA	A	21,761	2	195
3/18/2013	216	740	Broad River, GA	H	3,771	1	70
3/18/2013	220	784	Long Cane Creek, SC	A	27,866	1	195
3/18/2013	228	940	Broad River, GA	H	380	0	20
3/18/2013	236	685	Broad River, GA	H?	11,096	2	110
3/18/2013	251	630	Long Cane Creek, SC	M	2,989	2	155
3/18/2013	258	627	Long Cane Creek, SC	H	8,723	0	123
3/18/2013	260	850	Broad River, GA	A	8,918	0	178
3/18/2013	262	690	Long Cane Creek, SC	A	11,563	2	195

Table 2. Date of implantation, transmitter ID, Total Length (mm), location of implantation, fate, number of detections with receivers and while manual tracking, and the number of days tracked post implantation for transmitter implanted hybrid striped bass in Thurmond Reservoir, SC-GA through August 2013. Fate codes are; Alive (A), Dead (D), Transmitter Expired (E), Reported Harvested (H), Missing (M), and Tagging Mortality (TM).

Date	ID	TL	Location	Fate	Receiver	Manual	Days Tracked
3/1/2013	261	508	Little River, SC	M	2,874	0	29
3/1/2013	275	511	Little River, SC	A	31,639	1	213
3/6/2013	205	500	Little River, GA	A	14,747	2	208
3/18/2013	203	525	Broad River, GA	M	1,071	0	21
3/18/2013	264	552	Broad River, GA	A	12,148	1	196
4/10/2013	107	607	Little River, GA	H	1,794	0	57
4/10/2013	189	615	Little River, GA	A	12,321	0	173
4/10/2013	191	580	Broad River, GA	M	971	0	31
4/10/2013	197	572	Broad River, GA	M	400	0	102
4/10/2013	198	555	Broad River, GA	TM	4	0	0
4/10/2013	199	570	Little River, GA	A	12,301	0	172
4/10/2013	250	622	Broad River, GA	TM	19	0	6
4/10/2013	257	562	Broad River, GA	M	726	0	83
4/10/2013	273	565	Broad River, GA	TM	22	0	2

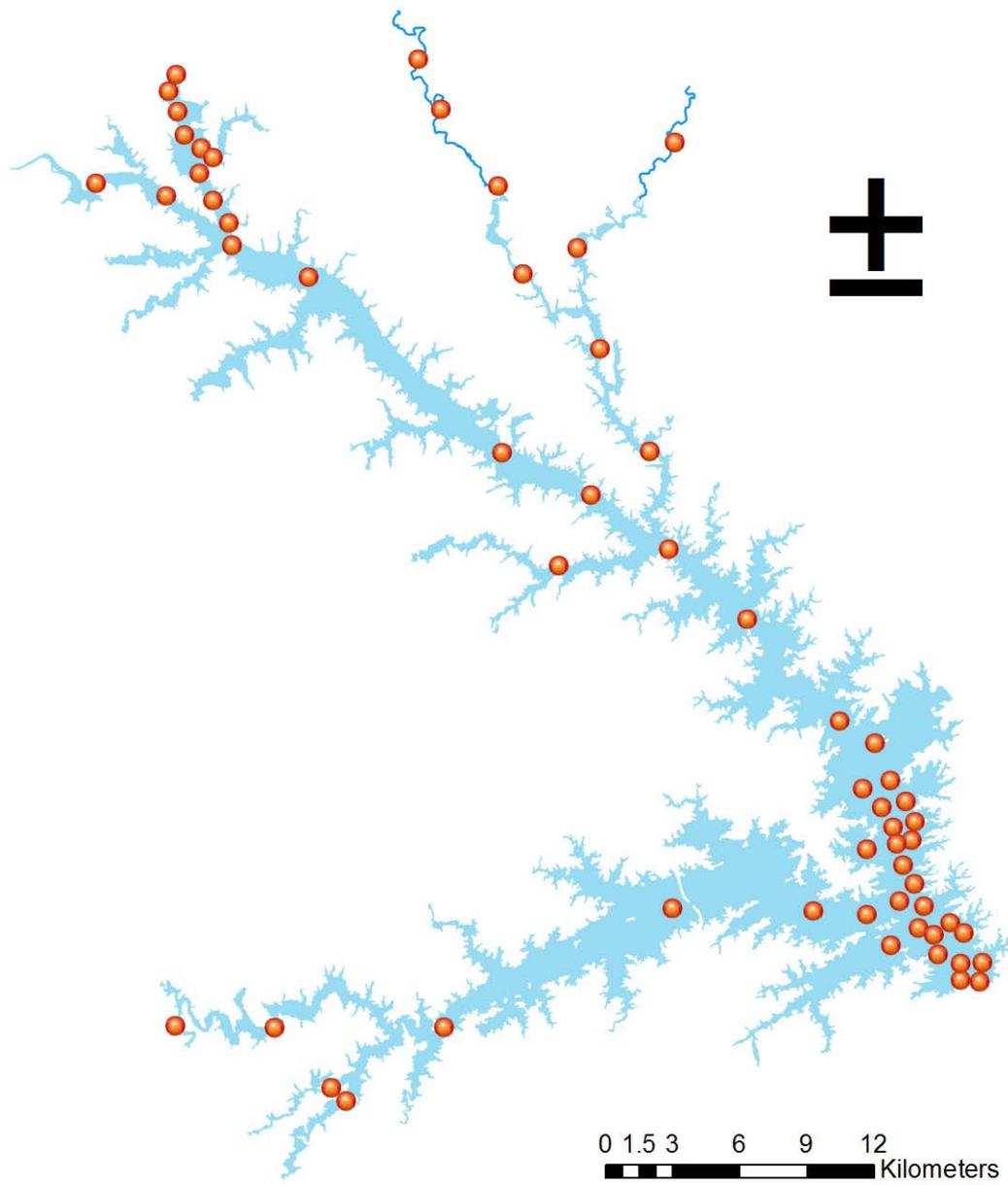


Figure 1. Acoustic receiver locations in J. Strom Thurmond Reservoir SC-GA, during 2010 -2013.

Table 3. Fate of striped bass implanted during 2010 – 2013 in J. Strom Thurmond Reservoir, SC-GA. Fish of “unknown” fate were transmitted and released before the receiver system was deployed, and their location history could not be used to successfully place them in another category.

Year Implanted	Alive	Dead	Transmitter Expired	Harvested	Assumed Harvested	Missing	Tagging Mortality	Unknown
2010	3	4	9	6	11	1	1	4
2011	5	3	5	3	15	1	4	0
2012	13	3	0	3	12	2	4	0
2013	22	0	0	12	3	1	1	0
<b>Total</b>	<b>43</b>	<b>10</b>	<b>14</b>	<b>24</b>	<b>41</b>	<b>5</b>	<b>10</b>	<b>4</b>

Water temperature and dissolved oxygen profiles were collected from nine sites located longitudinally from Thurmond Dam to Russell Dam during June, July, August and September of 2012 and 2013. Temperature and dissolved oxygen profiles were also collected at 26 fish locations during FY13.

**Discussion**

Location data downloaded from receivers during FY13 has been incorporated into an Access database; however, rigorous analysis of those data has not been completed. cursory examination of the data does show the importance of the Russell Tailrace and oxygenated area near Modoc as a summer habitat for striped bass. All fish have had their average monthly location during August located in the tailrace or oxygenated area except during 2012 when 2 fish moved between the two habitats during late August (Figure 2). Although, the proportion of fish utilizing the lower reservoir during August has increased it does not indicate an increase in the use of the lower lake, rather a propensity for fish tagged in the various tributaries to utilize different summer habitats. For

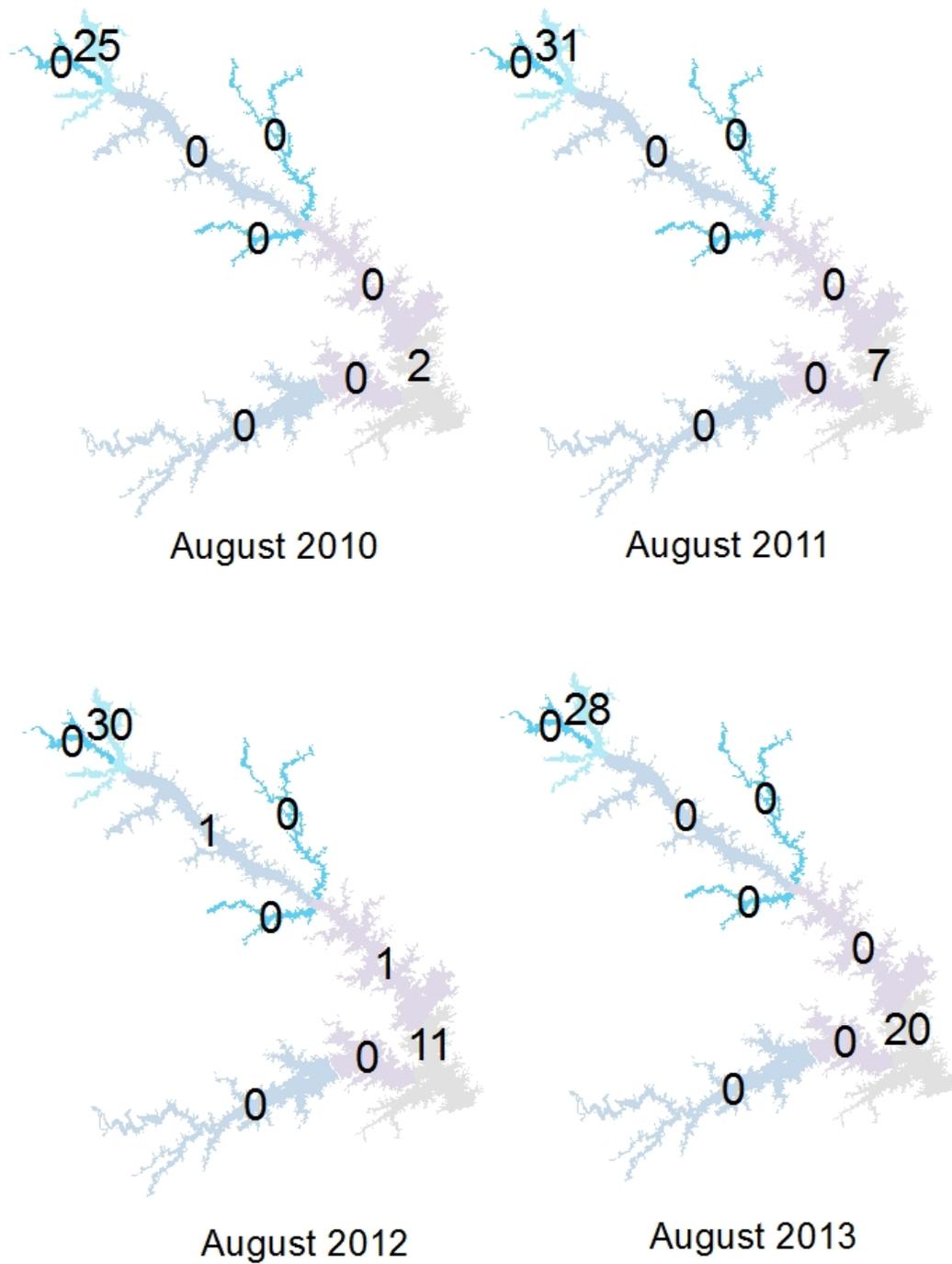


Figure 2. Number of striped bass, based on mean monthly August position in each section of Thurmond Reservoir during August 2010 - 2013.

example, the majority (17 of 20) of fish implanted in the Broad River, and all fish implanted in the tailrace (34 fish) and followed for at least one summer utilized the tailrace during summer. Fish implanted in Little River, South Carolina used the tailrace (17 fish) and lower reservoir (13 fish) in nearly equal proportions while fish implanted in Little River, Georgia were more likely to utilize the lower reservoir (14 fish) than tailrace (7 fish) during summer. The decrease in the proportion of fish that utilize the tailrace during summer is likely due to implanting fewer fish from the tailrace each year. During 2010 twenty-one (21) fish were implanted in the tailrace, but during 2011 and 2012 only 8 and 10 fish respectively, were captured from the tailrace and implanted with transmitters. No fish were captured from the tailrace during 2013 and implanted with transmitters. Forty-four (44) fish have been followed in subsequent summers, with 13 fish followed for at least three summers, and none of those fish have changed their summer habitat.

During 2013 we attached external reward tags to implanted striped bass to increase reporting rates of harvested striped bass and to validate assumptions about how we categorize the fate (i.e., “Alive”, “Dead”, or “Harvested”) of striped bass. The external tags were effective in increasing reporting rates and validated assumptions about how we categorize the fate of implanted fish. During 2010 – 2012 we had poor transmitter return rates; although we categorized more than 15 fish as harvested from each of the 2010 – 2012 implantations the majority (>64%) of those fates were based on location information that indicated that fish were removed from the lake and the absence of detections during manual tracking searches. For the 2013 implanted fish, which had external reward tags, 15 fish were reported as harvested and only three fish were classified as harvested based on location history and absence during manual searches.

## **Recommendations**

We will continue the study as planned. During spring of 2014 we will attempt to implant at least 10 additional fish, utilizing transmitters returned from fish harvested during 2013. Striped bass movements will be monitored with our receiver array and by manually tracking fish throughout the year.

**Job Title:** Condition of Stocked Striped Bass

**Period Covered** July 1, 2012 - June 30, 2013

### **Summary**

The condition of striped bass *Morone saxatilis* stocked into Lakes Marion and Moultrie in 2012 was evaluated. There was substantial variation of the condition of individual fish within a stocking batch. Likely sources of this variation were time of year, length, genetic family, and the pond rearing environment. However, average condition of a stocking batch may be a metric that allows determination of whether this factor is important in a particular batch achieving relatively high survival in a stocking year.

### **Introduction**

The stocking of striped bass is an important fishery management activity for the state's waters. Most South Carolina reservoirs depend on hatchery stocking of striped bass as natural reproduction is not possible. In the Santee-Cooper system, which includes Lakes Marion and Moultrie, natural reproduction does occur; however, stocking is used to augment natural reproduction, which exhibits high annual variability.

Somewhat surprisingly, the success of stocking striped bass in the Santee-Cooper system has also exhibited high annual variability. The reasons behind this variable annual survival are not well understood and need further inquiry.

Survival of juvenile fishes is strongly linked to body-tissue composition, particularly lipid, protein, and gross-energy stores (Pangle and Sutton 2005). Measurement of the body-tissue composition, or proximate composition, was used by Miranda and Hubbard (1994) to successfully predict over-winter survival potential of juvenile largemouth bass *Micropterus salmoides*. The

composition of fish tissue can be determined directly, which is time consuming, or estimated indirectly through condition factors (Anderson and Newmann 1996). Brown and Murphy (1991) showed a strong correlation between condition indices and the proximate composition of juvenile striped bass.

The objective of this study was to investigate the condition of striped bass stocked in 2012. Bulak (2012) previously evaluated the 2011 stockings, including an assessment of the correlation of the energy content of stocked fish, determined through calorimetry, with wet and dry weight. That investigation indicated 1) a significant correlation between energy density and dry and wet weight, 2) differences of average relative condition of stocking batches, 3) high variability of individual condition within a stocking batch, and 4) rearing pond was a contributing factor to condition of a stocking batch.

## **Materials and Methods**

A sample of approximately 25 striped bass was taken from each stocking batch going into Lakes Marion and Moultrie (a batch is defined as those fish used to fulfill an individual, unique stocking event; a batch was generally composed of a single genetic family, although that same family may fulfill several stocking batches). The sampled fish were immediately frozen. At a later time, these samples were defrosted and total length (mm) and wet weight (g) were determined. Wet weight samples were placed on a paper towel prior to weighing to remove excess moisture. The samples were then dried at 60 °C for at least 48 hours and dry weight (g) was measured.

Relative condition factor (K) was calculated for each fish as:

$$K = W_{\text{obs}}/W_{\text{pred}}$$

Where  $W_{obs}$  is the observed weight of an individual fish and  $W_{pred}$  is the length-specific predicted weight, as predicted by a length-weight equation. Length weight relations determined for 2011 stocked fish (Bulak 2012) were used; the equations were:

$$\text{Log}_{10} \text{ wet weight (mg)} = -2.54 + (3.35 * \text{log}_{10} \text{ total length, mm}),$$

$$\text{Log}_{10} \text{ dry weight (mg)} = -3.48 + (3.54 * \text{log}_{10} \text{ total length, mm}).$$

Relative condition factors were generated for observed wet and dry weight. We then defined the average relative condition factor for each stocking batch. A preliminary assessment of the effects of family, date of stocking, and rearing pond on condition was performed for fish reared at Dennis Center.

## **Results**

A total of 650 individual fish were sampled, measured, and weighed from a total of 27 different stocking batches from 8 distinct stocking families. Stocking began on May 7, 2012 and ended on May 29, 2012.

Relative condition varied by and within stocking batch (Figures 1 and 2). Relative condition factor tended to be higher in earlier stocked fish (Figure 3) and was dependent on fish total length.

The relation between condition and length was highly significant ( $P < 0.01$ ) and was defined as:

$$\text{Dry weight relative condition factor} = 1.21 + (-0.0070 * \text{TL, mm}); N = 650,$$

$$\text{Wet weight relative condition factor} = 1.14 + (-0.0058 * \text{TL, mm}); N = 650.$$

Relative condition varied substantially among genetic families used to produce the striped bass juveniles (Figure 4). When genetic families were stocked into at least three different culture ponds, there was substantial variation in relative condition among the ponds (Figure 5).

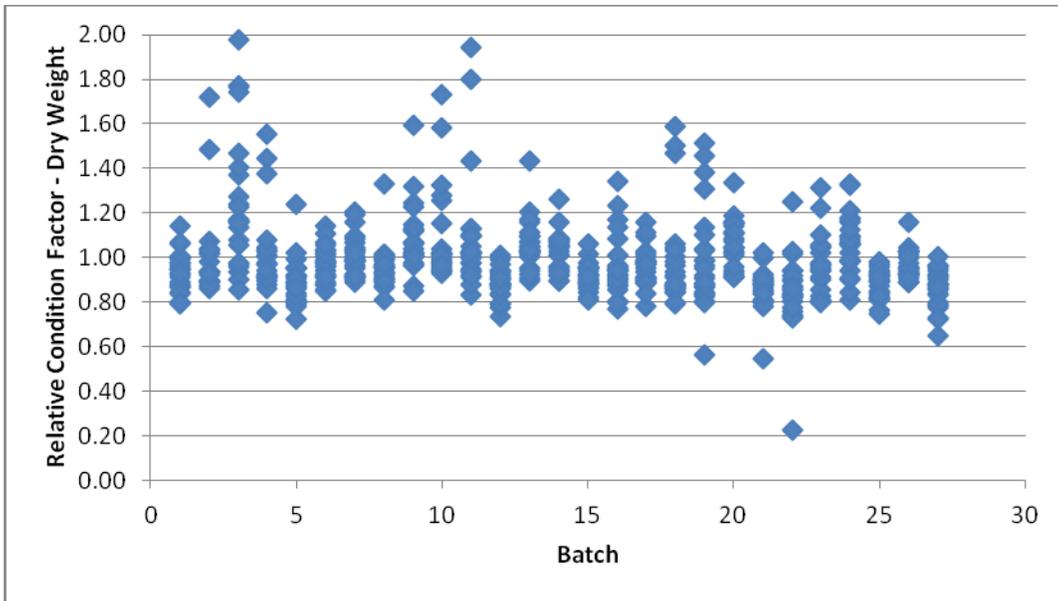


Figure 1. Relative condition factor, using dry weights, of striped bass juveniles stocked in May of 2012 from 27 distinct batches.

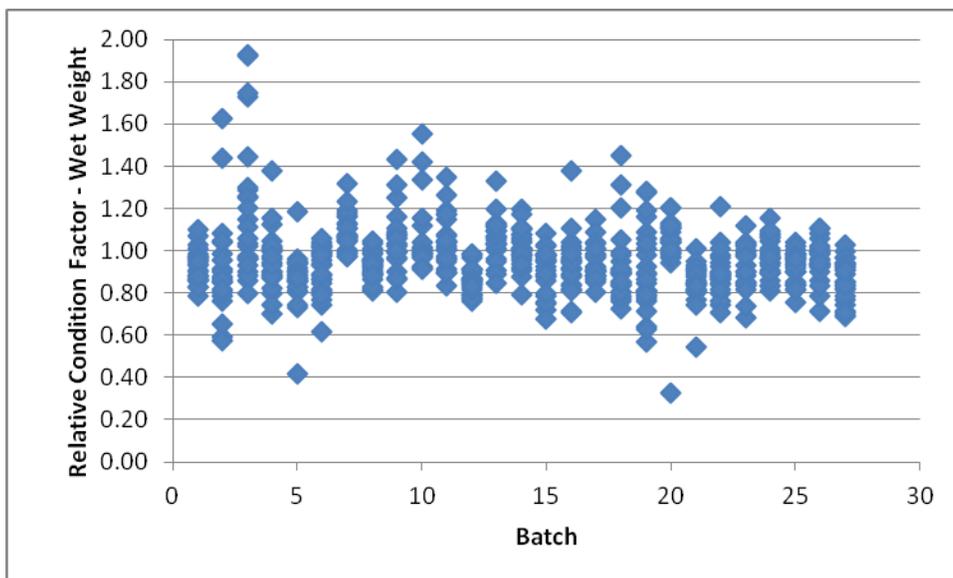


Figure 2. Relative condition factor, using wet weights, of striped bass juveniles stocked in May of 2012 from 27 distinct batches.

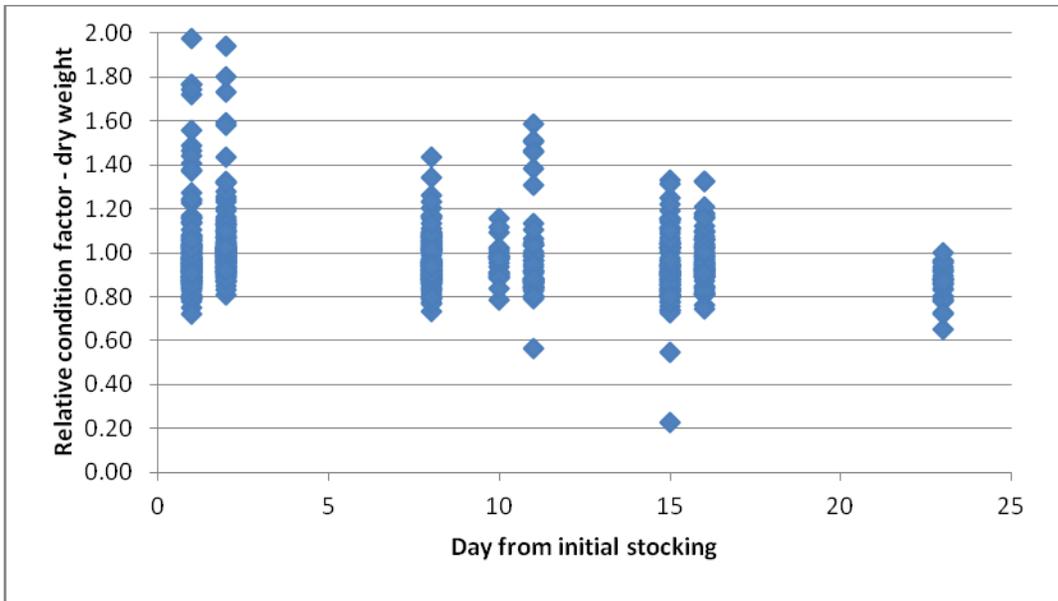


Figure 3. Variation and change in relative condition factor of striped bass juveniles stocked from May 7 through May 29, 2012.

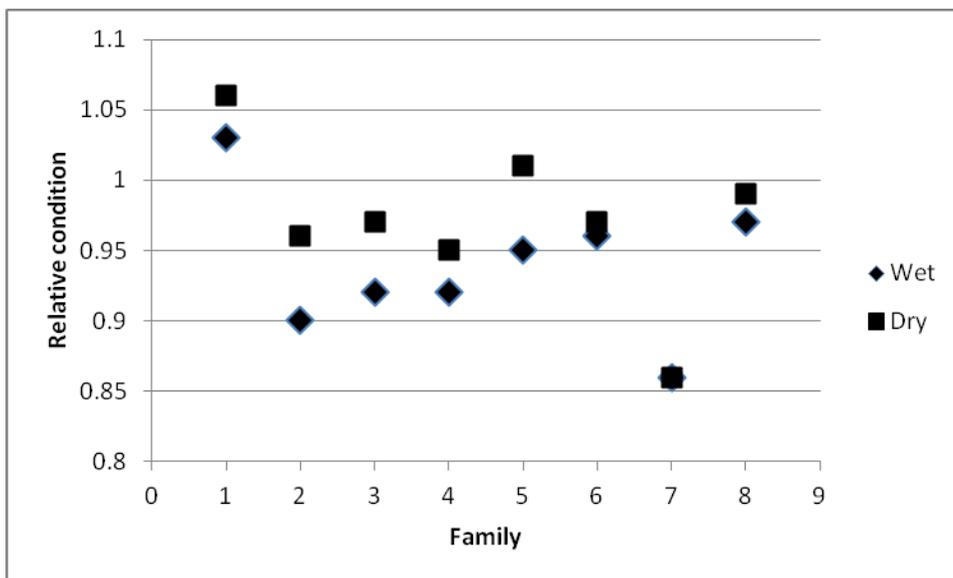


Figure 4. Average relative condition in 2012 of 8 distinct genetic families of hatchery-produced juvenile striped bass, using both wet and dry weights.

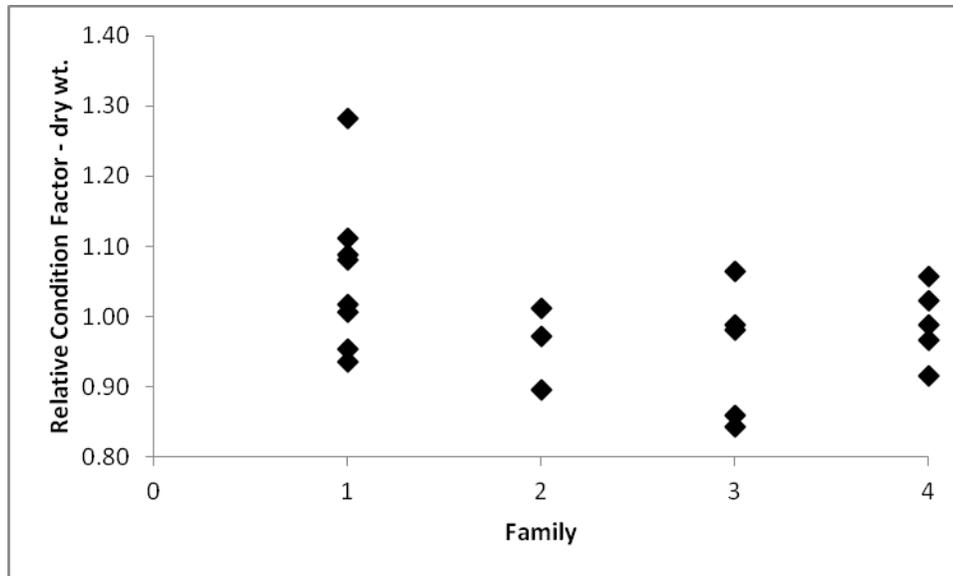


Figure 5. Variation in dry weight, relative condition factor among unique rearing ponds used to produce in the hatchery striped bass juveniles from 4 distinct genetic families.

## **Discussion**

Genetic markers now allow the evaluation of the relative stocking success of individual stocking batches. However, while genetic factors do allow a determination of times and stocking locations that produced relatively high survival for a stocking batch, there is currently not a metric that considers the condition of fish within a stocking batch. This effort attempted to define the condition of fish within a stocking batch so that its importance could also be evaluated.

However, there is substantial variation in condition of individual fish within a stocking batch that may make it difficult to assess the importance of fish condition on stocking success. For example, if a particular stocking batch had relatively high survival, one cannot determine whether that survival emanated from high or low condition fish. However, if enough samples (i.e. batches),

are stocked over several years, there may be sufficient sample size to detect the effect of condition on stocking success.

Genetic family, time of year, rearing pond, and size of stocked fish are all factors that can affect the condition of a stocked fish. In 2012, there was substantial variation in condition of fish among stocking batches, genetic family, time of year, and rearing pond. However, average condition factor of a stocking batch is metric that can, and should, be incorporated into the analysis of contribution of the various genetic families, stocking locations, and stocking times. In 2014, analysis should concentrate on incorporating the condition metric into this analysis, using a valid statistical technique that incorporates the variation in condition within each stocking batch.

### **Recommendations**

In 2014, assess the significance of average batch condition factor on stocking success during the 2011 and 2012 stocking seasons. Also, in 2014, continue to collect samples of fish from each stocking batch so the average condition - and accompanying variance - can be defined for each stocking batch. Based on current results, it appears that wet weights can be used to determine condition; use of only wet weights would reduce processing time associated with dry weight determinations; statistically consider the value of dry weight determinations for the 2011 and 2012 stocking years.

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**Job Title:** Pee Dee River Striped Bass

**Period Covered** July 1, 2012 - June 30, 2013

### **Summary**

A sample of 26 adult striped bass *Morone saxatilis* were obtained from the Pee Dee River. Fin clips were taken for genetic assessment. Genetic results will help clarify the current genetic composition of striped bass in the Pee Dee River. Additional sampling efforts are needed in the following project year.

### **Introduction**

The Pee Dee is a major South Carolina river. In South Carolina, the Pee Dee River freely flows approximately 175 miles from the North Carolina border to its junction with the Little Pee Dee River, just above Winyah Bay. Average streamflow at Pee Dee, SC, approximately 100 miles upstream from Winyah Bay, is 9,850 cubic feet per second (Snyder et al. 1983).

Striped bass are native to and naturally reproduce within the Pee Dee River, providing fishing opportunities along the entire length of the river. Historically, striped bass fingerlings from the Santee-Cooper system were intermittently stocked into this river, but this practice stopped about a decade ago when new policies required the use of endemic broodstock to supplement naturally reproducing populations.

Prior investigations have shown that the Pee Dee River has a distinct genetic signature from the Santee and ACE (Ashepoo, Combahee, and Edisto) drainages, suggesting the presence of a locally-adapted population (Bulak et al. 2004). Recently, genetic evaluations of striped bass from the Santee-Cooper lakes, Marion and Moultrie, revealed the presence of Roanoke River, NC, strain striped bass. This caused concern as managers wondered how those fish had gotten into the Santee-

Cooper system. One possible explanation was that Roanoke River striped bass stocked into the NC portion of the Pee Dee River had migrated into the SC portion and, eventually, into Santee-Cooper.

The goal of this study was to define the current genetic structure of the Pee Dee River population of striped bass. This information would help clarify whether escapement of striped bass from North Carolina was a major issue and provide guidance to possible, future hatchery augmentation efforts.

### **Materials and Methods**

Boat electrofishing was used to collect striped bass. Efforts were largely concentrated during the spring on the North Carolina portion of the Pee Dee River between the state line and Blewett Falls dam. Where possible, sampling efforts were coordinated with the North Carolina Wildlife Commission, who were conducting assessments of American shad *Alosa sapidissima* and robust redhorse *Moxostoma robustum*. Duke Energy, which operates the Blewett Falls dam, agreed to supply flows adequate for sampling, when possible. Once striped bass were captured, a fin clip was taken and placed in a preservative and the fish was then released. Also, plans were to implant a small number of striped bass with acoustic transmitters so that the location of areas where striped bass concentrate could be better understood. If transmitted striped bass migrated downstream, their acoustic signal would be picked up by acoustic receivers placed along the length of the Pee Dee River by a shortnose sturgeon *Acipenser brevirostrum* research project, conducted by the diadromous fisheries program of SC Department of Natural Resources (SCDNR).

### **Results**

A total of 26 striped bass were collected between April 18 and May 29. Total length of collected fish ranged from 551 to 780 mm, with an average of 642 mm. Fin clips were taken from all

these specimens and sent to the SCDNR genetics lab for processing. Results are expected by the end of 2013.

A total of five striped bass were implanted with acoustic transmitters on May 16. These fish ranged in total length from 595 to 780 mm. One fish immediately migrated downstream, reaching the confluence with the Little Pee Dee River (a distance of over 150 miles) on May 21, five days after it was transmitted. The fish entered the Waccamaw River and Winyah Bay on May 22 and then migrated throughout the lower reaches of the Pee Dee system through June 30.

Four of five transmitted striped bass apparently remained in the North Carolina portion of the Pee Dee River during the spring and summer of 2013, as they were not recorded on downstream receivers. Manual tracking of these four fish to confirm they were alive and pinpoint favored habitats were not attempted due to high flows during this period.

## **Discussion**

Collecting substantial numbers of striped bass during spring was difficult due to variable flows and the difficulty of navigation in the North Carolina portion of the Pee Dee River. Experience gained in 2013 should help future collection efforts.

Genetic results are expected by the end of the 2013 calendar year. These data will allow an initial glimpse at the contribution of Roanoke River, NC, and Santee River, SC fish to the Pee Dee population.

## **Recommendations**

We need to collect additional samples of striped bass from the Pee Dee River system to have an adequate sample size to determine the contribution of the three main genetic strains that we expect to find in this river. A sample size of 100 is desired. In the next year, attempts should be

made to collect samples from the downstream reaches of the Pee Dee River, in case there is a longitudinal separation of genetic types along the river's course; this sampling needs to be conducted before January 1, 2014 to avoid endangered shortnose sturgeon. Manual tracking in the North Carolina portion of the Pee Dee River is needed to assess whether the missing, four transmitted striped bass are still alive. Once initial genetic analysis is received, the results need to be discussed internally and shared with North Carolina.

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- Snyder, H.S., and 8 co-authors. 1983. *South Carolina State Water Assessment, Report No. 140*. South Carolina Water Resources Commission, Columbia, South Carolina. 367 pp.

**Job Title:** Striped Bass Fecundity - Santee-Cooper

**Period Covered** July 1, 2012 - June 30, 2013

### **Summary**

Ovary samples were obtained from female striped bass *Morone saxatilis* in 2011-2012 to histologically determine size at maturity. Results indicated that 100% of females were sexually mature at a total length of 604 mm, or 24 inches. This estimate indicates an earlier age at first maturity than was observed 20 years ago; heavy fishing pressure is suggested as a possible cause. Additional sampling is needed to confirm obtained results.

### **Introduction**

Knowledge of the maturity schedule is important when managing a reproducing population. Prior information obtained on the Santee-Cooper population of striped bass suggested that 100% of the females reached sexual maturity at age 5 (Bulak et al. 1995), though this was based on limited sampling of the population in 1990 (Bulak 1990).

Current harvest regulations were based on the premise that striped bass fully reach sexual maturity at age 5, or 26 inches in length. Current knowledge of the maturity schedule was needed.

The objective of this study was to define the current maturity schedule of Santee-Cooper striped bass.

### **Materials and Methods**

Striped bass were obtained from experimental gill nets (stretched mesh equals 2, 3, 4, 5, 6, 7, and 8 inch) fished each year in December, January, then February by Region 4 Fisheries, South Carolina Department of Natural Resources (SCDNR). In the 2011-2012 season, all collected striped

bass were sacrificed, measured (TL, mm), weighed, and sexed. Otoliths were removed to determine age. The ovaries of all females that showed any sign of sexual maturity were preserved in 10% formalin; those that showed no sign of sexual development were classified as immature. At a later time, ovaries were prepared for histological examination by the histology lab of SCNDR. Once histological preparations were prepared and dried, they were examined under the microscope to determine whether they would spawn during the coming, spring spawning season. After a maturity determination was made, a logistic regression was used to predict maturity as a function of length.

## **Results**

A total of 96 female striped bass were collected from winter gill netting on Lakes Marion and Moultrie during the December 2011 through February 2012 sampling period. Seventy-three (73) of these fish were classified as immature; their total lengths ranged from 203 to 566 mm (8 to 22 inches). Twenty-three (23) female striped bass showed signs of sexual maturity and their ovaries were removed, stored in formalin, and prepared for histological examination; total lengths of these fish ranged from 523 to 679 mm (21 to 27 inches). All ovaries examined histologically were judged to be sexually mature. Logistic regression indicated that 100% of females were mature at a total length of 604 mm (24 inches) (Figure 1).

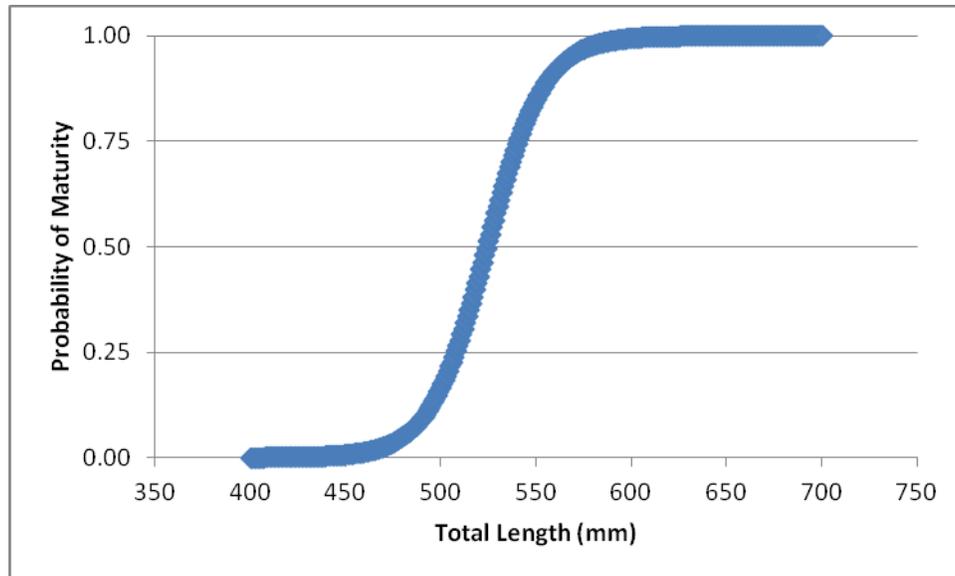


Figure 1. Logistic regression analysis of the maturity schedule of female striped bass from Lakes Marion and Moultrie, South Carolina.

## **Discussion**

Additional data is needed to confirm the results obtained from one sample year. Thus, ovary samples of all striped bass, including those macroscopically judged as immature, were obtained in winter gill netting conducted from December 2012 through February 2013. These ovaries were sent to the SCDNR histology lab. Once histological preparations are complete, the ovarian sections will be assessed for state of maturity.

Results indicated that 100% of striped bass females reached sexual maturity in 2012 at a length of 24 inches. This indicates that striped bass are reaching sexual maturity at a smaller size - and younger age - than was observed in a prior study in 1990. This new information should be incorporated into any future analysis that seeks to define an optimal harvest strategy for this population. However, it is well-documented that heavy fishing pressure can exert pressure on a

population to reach sexual maturity at a younger age (Trippel 1995, for example). Bulak (1995) estimated that a total fishing mortality of 45% between ages 2 and 4 for the Santee-Cooper striped bass population in the early 1990s. It is a reasonable hypothesis that the historic fishing pressure on Santee-Cooper striped bass has been sufficient to reduce the age at maturity of the population. Thus, future management decisions will need to debate the relative benefits of restoring the age at maturity to that observed in earlier times.

### **Recommendations**

In the coming year, process ovary samples obtained in the 2012-2013 sampling period. Combine these results with 2011-2012 data to obtain a more robust estimate of age at maturity. Examine the implications that earlier maturity may have on individual growth and population fecundity. Examine the potential effects of various fishing schedules on population fecundity.

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**Job Title:** Developing Sediment Management Guidelines to Enhance Habitat and Aquatic Resources in the Broad River Basin, South Carolina

**Period Covered** July 1, 2012 – November 6, 2013

### **Summary**

Data collection was conducted for phases of the Broad River Sediment Management study aimed at defining the relation between aquatic communities and changes in physical habitat (Objective 3 of a collaborative study with the SCDNR/South Carolina Geological Survey, “Developing Sediment Management Guidelines to Enhance Habitat and Aquatic Resources in the Broad River Basin, South Carolina”). Preliminary relationships among fish assemblage structure, stream habitat and sediment characteristics were explored for potential significance and to guide future analyses. Although data are limited at this point, results thus far suggest aquatic habitats and fish assemblage structure in streams and rivers of the Broad River basin vary in relation to substrate and sediment conditions (i.e. from anthropogenic activities, land use) in addition to natural stream features.

### **Introduction**

*Objective 3: Define the relation between aquatic communities and changes in physical habitat.*

Sedimentation is a predominant form of aquatic habitat degradation in lotic systems (Waters 1995). Many of the rivers of the South Carolina Piedmont exhibit chronic effects of sedimentation due to historic land use including widespread agriculture. In addition, acute sources such as in-stream sand mining operations may alter sediment dynamics.

The Broad River basin supports a diverse aquatic assemblage including approximately 60 fish species, or more than one third of South Carolina’s native freshwater fish fauna. Many of these

species require clean, undisturbed substrates for fulfillment of life history processes including reproduction. Shoal habitats in particular provide critical spawning grounds for many native fishes such as catostomids, yet these habitats are susceptible to excessive sediment deposition. Effective management of sediment in the Broad River basin is imperative to preserving habitat quality for sustaining these and other native aquatic species.

We aim to characterize relationships among sediment, aquatic habitat condition, and biological assemblages in the Broad River basin. Relationships will be used to develop management targets for maintaining suitable aquatic habitat and species populations in the Broad River basin.

## **Materials and Methods**

### *Relationships Among Stream Habitat, Sediment and Fish Assemblage Structure*

The major tributaries of the Broad River exhibit a wide range of sediment impacts and represent independent units in which downstream habitats are expected to reflect the cumulative influences of land uses and impacts within the watershed (e.g. sedimentation). Seven of the 11 study tributaries were sampled in spring 2013 and 10 of 11 were sampled in fall (Table 1). Unseasonably high rainfall in late spring and summer 2013 caused persisting high discharge in several of the larger streams and the main stem Broad River; these sites could not be sampled during one or more sample seasons (Table 1). Due to this reduction in spring/summer samples, all samples through 06 November 2013 were included in this report to provide a more complete summary of preliminary findings.

Sites were sampled using backpack electrofishing to assess the entire fish assemblage (species composition and relative abundance). Given the large size of most sites, fish sampling was accomplished by using 20 seine sets distributed throughout the sample section in proportion to the

Table 1. Sample sites for habitat and fish assemblage monitoring in the Broad River basin.

<b>Fish Assemblage / Habitat Assessment</b>	<b>Latitude</b>	<b>Longitude</b>	<b>Samples Completed (2013)</b>
Kings Creek	35.04313	-81.47615	Spring and Fall
Thicketty Creek	34.91475	-81.49633	Spring and Fall
Bullock Creek	34.85863	-81.45410	Spring and Fall
Turkey Creek	34.77659	-81.43230	Spring and Fall
Sandy River	34.59330	-81.39315	Spring and Fall
Duncan Creek	34.48915	-81.59143	Spring and Fall
Lawsons Fork Creek	34.94247	-81.78876	Spring and Fall
Buffalo Creek	35.12387	-81.56114	Fall Only*
Pacolet River	34.87400	-81.53132	*
Tyger River	34.53600	-81.54788	Fall Only*
Enoree River	34.50912	-81.59832	Fall Only*
Broad River (upstream of Tyger River confluence)	34.49545	-81.42275	Fall Only*
Broad River (downstream of Tyger River confluence)	34.48219	-81.42209	Fall Only*
<b>Fish Spawning / Habitat Assessment</b>	<b>Latitude</b>	<b>Longitude</b>	<b>Sample Status</b>
Kings Creek (reference/forested)	35.04313	-81.47615	Spring 2013 (6 samples)
Lawsons Fork Creek (impacted/urbanized)	34.94247	-81.78876	Spring 2013 (4 samples)
Bullock Creek	34.85863	-81.45410	Spring 2013 (1 sample)
Turkey Creek	34.77659	-81.43230	Spring 2013 (1 sample)
Broad River (upstream of Tyger River confluence; reference)	34.49545	-81.42275	Spring 2013 (2 samples)
Broad River (downstream of Tyger River confluence; impacted)	34.48219	-81.42209	Spring 2013 (2 samples)
<b>Sand Mine Assessment</b>	<b>Latitude</b>	<b>Longitude</b>	<b>Sample Status</b>
North Pacolet River (upstream of Slater Mine extraction)	35.18452	-82.08780	01 Nov 2012
North Pacolet River (downstream of Slater Mine extraction)	35.18471	-82.08370	01 Nov 2012
Tyger River (upstream of Theo Mine)	34.73447	-81.89027	09 Oct 2012

\*One or more samples could not be conducted due to persistent high flows (Figs. X-X).

amount of area represented by each habitat type (e.g. riffles/shoals, runs, pools). At each set, a 3.05-m (10-ft) seine was set at the downstream end of each habitat unit and an area of approximately 15 m<sup>2</sup> was sampled immediately upstream of the seine by a single backpack electrofisher, working all

fish downstream to the seine. A 6.10-m (20-ft) seine was used on the Broad River main stem to provide better coverage of the large shoal areas. All fish were identified and enumerated at each set, providing a measure of fish assemblage composition by habitat units as well as by site. In addition, habitat (depth, velocity and macrohabitat type) and substrate samples were obtained at each set in collaboration with SCDNR/South Carolina Geological Survey staff to provide a detailed measure of substrate and sediment characteristics of each site.

A preliminary assessment of potential relationships among habitat, sediment and fish assemblage structure was conducted. Habitat, substrate and sediment data are still being processed for most of the recent samples (e.g. fall 2013). However, to characterize potential influences of sediment on aquatic habitats and fish assemblages, available data on a range of substrate and sediment measures were obtained from the hydrogeological monitoring sites (K. Castle, SCDNR/South Carolina Geological Survey; Table 2), which are located at the fish sampling sites. Since aquatic habitats and biota may respond to both chronic and acute impacts of sedimentation, several measures of suspended sediment yield (LOADEST, SedYield and SPARROW) and deposited sediment composition (PctFine, D50) were explored. These data are preliminary and may vary slightly in time span among sites; they are used here solely to investigate potential relationships and guide future analyses. Most of the data were measured between spring/summer 2012 and summer 2013 and thus provide a reasonable representation of overarching habitat and sediment conditions among sites.

Non-metric multidimensional scaling (NMS) ordination was performed using PC-ORD (Version 5) on the fish assemblage data (abundance) from the 17 samples conducted in spring and fall 2013 to evaluate potential patterns in fish assemblage structure among samples (primary matrix). To explore relationships among fish assemblage structure and environmental, habitat and sediment characteristics, these additional measures were included as a secondary matrix in the ordination

(Table 2). Various transformations of the data were performed and the variation in fish assemblage structure among samples was examined in relation to correlations with the environmental, habitat and sediment variables.

Table 2. Environmental, habitat and sediment variables used in NMS ordination to investigate relationships among fish assemblage structure, habitat and sediment characteristics in tributaries of the Broad River, 2012-2013.

<b>Variable</b>	<b>Units</b>	<b>Definition</b>	<b>Mean</b>	<b>Range</b>
Elev	feet	Site elevation	410.6	316 – 551
LOADEST	tons/km <sup>2</sup> /yr	Modeled annual suspended sediment yield, standardized to watershed area	89.4	1.5 – 282.8
SedYield	tons/km <sup>2</sup> /yr	Observed annual suspended sediment yield, standardized to watershed area	90.1	2.5 – 235.6
SPARROW	tons/km <sup>2</sup> /yr	USGS SPARROW model annual suspended sediment yield, standardized to watershed area	157.6	103.1 – 305.8
D50	mm	Mean of all bed sample median particle diameters	1.2	0.7 – 3.3
PctFine	Percentage	Mean percentage by dry weight of fine sediment (sand $\leq$ 2 mm diameter and mud) in bed samples	78.1	42.2 – 93.0
Width	m	Mean wetted stream width	14.9	6.5 – 39.0
Depth	m	Mean water depth	0.5	0.3 – 0.6
DepthSD	m	Standard deviation of water depth	0.2	0.1 – 0.3
Veloc	m/sec	Mean current velocity, measured at 60% water depth	0.3	0.1 – 0.5
VelocSD	m/sec	Standard deviation of current velocity	0.2	0.1 – 0.3
Cond	$\mu$ S/cm	Conductivity	100.1	67 – 168

### *Evaluation of Fish Spawning Habitat Use in Relation to Substrate and Sediment Composition*

Sites possessing shoal habitats of contrasting expected sediment impacts were sampled at regular intervals during the fish spawning season on two tributaries of the Broad River, Kings Creek (forested watershed; low sediment impact) and Lawson's Fork Creek (urbanized watershed; high sediment impact). Aside from land use and sediment load, these streams are similar in drainage area (Kings = 175 km<sup>2</sup>; Lawsons Fork = 216 km<sup>2</sup>), size, elevation (Kings = 517 ft; Lawsons Fork = 551 ft) and support many of the same shoal/riffle-spawning fish species. However, Lawsons Fork Creek exhibits a disproportionately high observed and modeled sediment yield relative to its drainage area (193.5 tons/km<sup>2</sup>/yr observed) whereas Kings Creek is considerably lower (3.3 tons/km<sup>2</sup>/yr observed; K. Castle, SCDNR/South Carolina Geological Survey, pers. comm.). In addition to these tributaries, sites were sampled on the Broad River main stem upstream (reference) and downstream (impacted) of the confluence with the Tyger River, one of the major sources of sediment entering the Broad River.

With two exceptions, Kings Creek and Lawson's Fork Creek were both sampled on 23 April, 2 May, 10 May, 14 May, 21 May, and 30 May 2013. Lawson's Fork Creek was not sampled on 10 May 2013 (high flow) or 30 May 2013 (wastewater spill on 27 May 2013). Mean water temperature for Kings Creek during this period was 17.3 C (range 12.8 – 23.1 C) and mean temperature for Lawson's Fork Creek was 17.9 C (range 13.4 – 23.1 C). The Broad River upstream and downstream of the Tyger River was sampled on 17 April and 26 April 2013 but frequent rains beginning in early May 2013 caused discharge to remain too high for additional sampling (i.e. >3,000 cfs at Carlisle gauge). Shoals were sampled using a 0.09 m<sup>2</sup> (1 ft<sup>2</sup>) Surber sampler (Wildlife Supply Company, Inc., Yulee, FL, USA) at 10 – 20 sets (depending on shoal size) across one to two transects spanning each study shoal. The Surber sampler bag mesh and collection cylinder screen

mesh size were 500  $\mu\text{m}$ . At each set, the substrate within the sampler area was disturbed by hand for 20 seconds and to a substrate depth of no greater than 5 cm or the maximum possible depth if less than 5 cm. All material collected in the bag and cylinder was preserved in 5% formalin for laboratory examination for fish eggs, larvae and macroinvertebrates. Important habitat features including depth, current velocity, substrate composition and particle size distribution were measured at each collection point to facilitate an assessment of spawning in relation to habitat condition.

#### *Influence of Sand Mining on Local Habitat, Sediment and Fish Assemblage Structure*

The potential local impacts of sand mining on stream habitat and fish assemblage composition were examined at two sites bracketing an active sand mining operation on the North Pacolet River in the Broad River basin. The sand mining operation consisted of an approximately 250-m-long sand extraction zone within which a barge is used to vacuum substrate, which is then sorted to extract sand of various sizes. Extracted water was continuously returned to the river at the downstream end of the extraction zone. To assess potential local influences of this operation on adjacent habitats and fish assemblages, one sample site was selected immediately upstream of the extraction zone and another site was selected immediately downstream of the extraction reach. Sites were sampled using backpack electrofishing to assess the entire fish assemblage (species composition and relative abundance) in identical fashion to the tributaries as explained previously. In addition, habitat (depth, velocity and macrohabitat type) and substrate samples were obtained at each fish collection location in collaboration with SCDNR/South Carolina Geological Survey staff to provide a detailed measure of substrate and sediment characteristics of each site.

## **Results**

### *Relationships Among Stream Habitat, Sediment and Fish Assemblage Structure*

Forty (40) species of fish were collected altogether among the Broad River tributary monitoring sites in spring and fall 2013 (Table 3). Fish species richness among tributary samples averaged 15.2 and ranged from six (Tyger River, fall 2013) to 20 (Kings Creek and Thicketty Creek, spring 2013 and Sandy River, fall 2013). The most abundant species overall were *Hybognathus regius* (Eastern Silvery Minnow), *Cyprinella nivea* (Whitefin Shiner) and *Cyprinella chloristia* (Greenfin Shiner; Table 3). Species occurring in the most samples were *C. nivea* (all samples), *Notropis scepticus* (Sandbar Shiner) and *Lepomis auritus* (Redbreast Sunfish).

With all 17 samples included, NMS ordination showed a pattern in fish assemblage structure among samples that was more pronounced than expected by chance (Monte Carlo test,  $P = 0.004$ ; final stress = 11.80). About 88% of the total variation in fish assemblage structure among samples was represented by two dimensions in NMS, with Axis 2 representing the majority of variation (51%) and Axis 1 representing about 37% (Figure 1).

Correlations among environmental (including habitat and sediment) variables and the primary ordination axes indicated that fish assemblage structure varied in relation to both environmental/site characteristics and habitat/sediment conditions (Table 4). Variables associated most strongly with Axis 2 included mean width, mean depth and the SPARROW-modeled suspended sediment yield (Kendall's tau; Table 4). Variables associated most strongly with Axis 1 were mean velocity, site elevation, d50 (median bed particle size) and percent fine bed material.

Table 3. Fish species collected at 10 tributary monitoring sites in the Broad River basin, 2013. Presence and abundance data are totals including both spring (7) and fall (10) samples. Sites are listed in Table 1 in Methods.

Code	Scientific Name	Common Name	Samples	Total Catch	Relative Abundance
WHS	<i>Catostomus commersoni</i>	White Sucker	1	1	0.03%
CCS	<i>Erimyzon oblongus</i>	Creek Chubsucker	1	1	0.03%
NHS	<i>Hypentelium nigricans</i>	Northern Hogsucker	9	29	0.80%
NLR	<i>Moxostoma collapsum</i>	Notchlip Redhorse	1	1	0.03%
VLR	<i>Moxostoma pappillosum</i>	V-lip Redhorse	1	1	0.03%
STJ	<i>Scartomyzon rupiscartes</i>	Striped Jumprock	8	27	0.75%
BJR	<i>Scartomyzon sp.</i>	Brassy Jumprock	2	4	0.11%
FLR	<i>Centrarchus macropterus</i>	Flier	2	5	0.14%
RBS	<i>Lepomis auritus</i>	Redbreast Sunfish	16	162	4.48%
GSF	<i>Lepomis cyanellus</i>	Green Sunfish	6	14	0.39%
PPS	<i>Lepomis gibbosus</i>	Pumpkinseed	2	5	0.14%
BLG	<i>Lepomis macrochirus</i>	Bluegill	10	38	1.05%
RES	<i>Lepomis microlophus</i>	Redear Sunfish	1	2	0.06%
SMB	<i>Micropterus dolomieu</i>	Smallmouth Bass	4	5	0.14%
LMB	<i>Micropterus salmoides</i>	Largemouth Bass	5	7	0.19%
BLC	<i>Pomoxis nigromaculatus</i>	Black Crappie	1	2	0.06%
RSD	<i>Clinostomus funduloides</i>	Rosyside Dace	1	1	0.03%
GFS	<i>Cyprinella chloristia</i>	Greenfin Shiner	15	373	10.32%
TLC	<i>Cyprinella labrosa</i>	Thicklip Chub	6	16	0.44%
WFS	<i>Cyprinella nivea</i>	Whitefin Shiner	17	468	12.95%
STC	<i>Cyprinella zanema</i>	Santee Chub	10	85	2.35%
ESM	<i>Hybognathus regius</i>	Eastern Silvery Minnow	12	938	25.96%
HBC	<i>Hybopsis hypsinotus</i>	Highback Chub	2	2	0.06%
BHC	<i>Nocomis leptcephalus</i>	Bluehead Chub	14	354	9.80%
GHS	<i>Notropis chlorocephalus</i>	Greenhead Shiner	7	15	0.42%
STS	<i>Notropis hudsonius</i>	Spottail Shiner	14	184	5.09%
SWS	<i>Notropis procne</i>	Swallowtail Shiner	7	96	2.66%
SBS	<i>Notropis szepticus</i>	Sandbar Shiner	16	348	9.63%
SBH	<i>Ameiurus brunneus</i>	Snail Bullhead	5	11	0.30%
WCF	<i>Ameiurus catus</i>	White Catfish	1	3	0.08%
FBH	<i>Ameiurus platycephalus</i>	Flat Bullhead	5	7	0.19%
CCF	<i>Ictalurus punctatus</i>	Channel Catfish	3	6	0.17%
MGM	<i>Noturus insignis</i>	Margined Madtom	9	74	2.05%
FCF	<i>Pylodictis olivaris</i>	Flathead Catfish	1	1	0.03%
FTD	<i>Etheostoma brevispinum</i>	Carolina Fantail Darter	2	15	0.42%
SWD	<i>Etheostoma fusiforme</i>	Swamp Darter	1	1	0.03%
TSD	<i>Etheostoma olmstedii</i>	Tessellated Darter	13	170	4.71%
SGD	<i>Etheostoma thalassinum</i>	Seagreen Darter	11	98	2.71%
PDD	<i>Percina crassa</i>	Piedmont Darter	13	36	1.00%
MSQ	<i>Gambusia holbrooki</i>	Eastern Mosquitofish	4	7	0.19%

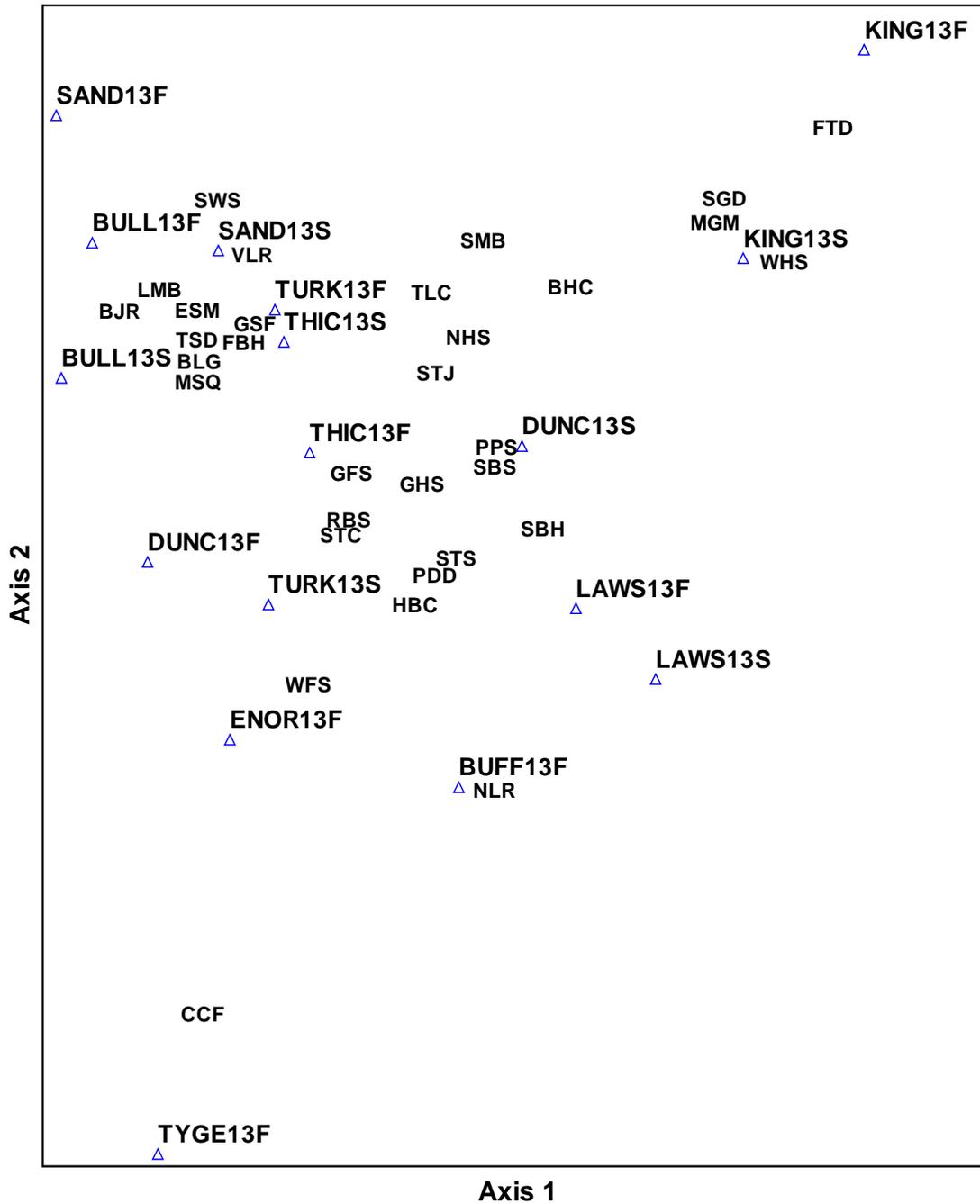


Figure 1. NMS ordination plot of 17 Broad River tributary samples. Sample labels show the first four letters of the site followed by the year (13) and season (S = spring; F = fall). Species are shown as three-letter codes (refer to Table 3). Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%.

Table 4. Correlations among environmental, habitat and sediment variables and fish assemblage structure with all 17 tributary samples included. Axis 2 represented the majority of variation in fish assemblage structure (51%) and Axis 1 represented an additional 37%. Variables are defined in Table 2.

	AXIS 1		AXIS 2	
	r	tau	r	tau
Elev	0.719	0.434	0.016	0.008
LOADEST	-0.197	-0.023	-0.190	-0.189
SedYield	-0.054	0.038	-0.453	-0.249
SPARROW	0.287	0.264	-0.516	-0.506
D50mm	0.723	0.385	0.443	0.219
PctFine	-0.666	-0.385	-0.457	-0.249
Width	-0.190	0.015	-0.772	-0.515
Depth	-0.045	0.075	-0.738	-0.508
DepthSD	-0.063	-0.008	0.412	0.219
Veloc	0.596	0.444	-0.461	-0.385
VelocSD	0.485	0.367	0.040	-0.112
Cond	-0.108	0.000	0.593	0.400

Based on the initial ordination, general site characteristics including mean width and depth were playing a large role in the variation in fish assemblage structure among samples. Examination of these variables showed an apparent disproportionate influence of two much larger sites, Enoree River (mean width = 31.4 m) and Tyger River (39.0 m), on the ordination. The mean width of all other sample sites was 12.2 m and none exceeded 18.4 m. To reduce the influence of these two significantly larger sites on the ordination, a second run was performed excluding the Enoree River and Tyger River.

With 15 samples (Enoree and Tyger excluded), NMS ordination in three dimensions represented about 95% of the total variation in fish assemblage structure among samples (Monte

Carlo test,  $P = 0.004$ ; final stress = 6.36). Axis 1 represented the majority of the variation (56%), with Axes 2 and 3 representing about 18% and 21%, respectively.

Correlations among environmental (including habitat and sediment) variables and the primary ordination axes again suggested that fish assemblage structure varied in relation to both environmental/site characteristics and habitat/sediment conditions (Table 5). Variables associated most strongly with Axis 1 (Kendall's tau) included mean velocity, d50 (median bed particle size) and percent fine bed material (Table 5). Variables most strongly associated with Axis 3 were SPARROW-modeled suspended sediment yield, elevation, LOADEST-modeled sediment yield and observed suspended sediment yield.

Table 5. Correlations among environmental, habitat and sediment variables and fish assemblage structure for 15 tributary samples (Enoree and Tyger excluded). Axis 1 represented the majority of variation in fish assemblage structure (56%), Axis 3 about 21% and Axis 2 about 18%. Variables are defined in Table 2.

	AXIS 1		AXIS 2		AXIS 3	
	r	tau	r	tau	r	tau
Elev	0.659	0.353	0.585	0.373	0.401	0.255
LOADEST	-0.136	-0.157	-0.128	0.177	-0.347	-0.177
SedYield	0.070	-0.078	0.217	0.255	-0.266	-0.177
SPARROW	0.411	0.314	0.531	0.255	-0.360	-0.490
D50mm	0.639	0.471	-0.409	-0.137	0.599	-0.020
PctFine	-0.612	-0.432	0.438	0.177	-0.468	0.098
Width	0.133	0.067	0.421	0.410	-0.181	-0.124
Depth	0.172	0.105	0.540	0.392	-0.187	-0.105
DepthSD	-0.215	-0.156	-0.295	-0.234	0.076	-0.020
Veloc	0.754	0.587	0.210	0.125	0.012	-0.067
VelocSD	0.502	0.332	0.225	0.254	0.021	-0.039
Cond	-0.331	-0.125	-0.557	-0.490	0.132	0.067

*Evaluation of Fish Spawning Habitat Use in Relation to Substrate and Sediment Composition*

Apparent fish eggs and larvae were collected on multiple dates at Kings Creek and Lawson’s Fork Creek (Table 6). Apparent fish eggs and larvae were collected from the Broad River immediately upstream of the confluence with the Tyger River and an apparent fish larva was collected from the Broad River downstream of the Tyger River. These specimens will be further examined and identified to the finest taxonomic level possible through consultation with experts. Once identifications are complete, differences in the presence, abundance and taxonomy of fish eggs and larvae among sites will be analyzed in relation to habitat/substrate, temperature and sediment levels. Shoals receiving and exhibiting greater quantities of fine sediment are expected to provide less suitable spawning habitat for certain fish species including rock/crevice spawners.

Table 6. Preliminary results for fish egg and larva collections at study sites in the Broad River basin. Confirmation of fish origin and taxonomic identification are pending.

Date (2013)	Surber Sets	Kings Creek		Lawson’s Fork Creek	
		Eggs	Larvae	Eggs	Larvae
23-Apr	10	0	0	1	1
2-May	10	3	0	0	0
10-May	10	0	0	No Sample	
14-May	10	2	0	1	0
21-May	10	8	0	0	1
30-May	10	0	2	No Sample	
<b>Total</b>		<b>13</b>	<b>2</b>	<b>2</b>	<b>2</b>

Date (2013)	Surber Sets	Broad River – Upstream of Tyger Confluence		Broad River – Downstream of Tyger Confluence	
		Eggs	Larvae	Eggs	Larvae
17-Apr	10	5	3	0	0
26-Apr	15	12	0	0	1
No additional samples conducted (high flows)					
<b>Total</b>		<b>17</b>	<b>3</b>	<b>0</b>	<b>1</b>

*Influence of Sand Mining on Local Habitat, Sediment and Fish Assemblage Structure*

Sixteen species were collected altogether in fall 2012 and fall 2013 from the North Pacolet River adjacent to the active sand mine (Table 7). Species richness ranged from 8 (downstream, fall 2013) to 10 (upstream, fall 2013). Analyses investigating differences between up- and downstream sites within and across sample periods and how these may be influenced by sand mining will continue.

Table 7. Species abundance by sample for sites upstream versus downstream of an active sand mine on the North Pacolet River, Fall 2012 and Fall 2013.

	01 November 2012		29 October 2013	
	Downstream	Upstream	Downstream	Upstream
White Sucker	0	1	0	0
Notchlip Redhorse	0	0	2	0
Brassy Jumprock	0	0	3	0
Redbreast Sunfish	13	4	8	7
Warmouth	1	0	0	0
Bluegill	1	0	10	3
Largemouth Bass	0	1	0	0
Greenfin Shiner	63	145	1	31
Santee Chub	22	25	21	14
Bluehead Chub	19	63	13	12
Greenhead Shiner	0	14	0	1
Sandbar Shiner	0	8	0	0
Flat Bullhead	0	0	0	2
Margined Madtom	7	3	2	6
Seagreen Darter	1	0	0	1
Eastern Mosquitofish	11	0	0	1
<b>Species Richness</b>	<b>9</b>	<b>9</b>	<b>8</b>	<b>10</b>
<b>Total Fish</b>	<b>138</b>	<b>264</b>	<b>60</b>	<b>78</b>

## **Discussion**

In this analysis, fish assemblage structure varied in relation to a combination of natural site features (e.g. mean width, current velocity and elevation) and sediment-related conditions (e.g. d50, percent fine bed material and suspended sediment yield). The strength and direction of these relationships will be investigated further as more data become available. Because sedimentation of streams is largely related to land use and management practices, the existence of potential relationships between these measures and fish assemblage structure suggests that sediment control measures may have measurable conservation value for aquatic habitats and species in the Broad River basin.

## **Recommendations**

Continue analyses with updated habitat, substrate and sediment data. Examine relative influence of anthropogenic sediment impacts versus natural conditions on fish assemblage structure and aquatic habitat conditions in the basin. Examine responses to changes in aquatic habitat and sedimentation among fish species, taxonomic and functional groups, including thresholds in habitat / sediment conditions at which populations or groups exhibit significant decline. Incorporate findings into management targets to reduce negative impacts of sedimentation on aquatic habitats and species in the Broad River basin.

## **Literature Cited**

Waters, T. F. 1995. Sediment in streams: sources, biological effects, and control. American Fisheries Society Monograph 7.

Prepared By: Kevin Kubach

Title: Fisheries Biologist

**Job Title:** South Carolina Stream Assessment

**Period Covered** July 1, 2012 – June 30, 2013

**Summary**

We continued analyzing and compiling South Carolina Stream Assessment data for a forthcoming completion report summarizing estimates of stream conditions across the state. Yearly summaries of Stream Assessment activity can be found in prior annual reports for Freshwater Fisheries Research (2006 – 2012).

Prepared By: Kevin Kubach

Title: Fisheries Biologist

**Job Title:** South Carolina Stream Conservation Planning Tool

**Period Covered** July 1 2012 - June 30, 2013

### **Summary**

Identifying and communicating the relationships between natural gradients, human activities, and aquatic habitat integrity is crucial to aquatic conservation. The South Carolina Department of Natural Resources (SCDNR), in conjunction with Clemson University, has developed a novel web-based South Carolina Stream Conservation Planning Tool that enables a spatially explicit understanding of how human activities affect the biological condition of wadeable streams, intended to support decisions about aquatic conservation actions. The web mapping application communicates findings from the South Carolina Stream Assessment (SCSA) to a broad audience, allowing users to visualize predicted biological conditions based on their status and severity across all South Carolina wadeable stream catchments. Additionally, an interactive catchment management tool allows users to explore and forecast the impacts of customized land management scenarios on aquatic resource indicators at any user-specified location across South Carolina, and so engages users in the process of modeling and forecasting stream conditions.

We selected stream condition metrics from over 200 measurements taken at approximately 700 streams locations sampled during the SCSA from 2006 to 2011. Metrics were related to spatial predictor data created under the National Fish Habitat Assessment. We generated prediction models using the Random Forest machine-learning technique from the sample data, and applied the predictions to the entire population of wadeable stream reaches in the state. The mapping application provides users with a browser-based interface to modify predictors at the catchment (local) scale. A web service dynamically generates predictions based on these user inputs, and

results are mapped at watershed (network) scales to display cumulative effects of the changes. The dynamic execution of models broadens the utility of the application and opens the forecasting process to a non-technical audience. By providing an accessible means of forecasting the effects of management decisions, the tool encourages a watershed perspective towards aquatic conservation. The application is targeted to stakeholders at the policy making and conservation planning levels. The approach described has been set up for South Carolina but is applicable to assessment programs at the regional and national levels.

## **Introduction**

The project described here is conceptually rooted in a watershed perspective that recognizes the pervasive nature of cumulative impacts to our waterways, recognizing that a landscape approach is critical to successful aquatic conservation efforts. Fishery and aquatic scientists often assess habitats to understand the distribution, status, stressors, and relative abundance of aquatic resources. Due to the spatial nature of aquatic habitats and the increasing scope of management concerns, using traditional analytical methods for assessment is often difficult. However, advancements in the geographic information systems (GIS) field and related technologies have enabled scientists and managers to more effectively collate, archive, display, analyze, and model spatial and temporal data. For example, spatially explicit habitat assessment models allow for a more robust interpretation of many terrestrial and aquatic datasets, including physical and biological monitoring data, habitat diversity, watershed characteristics, and socioeconomic parameters. The geospatial data produced as a result of this project proposal are intended to enable a unique, broad, and spatially explicit understanding of the links between natural habitat conditions, human influences on aquatic habitats, and aquatic ecosystem integrity. The ultimate goal is to improve understanding of how local and

regional processes influence stream conditions in the state and to provide SCDNR with additional knowledge, data, and tools to help prioritize and drive conservation planning and action.

### *The South Carolina Stream Assessment*

The Southeastern U.S. is rich in aquatic biodiversity, but has been suffering long-term declines in native aquatic species, particularly those sensitive to environmental change. The South Carolina Department of Natural Resources (SCDNR) has described over 125 species of fish, herpetofauna (i.e. reptiles and amphibians), mussels, crayfish, and snails that are directly dependent on aquatic systems for some or all of their life-stages as state priority species of conservation concern (SCDNR 2005). The most pervasive threats to aquatic species biodiversity are instream habitat alteration, pollution from point and nonpoint sources, and population fragmentation due to loss of hydrologic connectivity. Such threats to aquatic habitats and biological communities commonly manifest as a repercussion of human-induced landscape disturbances.

In response to concerns over declines in aquatic biodiversity, the South Carolina Department of Natural Resources in conjunction with Clemson University initiated the South Carolina Stream Assessment (SCSA) in 2006 (Scott 2008). An assessment of nearly 500 wadeable streams was completed in 2011, with a collection of biological, chemical, and physical data necessary to support proactive decision making with respect to aquatic resources in the state (Figure 1). The SCSA employs two methods of site selection for data collection. One method established long-term annual monitoring of 85 streams in least-impacted watersheds. This method is intended to provide expected aquatic resource conditions for comparative purposes as well as range due to temporal variability. The second method employs a probabilistic or random-design stream sampling program designed to provide unbiased estimates of aquatic resources throughout the state at various spatial scales. Sample reaches are selected with a known probability from a list frame of all 100 m stream segments

in the state that drain catchments 4-150 km<sup>2</sup> in size. Sample locations are stratified and allocated proportionally by ecobasin (a unique combination of EPA level IV ecobasin and major drainage basin), and by stream size. This site selection procedure ensures independence among samples and allowed for statistically defensible estimates of statewide aquatic resource parameters.

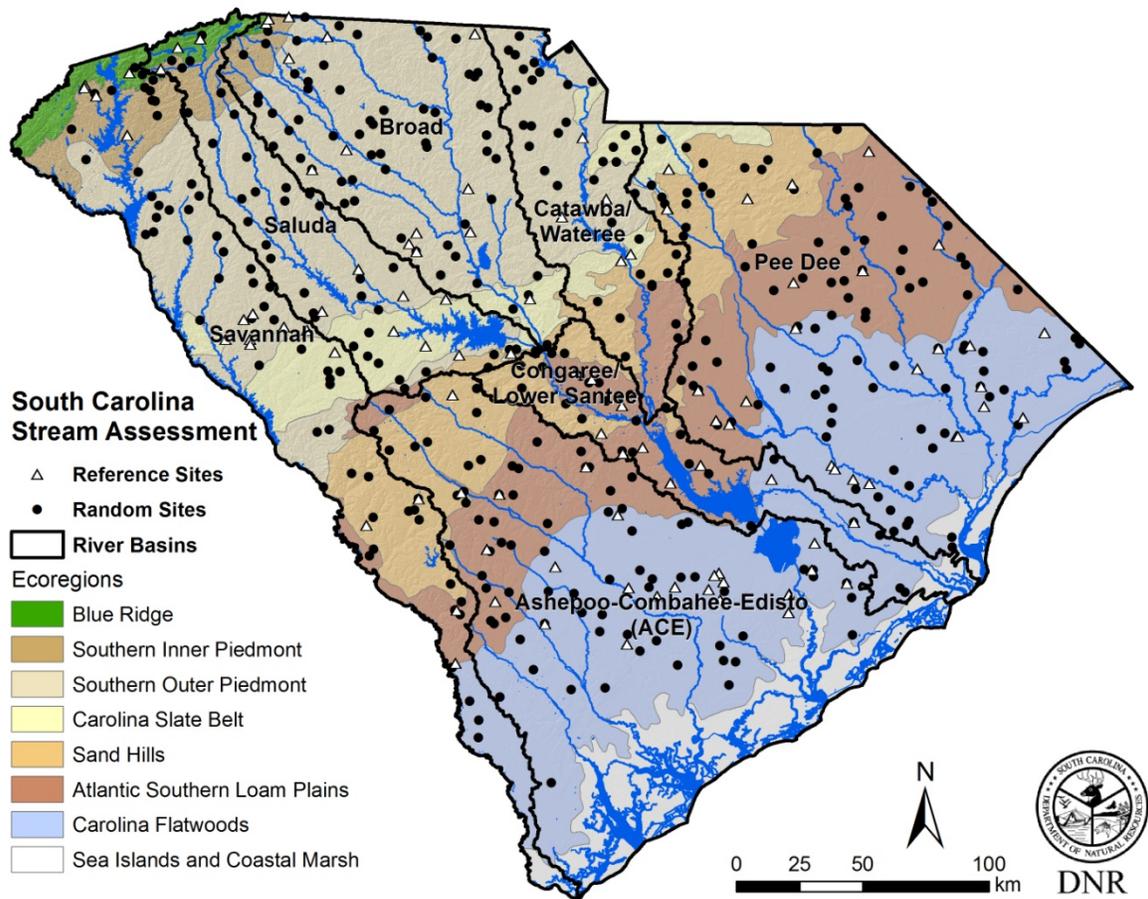


Figure 1. SC Stream Assessment sample locations apportioned among major river basins and EPA level IV ecoregions.

The South Carolina Stream Assessment provided data necessary to support proactive decision-making with respect to aquatic resources in the state. A reversal of the decline of native species requires an explicit understanding of the interconnected relationship between land and water, and the identification of the landscape features that are critical for maintenance of aquatic habitats capable of supporting sensitive species. The overall goals of our data analyses were to understand how aquatic resources and species compositions naturally vary across the landscape, evaluate how human-induced landscape activities alter aquatic resources and species compositions, and develop ecological forecasts of current aquatic resource compositions and species compositions for any given watershed in the state. Modeling such relationships with known confidence is critical to proactive management and sustainability of South Carolina's aquatic resources.

## **Materials and Methods**

### *Data Description*

Our statistical modeling approach is conceptually rooted in a watershed perspective that recognizes links between landscape activities and stream condition; the quality of water and aquatic habitats reflect the condition of the uplands drained by the stream. Streams integrate the entire drainage area due to the cumulative nature of hydrologic systems, with the consequences of poor landscape practices (e.g. urbanization, excessive nutrients, pollutant discharges) eventually impacting the waterbodies of the state. Nearly 80% South Carolina's landscape drains to a wadeable stream, indicating the ubiquitous need for landscape-based conservation management consideration.

Our Conservation Planning Tool is based on predictive statistical models developed using our robust South Carolina Stream Assessment data collection. We utilize two primary data inputs in our statistical modeling process: response variables and predictor variables. Response variables are

either biological indicators (e.g., species richness, % conservation priority species, etc.), or physical outcomes (e.g., % large wood, average velocity, temperature, etc.) whose values are dependent on an interacting suite of predictor variables (e.g., elevation, slope, drainage area, land use categories, etc.). Response variables are derived from South Carolina Stream Assessment data collections. Predictor variables are derived from an assessment and geodatabase (Wang et al. 2011) made under the National Fish Habitat Action Plan (NFHAP).

The first step of our modeling process involves selection of aquatic resource condition response variables. This may represent the occurrence of a particular species, habitat feature, or water quality parameter of interest, or the development of biological and habitat metrics that best indicate healthy versus altered aquatic habitats. Examples of potential response variables include fish species richness, conservation priority species density, American Eel *Anguilla Rostrata* presence, large wood occurrence, average velocity, etc. Response variables can be categorical or continuous, although we suggest that model fit and interpretation are both improved by the development of categorical response variables (e.g. low, intermediate, high). We developed biological and aquatic indicators unique to either the upstate or coastal plain, because taxa distributions and aquatic habitats vary greatly between the two geographic regions.

The NFHAP hierarchical spatial framework and database provides spatial predictor data for catchments across the entire state, thereby enabling us to both maintain our watershed-based analysis approach and meet our objective of extrapolating our models across unsampled areas of the state. The NFHAP spatial framework and database was created using the National Hydrography Dataset Plus v.1 (NHDPlus). The NHDPlus is a vector dataset describing hydrological networks and associated catchment spatial characteristics at a spatial scale of 1:100,000. The smallest basic spatial unit of the NHD+ are fluvial networks represented by confluence to confluence stream reaches

(flowlines; Figure 2). Within the NFHAP database, each flowline is attributed with predictor data at two spatial levels: 1) local catchment spatial attributes, and 2) network catchments spatial attributes (Figure 2). Local catchments are defined as the elevation-derived drainage boundary that has a 1:1 relation to a given NHD+ flowline. Network catchments are defined as the cumulative aggregation of local catchments that represent the entire upstream drainage boundary for a given NHDPlus flowline. Spatial predictor data attributed to each level includes a series of catchment-natural (physical) and human-disturbance factors that are known to influence stream characteristics and biota (Table 1).

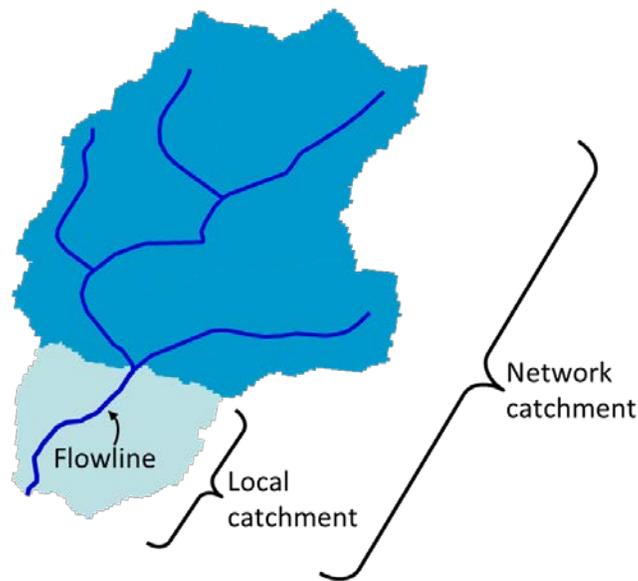


Figure 2. NHDPlus flowlines and associated local catchments. The NFHAP database additionally attributes flowlines with network catchment spatial data.

Table 1. NFHAP database spatial predictor variables included in random forests models.

Predictor Variable	Coverage	Type	Description	Units	Source	Production	Source Scale/Resolution	Currentness
COMID	N/A	ID	Unique feature identifier	N/A	NHDPlus	NFHAP	1:100,000	2005
AREASQKM	CATCHMENT	Physical	Local catchment area	square kilometers	NHDPlus	NFHAP	1:100,000	2005
AreasqkmC	CATCHMENT	Physical	Network catchment area	square kilometers	NHDPlus	NFHAP	1:100,000	2005
Barr_coC	CATCHMENT	Human Disturbance	Number of barriers (pbstrctions for fish passage both natural and nonnatural)	count	USFWS Fish Passage Decision Support System Barrier Dataset	NFHAP	N/A	2002
Dam_coC	CATCHMENT	Human Disturbance	Number of dams	count	USACE National Inventory of Dams	NFHAP	N/A	2002-2004
Road_crC	CATCHMENT	Human Disturbance	Number of road crossings	count	US Census 2000	NFHAP	1:100,000	2000
Road_lenC	CATCHMENT	Human Disturbance	Length of roads in network catchment	meters	US Census 2000	NFHAP	1:100,000	2000
Epa_303dC	CATCHMENT	Human Disturbance	Length of streams in Section 303(d) Listed Waters	meters	EPA	NFHAP	1:100,000	2002
PcsC	CATCHMENT	Human Disturbance	Number of sites from the National Pollutant Discharge Elimination System (NPDES) Majors from the Permit Compliance System (PCS)	count	EPA	NFHAP	N/A	2007
Tric	CATCHMENT	Human Disturbance	Number of sites from the Toxics Release Inventory (TRI) Program	count	EPA	NFHAP	N/A	2007
ImpervC	CATCHMENT	Human Disturbance	Percentage of impervious surfaces	%	NLCD 2001	NFHAP	30 meter grid cell	2001
PopdensC	CATCHMENT	Human Disturbance	Population density	population density per km <sup>2</sup>	NOAA	NFHAP	1 kilometer grid cell	2000
Mine_coC	CATCHMENT	Human Disturbance	Number of mines or mineral processing plants	count	USGS MIT	NFHAP	N/A	2003
C_H2O_01	CATCHMENT	Physical	Open Water (NLCD 11)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_URBAN_01	CATCHMENT	Human Disturbance	Developed: Open Space, Low Intensity, Medium Intensity, and High Intensity (NLCD: 21,22,23,24)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_BARREN_01	CATCHMENT	Physical	Barren Land (NLCD 31)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_FOREST_01	CATCHMENT	Physical	Deciduous, Evergreen, and Mixed Forest (NLCD: 41,42,43)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_GRASSHRUB_01	CATCHMENT	Physical/Human Disturbance	Shrub/Scrub, Grassland/Herbaceous (NLCD: 52,71)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_AGRICULTURE_01	CATCHMENT	Human Disturbance	Cultivated Crops, Pasture/Hay (NLCD: 81,82)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_WETLAND_01	CATCHMENT	Physical	Woody Wetlands, Emergent Herbaceous Wetlands (NLCD: 90,95)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_DECIDUOUS_01	CATCHMENT	Physical	Deciduous Forest (NLCD: 41)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_EVERGREEN_01	CATCHMENT	Physical/Human Disturbance	Evergreen Forest (NLCD: 42)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
C_ROWCRP_01	CATCHMENT	Human Disturbance	Cultivated Crops (NLCD: 82)	%	NLCD 2001	SCDNR	30 meter grid cell	2001
LENGTHKM	LOCAL	Physical	Reach length	kilometers	NHDPlus	NFHAP	1:100,000	2005
LengthkmC	CATCHMENT	Physical	Reach length	kilometers	NHDPlus	NFHAP	1:100,000	2005
SLOPE	LOCAL	Physical	Mean watershed slope	degrees	NED	NFHAP	30 meter grid cell	2004
SlopeC	CATCHMENT	Physical	Mean watershed slope	degrees	NED	NFHAP	30 meter grid cell	2004
SOILHYGRP	LOCAL	Physical	Mean soil index variable * 10.	soil index variable * 10	STATSGO	NFHAP	1:250,000	1995
SoilhygC	CATCHMENT	Physical	Mean soil index variable * 10.	soil index variable * 10	STATSGO	NFHAP	1:250,000	1995
SOILPERM	LOCAL	Physical	Permeability rates (inches/hour) * 100	inches/hour * 100	STATSGO	NFHAP	1:250,000	1995
SoilpermC	CATCHMENT	Physical	Permeability rates (inches/hour) * 100	inches/hour * 100	STATSGO	NFHAP	1:250,000	1995
ELEV_MEAN	LOCAL	Physical	Mean elevation	centimeters	NED	NFHAP	30 meter grid cell	2004
Ele_meanC	CATCHMENT	Physical	Mean elevation	centimeters	NED	NFHAP	30 meter grid cell	2004
Elev_maxC	CATCHMENT	Physical	Maximum elevation	centimeters	NED	NFHAP	30 meter grid cell	2004
CanopyC	CATCHMENT	Physical	Percentage of tree canopy	%	NLCD 2001	NFHAP	30 meter grid cell	2001
PRECIP	CATCHMENT	Physical	Mean annual precipitation	mm	PRISM	NHD+	4 km grid cell	1960-1990
TEMP	CATCHMENT	Physical	Mean annual air temperature	degrees centigrade * 10	PRISM	NHD+	4 km grid cell	1960-1990

### *Random Forests*

We used classification Random Forests (RF) analysis on our ‘training’ data set to explore associations among SCSA response variables and NFHAP spatial predictor variables (Breiman 2001, Cutler et al. 2007). Machine learning techniques such as RF provide an alternative modeling paradigm to traditional statistics, where no a priori model is defined, and complex data structures (e.g., non-normal distributions, nonlinearity, interactions) are accommodated. Machine learning techniques use an algorithm to learn the relationship between the response and its predictors by identifying dominant patterns in the dataset (Breiman 2001, Elith et al. 2008). Random Forests represent an advance in machine learning techniques that have increased the accuracy and prediction power of single classification and regression trees by the creation of an ensemble of trees (Breiman 2001). Random forests are non-parametric, can handle both categorical and continuous data as either predictor and/or response variables, can handle high-order interactions, are insensitive to outliers, and can accommodate missing data by using surrogates (Breiman 2001, De’ath and Fabricius 2000, Urban 2002). Categorical Random Forests fit an ensemble of trees to a dataset, where each individual tree in the forest is built using a randomly selected bootstrap sample of the training dataset. In addition, only a random subset of predictor variables is considered for node and splitpoint selection (Amit and German 1997). In this way, two elements of randomness are injected into the procedure. Observations not included in the bootstrap samples are passed down their respective trees, and each tree’s terminal nodes contain a predicted categorical response to different combinations of observed values among predictor variable pathways. Each tree has a ‘vote’ in the most important predictive variables to split on, and on the categorical responses of different values of input combinations; and the majority of votes among the ensemble of trees ‘wins’. Therefore, we can a) predict and rank variables that most strongly influence an outcome (variable importance plot:

Figure 3a, and 3b) isolate and examine the behavior of individual predictors on the outcome, while holding the effect of all other predictive variables constant (partial dependence plots: Figure 3b).

RF modeling of 'training' data was conducted by building 5000 trees using default values for other parameters in the randomForest package in the R programming environment (R Core Team 2012). RF models have known biases in variable importance selection for highly correlated predictor variables; therefore we conducted a preliminary screening of our abiotic variables to eliminate highly correlated variables.

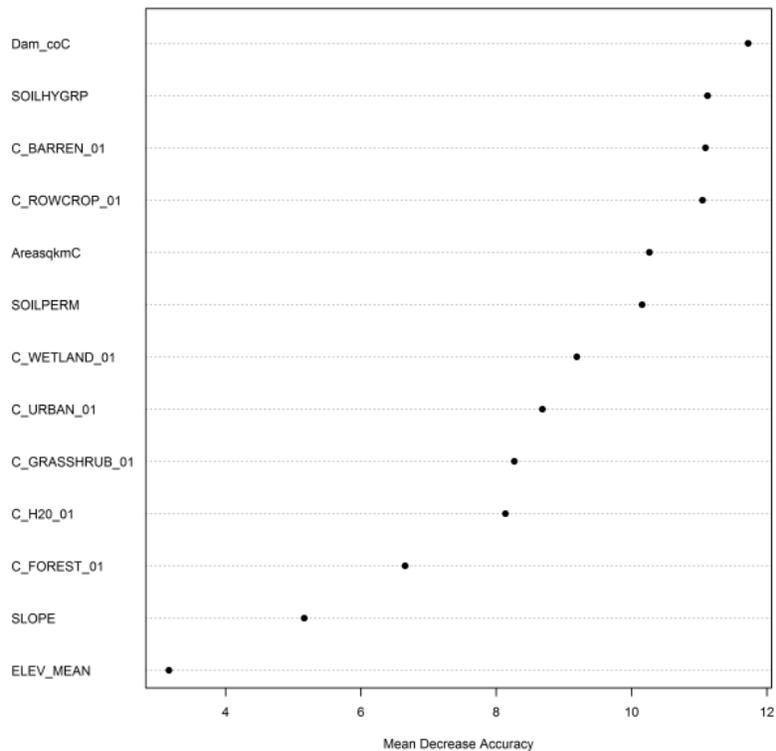


Figure 3a. Depicts a random forests variable importance plot.

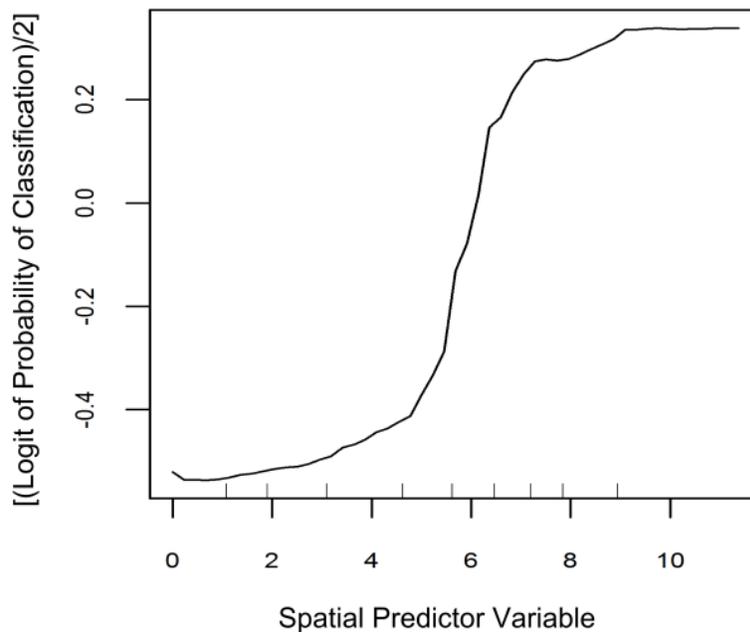


Figure 3b. Depicts a random forests partial dependence plot.

### *Error Estimates Procedure*

The RF algorithm builds trees based on repeated randomized samples of the dataset, hence it is not essential to hold back data for testing after model creation to obtain an unbiased estimate of error. Model performance was evaluated with three accuracy measures calculated using the resubstitution method (Theodoridis and Kourtroumbas 2006). The three measures were the Proportion Correctly Classified (PCC), Cohen's weighted Kappa statistic (weighted  $\kappa$ ), and the area under the receiver operating curve (AUC). Both PCC and weighted  $\kappa$  are derived from the model confusion matrix, which gives the number of actual versus predicted classifications of group membership. PCC performance measures are given in two forms: 1) an overall PCC percentage

(accuracy) representing the number of correctly classified cases divided by the total number of cases across all outcome classes, and 2) a measure of accuracy for a specific outcome class (precision). Weighted  $\kappa$  corrects the overall PCC for agreement caused by chance, and gives a value ranging from -1 to 1 (Cohen 1968). A positive value indicates greater agreement between modeled and measured classifications than expected by chance alone, and a negative value indicates less agreement than expected by chance alone. Cohen's weighted  $\kappa$  was calculated using the vcd package in R (R Core Team 2012). The AUC is derived from plotting the true positive rate (sensitivity) against the false positive rate (specificity), with each point plotted representing a sensitivity/specificity pair. The area under the resulting plot is a measure of how well the model correctly classifies groups. AUC values range from 0 to 1, with values  $> 0.5$  indicating better model performance than expected by chance alone (Swets 1988). We used the ordROC function in the nonbinROC R package in R to calculate AUC values

### *Random Forest Model Documentation*

Each model is associated with a .pdf file termed 'Random Forest Documentation for Model' containing the following information.

1. **Modeling Procedure**: Information regarding random forests statistical modeling.
2. **Error Estimates Procedure**: Information regarding the error estimates used in model.
3. **Response Variable Definition**: A description of the response variable used in the model; includes background information, definition, ecological significance, and calculation procedure.
4. **Variables Retained in Model**: Subset of variables retained in final model after exclusions based on correlations and model importance.
5. **Model Call**: The original R call to randomForest, indicates model parameterization.

6. **Correlations Remaining in Model**: Highly correlated predictor variables are known to cause variable selection bias in random forests models; variable selection of individual tree algorithms is biased in favor of highly correlated variables. Therefore we run a series of data reductions to remove highly correlated variables from our final model. Final correlations remaining in model are presented.
7. **List of Important Variables (Mean Decrease Accuracy)**: Variables with large mean decrease in accuracy are more important for classification of the data. Variables are listed in order of highest to lowest mean decrease in accuracy.
8. **Variable Importance Plot**: Plot of mean decrease in accuracy showing the relative importance of each variable's importance in classifying data. The plot shows predictor variables on the y-axis and their importance (mean decrease in accuracy) on the x-axis.
9. **Partial Dependence Plots**: Partial dependence plots isolate and examine the behavior of individual predictors on the outcome, while holding the effect of all other predictive variables constant. Plots show the logit of probability of classification/2 on the y-axis, and values of the predictor variable on the x axis.
10. **PCC Result and Confusion Matrix**: PCC performance measures are given in two forms: 1) an overall PCC percentage (accuracy) representing the number of correctly classified cases divided by the total number of cases across all outcome classes, and 2) a measure of accuracy for a specific outcome class (precision). PCC calculations are based on the confusion matrix, which shows how predictions are made by the random forests model.
11. **Weighted K Result**: Weighted  $K$  corrects the PCC for agreement caused by chance, and gives a value ranging from -1 to 1 (Cohen 1968). A positive value indicates greater agreement

between modeled and measured classifications than expected by chance alone, and a negative value indicates less agreement than expected by chance alone (Table 2).

12. **AUC Result:** The AUC is derived from plotting the true positive rate (sensitivity) against the false positive rate (specificity), with each point plotted representing a sensitivity/specificity pair. The area under the resulting plot is a measure of how well the model correctly classifies groups. AUC values range from 0 to 1, with values  $> 0.5$  indicating better model performance than expected by chance alone (Swets 1988).

## **Results and Discussion**

### *South Carolina Stream Conservation Planning Tool*

The South Carolina Stream Conservation Planning Tool enables a spatially explicit understanding of how human activities affect the biological and aquatic conditions of South Carolina's wadeable streams. This tool has two primary functionalities: 1) a web mapping application allows users to visualize predicted aquatic resource conditions based on their status and severity across all South Carolina wadeable stream catchments; 2) an interactive catchment management tool allows users to explore and forecast the impacts of customized land management scenarios on aquatic resource indicators at any user-specified location across South Carolina.

### *Mapping Application*

The map viewer displays 'static' predictions of current biological and aquatic resource conditions for South Carolina catchments ( $<150\text{km}^2$ ) based on extrapolations from random forests models. GIS services are implemented using ESRI ArcGIS Server. A web browser client supports dynamic mapping and scale-dependent detail views of stream condition and prediction metrics. One predictive map is available per model generated; individual maps display the predicted status of a

unique biological or aquatic indicator. Because we restricted biological and aquatic indicators and corresponding models to either the upstate or coastal plain, catchment predictions are likewise restricted to either the upstate or coastal plain. A brief description of the response variable and associated map legend is located on the left side of the map viewer. A link to each models ‘ Random Forest Model Documentation’, a detailed report describing response variable construction, random forests model results, and error metrics are also located on the left side of the map viewer.

### *Catchment Management Tool*

The interactive catchment management tool allows users to explore and forecast the impacts of customized land management scenarios on aquatic resource indicators at any user-specified location across South Carolina, engaging users in the process of modeling and forecasting stream conditions. Users may modify human disturbance factors within a single catchment or multiple catchments within a network, and visually examine the predicted changes in a given aquatic resource indicator. The SC Conservation Planning Tool software recalculates response values for each selected catchment and conducts a downstream analysis. All downstream catchments impacted by user-modifications are returned to the user and displayed in the map. Users have access to prediction results for 24 hours, and may export results in .csv or JSON formats.

While web mapping applications are commonly used as the basis for decision support tools, these applications traditionally rely on statically generated spatial layers. Our Conservation Planning Tool software and web mapping application is unique in that it provides a dynamic execution of models based on user-specified inputs. The capacity for users to dynamically execute models greatly broadens the utility of the mapping application, and opens the forecasting process to a non-technical audience.

Forecasted catchment management simulations can aid in municipal and county government land planning and permitting; state agency permitting, land acquisition and management activities; federal agency land and resource management; and assist non-governmental organizations with land management and/or advocacy responsibilities. Our Conservation Planning Tool should reflect pathways of threats to aquatic resources, communicate aquatic resources status and expected responses to interested stakeholders, and provide resource conservation guidance at the planning stages of land management and development projects that effectively mitigates impacts.

### **Recommendations**

The South Carolina Stream Conservation Planning Tool is a decision support system that is now completely functional and ready for live web deployment on a host server. Development of several models has been completed and they have been implemented in the tool.

- While SCDNR IT has indicated interest in hosting the tool, their staff have been unable to devote time and resources at this point to this task. It is imperative that a hosting solution be implemented, either externally or within DNR IT, before grant resources are expended at the end of calendar 2013 and we lose support from the system architect at Clemson, Dr. Sam Esswein.
- Develop and refine additional response models as the StreamWeb database (repository for SCSA data) is mined for information. The planning tool is designed to be easily updated with additional models and predictor variables as they become available, making it a very flexible system.

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**Job Title:** Fish Community Response to Dam Removal in Twelvemile Creek, Pickens County, South Carolina

**Period Covered** January 1, 2013 – December 31, 2013

### Summary

A rare opportunity to study the ecological effects of dam removal in the Southeastern U.S. has presented itself with the removal of two mainstem dams on Twelvemile Creek, Pickens County, South Carolina. We sampled sites above and below two dams before, during, and after dam removal to document changes in stream habitat and fish communities. We plotted fish metrics by site and year to evaluate temporal trends, and used non-parametric multidimensional scaling to examine, visualize, and interpret changes in community composition across time. Prior to dam removal, habitat and fish community compositions in the small impoundments above both dams were distinct from their immediate downstream free-flowing reach counterparts. Impoundments were shallow with low velocities and were characterized by greater densities of lentic species such as sunfish and bass, whereas free-flowing sections were characterized by greater depth-diversity and velocity and had greater densities of lotic species such as darters, shiners, and madtoms. After dam removal, fish assemblage and habitat conditions of the former impoundments changed rapidly, showing increased similarity to habitats found in immediate downstream free-flowing areas. Our analyses showed that overall community composition and species density metrics at all sample locations largely recovered within 2 years of the removal of the lower-most dam.

Prior to dam removal we routinely captured *Micropterus coosae* (redestye bass) at all sample sites. We began to capture non-native *Micropterus punctulatus* (spotted bass) beginning one month immediately following the removal of the lower-most dam. We have documented spotted bass in all sample reaches below a third dam that remains on the river, however it is important to note that

genetic verification of our field identifications is still pending. We captured the majority of spotted bass (to date) within 9 months of the removal of the lower-most dam, and have observed less catch occurrences since that time. The presence of Alabama spotted bass in post-dam removal samples causes concern regarding potential hybridization with the drainage's native redeye bass population.

## **Introduction**

Dams convert lotic aquatic systems to lentic systems, fundamentally altering the natural hydrological regime, thermal regime, physical habitat, benthic substrate composition, and longitudinal connectivity of aquatic ecosystems (Bendnarek 2001). Consequently, dams alter the abundance, composition, and distribution of native fish communities (Martinez et al. 1994, Taylor et al. 2001, Santucci et al. 2005). Dam removal is a restoration tool intended to reestablish the natural ecological conditions of aquatic systems. Over 1,000 dams have been removed from U.S. streams and rivers to date, with the vast majority of removals occurring in the northeastern and western U.S. ([www.americanrivers.org](http://www.americanrivers.org)). A rare opportunity to study the ecological effects of dam removal in the southeastern U.S. has presented itself with the removal of two mainstem dams on Twelvemile Creek, Pickens County, South Carolina.

Twelvemile Creek was extensively polluted with PCBs originating from a capacitor manufacturing plant from 1955-1975; the waste site and its receiving waters were listed with the EPA Superfund Program in 1990. Under CERCLA statute (Superfund law), a natural resources board of trustees is authorized to act as trustees of natural resources on behalf of the public, and within that role they may assess and recover damages for injuries and losses to natural resources caused by a hazardous waste site. As part of the settlement for damages caused by PCB contamination, a natural resources board of trustees facilitated the removal of two mainstem dams on

Twelvemile Creek in order to 1) remove any remaining contaminated sediments that have accumulated behind the dams, 2) to promote sediment transport to further 'cap' contaminated sediments downstream and in Lake Hartwell, and 3) provide recreational fishing and boating opportunities. Dam removal began in August 2009 with the initial dredging behind the upper dam (Woodside I Dam); this dam was completely removed by April 2011. Dredging and removal preparations on the lower dam (Woodside II Dam) began in April 2011, and removal was completed in September 2011.

The objective of this investigation was to document changes in the fish communities of Twelvemile Creek before and after the removal of the two dams (Woodside I and Woodside II). We utilized two methods to examine changes in fish assemblages through the process of dam removal. We plotted fish metrics by site and year to evaluate temporal trends, and used non-parametric multidimensional scaling (NMDS) to examine, visualize, and interpret changes in community composition.

### **Materials and Methods**

Six sampling stations were established for collecting biological and habitat data (Figure 1). The sampling stations are distributed as follows: 1) an alluvial stream section downstream of Woodside II Dam (Downstream), 2) a bedrock-constrained free-flowing stream section downstream of Woodside II Dam (Woodside II Below), 3) an impounded area above Woodside II Dam (Woodside II Above), 4) a bedrock-constrained free-flowing stream section downstream of Woodside I Dam (Woodside I Below), 5) an impounded area above Woodside I Dam (Woodside I Above), and 6) an upstream reference station located upstream of both Woodside I and II, as well as upstream of a third dam (Upstream; Figure 1).

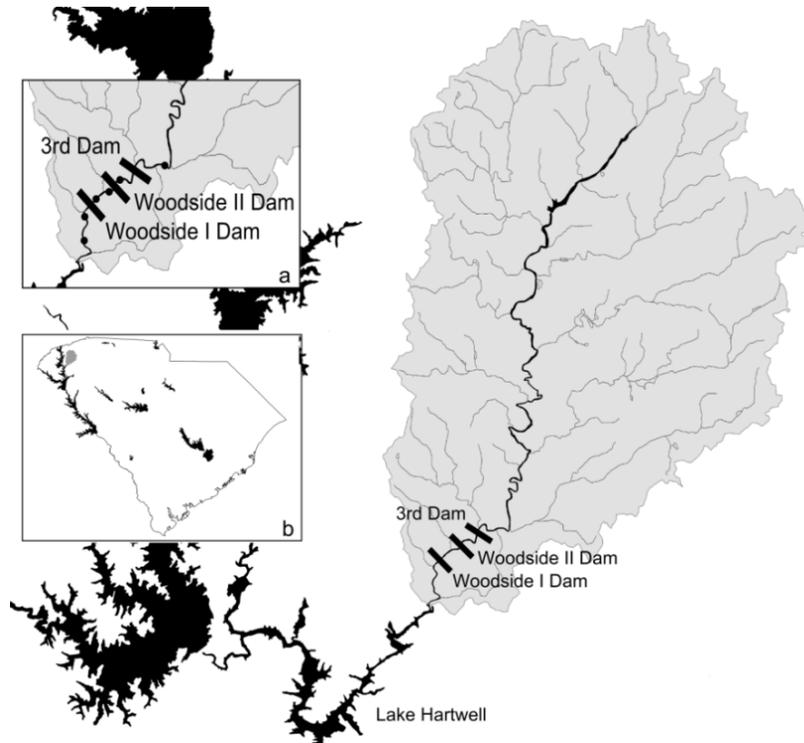


Figure 1. Twelvemile Creek drainage shaded in gray. Inset (a) shows sample locations (black circles), locations of two former mainstem dams (Woodside I and Woodside II), and the location of a remaining third dam (Easley-Central Dam). Inset (b) shows watershed location in SC.

This analysis references 10 samples collected before, during, and after dam removal (December 2006, August 2009, April 2010, September 2010, April 2011, October 2011, April 2012, October 2012, April 2013, October 2013). Fishes were collected at 20 wadeable stream segments of approximately 15m<sup>2</sup> within 300m segments at each site with a standardized effort using electrofishing gear and seines. All fishes encountered were collected, field identified to species level, recorded, and released. Habitat measurements of depth, velocity, and substrate were recorded at each of the 20 replicates; widths and turbidity measurements were recorded at each site.

Fish assemblage metric scores were plotted by site and year to evaluate temporal trends before and after dam removal. Metrics evaluated included: total density, cyprinid invertivore density, benthic invertivore density, round bodied catostomid density, native centrarchid density, and non-native species density (Table 1). Densities were calculated as number per replicate (out of 20 replicates). I additionally used non-metric multidimensional scaling (NMDS) to examine changes in community composition before and after dam removal. NMDS is a non-parametric ordination technique that translates the n-dimensional (n=# taxa) community in relatively few dimensions (usually 2 or 3) so that differences between sites are readily interpreted visually. In a robust NMDS plot, distances between points are directly representative of the differences in species composition of communities. All current analyses focused on metric and compositional changes at the four sample sites flanking each dam.

Table 1. Fish metric definitions.

<b>Metric</b>	<b>Definition</b>
Total Density	total number of fish captured / total number of seine sets
Cyprinid Invertivore Density	total number of ESM, RFC, STS, WFS, YFS / total number of seine sets
Benthic Invertivore Density	total number of BBD, MGM, TQD / total number of seine sets
Round Bodied Catostomid Density	total number of NHS, NLR, STS / total number of seine sets
Native Centrarchid Density	total number of BLG, LMB, RBS, REB, WAR / total number of seine sets
Non-Native Species Density	total number of FCF, GSF, SPB / total number of seine sets

## **Results and Discussion**

Fish assemblage metric scores were plotted by site and year (Figure 2). Total density at the two formerly impounded sites above each dam increased rapidly at 6 months after each dam removal,

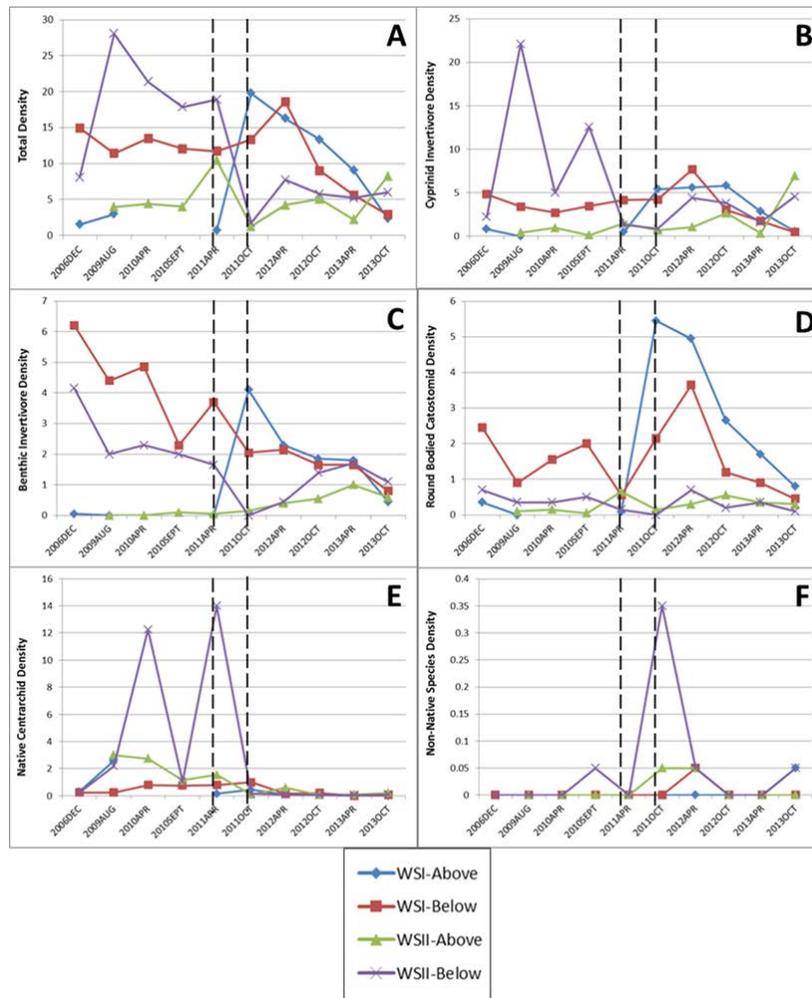


Figure 2. Total density, cyprinid invertivore density, benthic invertivore density, round bodied catostomid density, native centrarchid density, and non-native species density through time at Twelvemile Creek sample sites immediately upstream and downstream of the Woodside I and Woodside II Dams. The left-most vertical dashed line represents the complete removal of Woodside I Dam, and the right-most vertical dashed line represents the complete removal of Woodside II Dam.

then generally decreased and stabilized over time (Figure 2A). Total densities at both formerly impounded sites resembled those found at the free flowing sites by 2 years after the removal of the Woodside I Dam, and 1.5 years after the removal of the Woodside II Dam. Total density at the free flowing site below the former Woodside I Dam remained relatively constant during and immediately after dam removal, but decreased at one year after dam removal. This decrease likely reflected natural variation in population numbers. Total density at the free flowing site below the Woodside II Dam dropped sharply after the removal of its upstream dam, but resembled total densities observed at other sites by 1 year after the removal of the Woodside II Dam.

Cyprinid invertivore densities at both formerly impounded sites increased modestly at 6 months after each dam removal, and resembled densities observed at the free-flowing sites by 1.5 years after the removal of the Woodside I Dam, and 1 year after the removal of the Woodside II Dam (Figure 2B). Cyprinid invertivore densities at the free flowing site below the former Woodside I Dam did not appear to be affected by dam removal. However, cyprinid invertivore densities below the former Woodside II Dam dropped sharply after the removal of Woodside II, but resembled the densities of other sites by 1.5 years after the removal of the Woodside II Dam.

Benthic invertivore densities at the former impoundment above Woodside I increased sharply at 6 months year after the removal of the Woodside I Dam, and resembled the densities observed at all other sites since that time period (Figure 2C). Densities of benthic invertivores at the former impoundment above Woodside II increased slowly after dam removal, and resembled the densities observed at all sites by 1.5 - 2 years after the removal of the Woodside II Dam. Densities of benthic invertivores at both free flowing sites decreased immediately after dam removal; densities at the free flowing site below the Woodside II Dam decreased more sharply than observed at the site below the Woodside I Dam. Benthic invertivore densities at the free flowing site below the Woodside I Dam

stabilized at 6 months after dam removal, while densities at the free flowing site below the Woodside II Dam did not stabilize until 1 year after the removal of the Woodside II Dam.

Round bodied catostomid densities increased sharply at both sites flanking the former Woodside I Dam after its removal, then decreased and resembled the densities observed in other sites by 2.5 years after the removal of the Woodside I Dam (Figure 2D). Round bodied catostomid densities remained relatively stable at the sites flanking the former Woodside II Dam before and after its removal.

Native centrarchid densities decreased at both formerly impounded sites after the removal of each location's dam, and the densities at each former impoundment resembled densities at the free flowing sites by 6 months after dam removal (Figure 2E). The densities of native centrarchids showed considerable natural annual variation at the free flowing site below the lowest dam (Woodside II) prior to dam removal, and this seasonal variation has not recovered after the removal of the Woodside II Dam.

Non-native species density increased sharply at both sites flanking the former Woodside II Dam at 1 month after the removal of the Woodside II Dam, and increased at the free flowing site below the former Woodside I dam at 6 months after the removal of the Woodside II dam (Figure 2F). The observed increase was primarily due to the presence of *Pylodictis olivaris* and *Micropterus punctulatus*, two non-native species that we captured in relatively low abundances prior to the dam removals. Of concern, we captured *M. punctulatus* (spotted bass) in our samples for the first time one month after the removal of the lower dam (October 2011). In the October 2011 sample, we captured spotted bass at the Downstream site, and at the two sites flanking the former lower dam (Woodside II Above and Below). In April 2012, we additionally captured spotted bass below the former upper dam (Woodside I Below). This capture pattern indicated that *M. punctulatus* may have

been moving in an upstream direction from Lake Hartwell into the newly restored river section. We captured the majority of spotted bass (to date) within 9 months of the removal of the lower dam, and have observed less catch occurrences since that time. In total, we captured 9 spotted bass within 9 months of the removal of the lower dam (Woodside II Dam), and have captured only 1 spotted bass between 9 months and 2 years of dam removal.

The upstream movement of spotted bass poses an ecological concern because spotted bass readily hybridize with and deplete the genetic integrity of redeye bass (*Micropterus coosae*), a fish native to water bodies of the Savannah River Drainage. The presence of spotted bass is well documented in the major reservoirs of the Savannah River, but little is known about their distribution in tributary systems. Prior to their removal, it is possible that the Woodside Dams acted as barriers to an upstream invasion of *M. punctulatus* from Lake Hartwell. A third dam (Easley-Central Dam) remains on Twelvemile Creek and effectively blocks the upper reaches from invasion in its current condition. To date, we have not genetically verified the capture of any pure strain spotted bass or redeye/spotted hybrids above the third dam.

The NMDS analysis showed that differences in community composition among sites were strongly related to changes in habitat conditions before and after dam removal, and showed that assemblages in sample sites varied longitudinally (Figure 3). An examination of the scree plot indicated that a 2-dimensional solution provided far greater reductions in stress than later axes. The final stress for the 2-dimensional solution was 15.67, the final instability was 0.0098, and the Monte-Carlo test was significant at  $p < 0.0001$ , indicating that the derived solution produced stronger axes than expected by chance.

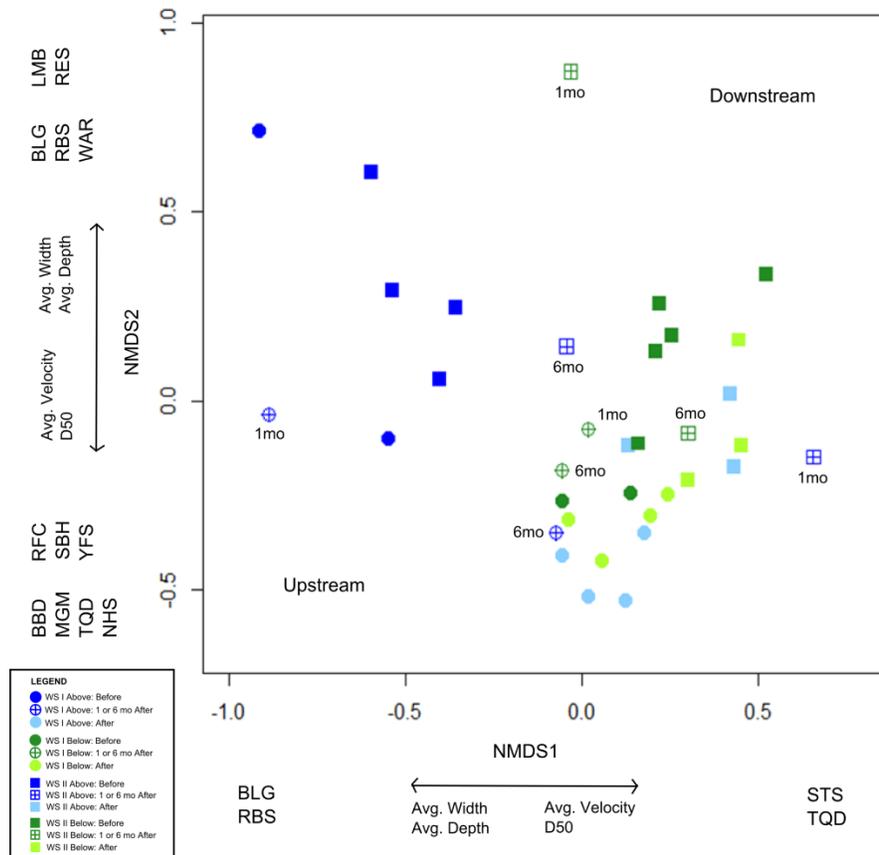


Figure 3. Non-metric multidimensional scaling of fish species by site. Points closer to one another in the ordination are more similar in species composition. Species names in gray refer to species that correlate strongly on each axis, whether positively or negatively. Environmental variables in red are parameters that were strongly correlated with each axis. Species correlations are inherent weights (i.e. the ordination is based on the species) whereas environmental correlations are post-hoc. Inferred groups are indicated with black circles.

Prior to dam removal, the species compositions of impoundments (Woodside I and II Above) were similar. The impoundments had sand-dominated substrates (low D50) and greater average widths and depths, and were characterized by lentic species such as *Lepomis auritus*, *Lepomis*

*gulosus*, *Lepomis macrochirus*, *Lepomis microlophus*, *Micropterus salmoides*. We also observed species compositional similarity in both free flowing sites (Woodside I and II Below) before dam removal, although these sites showed natural longitudinal differences. The free flowing sites had higher average velocities and substrate size, and were characterized by lotic species such as *Ameiurus brunneus*, *Etheostoma inscriptum*, *Hybopsis rubrifrons*, *Hypentelium nigricans*, *Notropis hudsonius*, *Noturus insignis*, *Notropis lutipinnis*.

After the removal of the upper dam (Woodside I Dam), species composition of the former impoundment (Woodside I Above) was similar in fish and habitat composition to its downstream free flowing counterpart (Woodside I Below) and the free flowing site below the lower dam (Woodside II Below) by 6 months after dam removal. The free flowing site below the former upper impoundment (Woodside I Below) showed little variation in species composition after the removal of the Woodside I Dam, indicating little impact to the species composition of this site as a result of dam removal.

After the removal of the lower dam (Woodside II Dam), habitat and species composition of the former impoundment (Woodside II Above) was similar in composition to its downstream free flowing counterpart (Woodside II Below) and the free flowing site below the upper dam (Woodside I Below) by 1 year after dam removal. The species composition of the free flowing site below the lower dam (Woodside II Below) was very dissimilar to the other free flowing sites at 1 month after dam removal, indicating an initial compositional disturbance. However, the species composition of this site returned to compositional similarity with the other free flowing sites at 6 months after dam removal, indicating a relatively quick compositional recovery.

The culmination of our initial analyses indicated that the overall fish compositional similarity of sample sites flanking each dam occurred by approximately 1 year after the removal of each dam,

however species densities recoveries lagged behind. Total densities of impounded sites were similar to free flowing by 2 years, cyprinid densities of impounded sites were similar to free flowing sites by 1.5 years, and benthic invertivore densities of impounded sites were similar to free flowing sites by 2 years. We observed minimal assemblage disturbance at the upper free flowing site (Woodside I Below) due to dam removal, but we did observe an assemblage disturbance at the free flowing site below the lower dam (Woodside II Below). The densities of insectivorous cyprinids and benthic invertivores at Woodside II Below were initially reduced immediately following dam removal, but each recovered within 1.5 years. We largely captured the non-native *Micropterus punctulatus* at sites below the third dam in the first 9 months after the removal of the lower dam (Woodside II Below Dam), and have only 1 reported capture for the subsequent 2 years of sampling. Fish assemblage and habitat monitoring will continue through 2015 to provide a multi-year record of post dam-removal ecological conditions.

### **Recommendations**

We will continue standardized sampling according to schedule at Twelvemile Creek to provide a multi-year record of post dam-removal ecological conditions.

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Prepared By: Cathy Marion

Title: Fisheries Biologist

**Job Title:** Assessing introgressive hybridization within and habitat requirements of native South Carolina redeye bass

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

In the last year, stream collection and genetic data from 2004 – 2010 was compiled, completing our initial effort to assess hybridization among black bass in Savannah basin stream populations. Work to determine the origin of redeye bass *Micropterus coosae* populations in the neighboring Santee drainage and their status with respect to hybridization was completed. The Tyger River was sampled for redeye bass following discovery of the species in the adjacent Enoree River, though no black bass other than native largemouth *Micropterus salmoides* were collected. Work was begun and is continuing on development of fast genetic assays for use in furthering our understanding of the extent of hybridization in Savannah basin streams. Staff, together with colleagues outside of the agency, presented aspects of our ongoing work in the conservation of redeye bass at a symposium on native Southeastern black bass species. Both oral presentations and submitted manuscripts were produced.

### **Introduction**

The redeye bass (Hubbs and Bailey 1940) is one of two black bass native to South Carolina, and has been identified by South Carolina's Comprehensive Wildlife Conservation Strategy as a Species of Highest Priority due to its restricted range and threats from introduced species (Kohlsaatt et al. 2005). The species' native range is restricted compared to others of its genus and includes the Savannah, Altamaha and Ogeechee River drainages on the Atlantic slope, and the Mobile Bay and Apalachicola drainages on the Gulf slope. Redeye bass occupy habitats above the Fall Line in fast

moving, cool-water streams (Rhode et al. 2009). In addition to native headwater streams and tributaries, *M. coosae* has thrived within four of the Savannah River basin's man-made reservoirs; Jocassee, Keowee, Hartwell and Russell (Koppelman and Garret 2002).

Recent studies have examined the relationship among populations of redeye bass across the range of the species. Mobile Bay drainage redeye bass are morphologically distinct from Atlantic Slope populations, with the common name Bartram's bass assigned to the latter (Bud Freeman, unpublished data). DNA sequence data supports this distinction, and further suggests species-level divergence between Savannah River redeye bass and those of other Atlantic Slope drainages. Savannah River redeye bass represent a highly divergent and distinct evolutionary lineage (Oswald 2007), as is one of three focus species in the National Fish and Wildlife Foundation's Native Black Bass Initiative (Birdsong et al. 2010).

Introductions of the non-native Alabama bass *Micropterus henshalli* into lakes Keowee and Russell have put Savannah River redeye bass at risk due to introgressive hybridization (Barwick et al. 2006). Genetic surveys in 2004 and 2010 showed that Alabama spotted bass have expanded within the drainage, as have their hybrids with redeye bass (Oswald 2007). Both are present in all four lakes surveyed, and in 2010 together they comprised from 48% to 68% of black bass collected from each reservoir. The survey of tributaries of the drainage indicated in 2004 that those redeye populations were for the most part still unimpacted by hybridization, but in 2010 an increase in Alabama bass alleles was noted for several tribs. Alabama bass are known to take advantage of stream habitats, and the continued spread of their alleles throughout the drainage is a possibility.

Objectives of this study have included an assessment of genetic change over time in Savannah basin redeye bass populations, and a genetic evaluation of redeye bass and other co-distributed species in Santee drainage to further evaluate the redeye's status in Santee drainage as

introduced. Work in the last year has focused on compilation of collection and genetic data for Savannah basin streams, completion of assessment of native or introduced status of Santee basin redeye bass populations, presentation of related work orally and in submitted manuscripts, and on the development of fast assays to be used to further our work on Savannah basin stream populations.

### **Materials and Methods**

For all fish collected sequences have been generated for one mitochondrial and three nuclear DNA loci following the procedures outlined by Oswald (2007). Genetic sequence data previously generated for black bass collected from Savannah drainage tributary populations in 2009 and 2010 were compiled and compared to data from 2004. New or increased incidences of Alabama bass alleles were noted.

DNA sequences from five species of minnow were evaluated for use in comparison of diversity and divergence in co-distributed redeye bass. Minnow used were collected from sites within the Santee, Tennessee (French Broad) and Savannah River drainages. A total of 120 individuals were captured including 47 Saffron Shiners *N. rubricoceus*, 27 Mirror Shiners *N. spectrunculus*, 20 Stonerollers *C. anomalum*, 10 Whitetail *C. galactura* and 16 Warpaint Shiners *L. coccogenis*. Whitetail shiners could not be captured from the Broad River collection location despite repeated attempts; therefore, this taxon was not included in the statistical analyses. Three loci consistently amplified and were assayed for all individuals, one mitochondrial locus (ND2) and two bi-allelic nuclear loci (CAL and ITS). Saffron and Warpaint shiners were sufficiently variable for both ND2 and Calmodulin and these two species/loci were used in comparisons to redeye bass divergence.

Work was begun on development of fast genetic assays. Molecular Beacon software was used to identify suitable probe sequences for three loci, Actin, Calmodulin and ITS. Where promising probe sequences were identified, hydrolysis probes were designed and synthesized. Where unsuccessful, an alternative approach using species specific PCR primers has been employed. Once fully developed, these assays together with analysis at the mitochondrial ND2 locus will be used to assess hybridization and to delineate possible refuge areas for redeye bass in seven high priority tributaries.

## **Results**

Genetic analysis of black bass collected from Savannah basin tributaries in 2009 and 2010 confirmed non-natives and/or hybrids from 5 of 9 collection sites. Hybrids were collected from at least one tributary associated with each of three reservoirs (Table 1). Three of these collections, Chauga River lower, Big Generostee Creek and Little Coldwater Creek represent new documentation of Alabama bass hybrids, as we collected only native black bass from each of these sites in 2004. Some hybrids collected from Chauga River lower carried a rare mtDNA haplotype previously only seen in Lake Hartwell. We did not sample any tributaries associated with Lake Jocassee in 2009/2010, but we did collect one hybrid from the Toxaway River in 2004. In general, tributary site collections that generated non-native alleles were those in closest proximity to one of the four reservoirs known to support an Alabama bass and hybrid population (Figure 1). The potential for the spread of Alabama bass and their hybrids from the reservoirs to additional tributary populations is indicated.

Table 1. Genetic identifications of black bass collected from Savannah basin streams in 2009 and 2010; redeye bass (REB), largemouth bass (LMB), Alabama bass (ASB), smallmouth bass (SMB), hybrid (HYB). Streams are grouped by the reservoir they are associated with, or as a direct tributary to the Savannah River.

Tributary to	Stream	Date	Species (N)					
			REB	LMB	ASB	ASB x REB	SMB	SMB x REB
L. Keowee	Eastatoee Ck.	9/24/09	8	0	0	0	0	0
	Little River	9/30/09	2	0	0	2	0	0
L. Hartwell	Chauga River lower	9/14/09, 9/29/09	9	2	0	8	0	0
	Chauga River - upper	9/29/09	15	0	0	0	0	0
	Chatooga River	8/4/10	18	0	0	0	0	0
L. Russell	Big Generostee Ck.	7/30/09	14	0	0	1	0	0
	Little Coldwater Ck.	9/1/10	18	3	0	3	0	0
Savannah R.	Steven's Ck.	7/29/09	15	6	0	0	0	0
	Savannah River	9/16/10	15	4	0	0	6	2

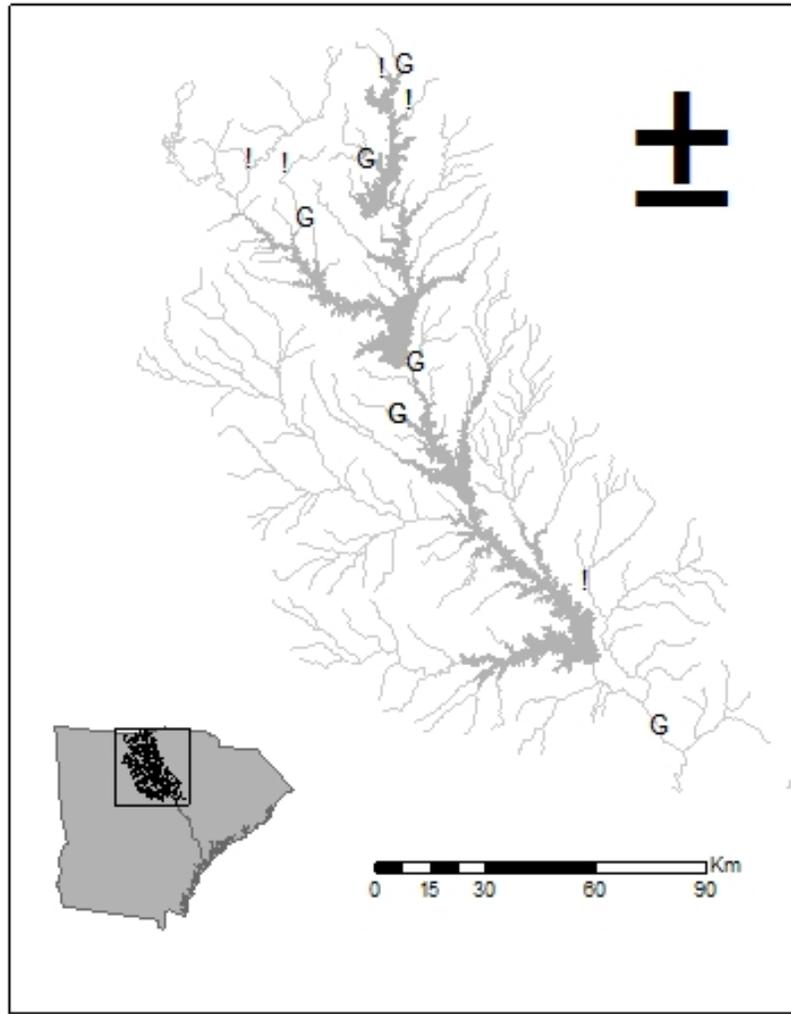
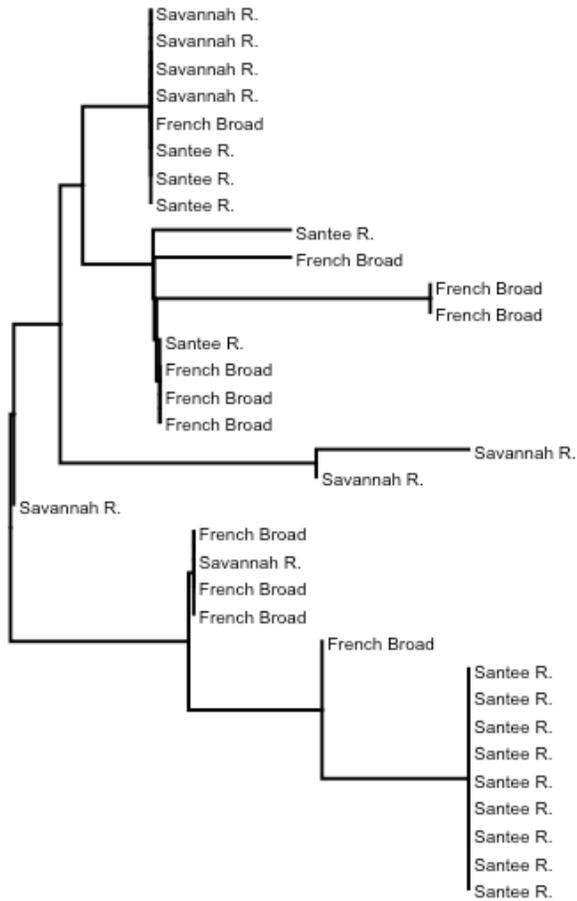


Figure 1. Spatial distribution of Savannah Basin tributary black bass collections from 2004 – 2010. Circles mark collection sites where only genetically pure redeye were collected. Crosses mark those sites where congeneric hybrids with redeye were collected. The lower most site depicted is the Augusta Shoals area of the Savannah River which produced smallmouth bass and their hybrids with redeye. All other hybrid collections were Alabama x redeye bass.

Divergence in Saffron and Warpaint shiners was found to be relatively shallow, much like redeye bass from the Santee basin. Most drainages appear to share identical or phylogenetically similar ND2 haplotypes (Figures 2 and 3). Unlike redeye bass however, ND2 diversity in Saffron and Warpaint shiners was relatively high in the Santee river drainage. These patterns are mirrored somewhat by variation surveyed at the nuclear Calmodulin locus (Fig. 4 and 5). While redeye bass are monomorphic in the Santee River (Oswald 2007), both Saffron and Warpaint shiners segregate for at least two alleles in this drainage and both alleles occur at appreciable frequencies.

The Santee population of redeye bass is not genetically differentiated from populations collected throughout the upper Savannah River drainage. In contrast, Saffron and Warpaint shiner populations collected in the Savannah and Santee drainages are significantly differentiated from each other, shown by pairwise comparisons in Table 2. Results indicate that the Santee Basin redeye bass populations evaluated here are the result of a more recent and likely human mediated introduction of fish originating from the Savannah basin. Further, collections from shoals throughout the North, Middle and South Tyger Rivers, and from the Tyger River below their confluences, did not produce any redeye bass. Similar sampling has shown the redeye bass to be established and widespread in the neighboring Enoree River.



ND2	Savannah	French Broad	Santee
1			9
2		1	
3	1	3	
4	1		
5	2		
6	1		
7		3	1
8		2	
9		1	
10			1
11	3	1	4
<i>h</i>	0.82	0.60	0.55

Figure 2. Neighbor-joining tree relating ND2 sequences collected from Saffron Shiners (*Notropis rubricroceus*).



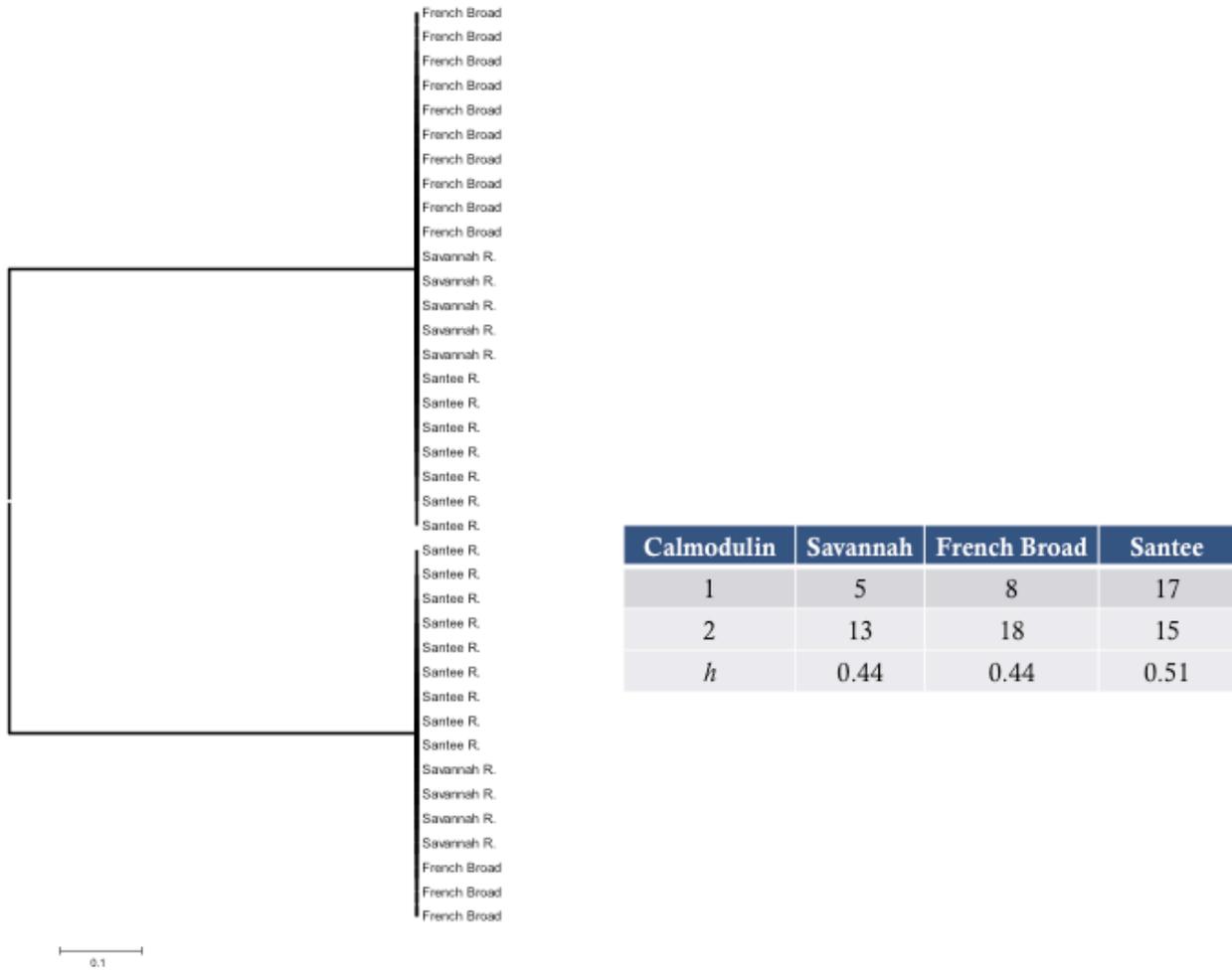


Figure 4. Neighbor-joining tree relating Calmodulin sequences collected from Saffron Shiners (*Notropis rubricroceus*).

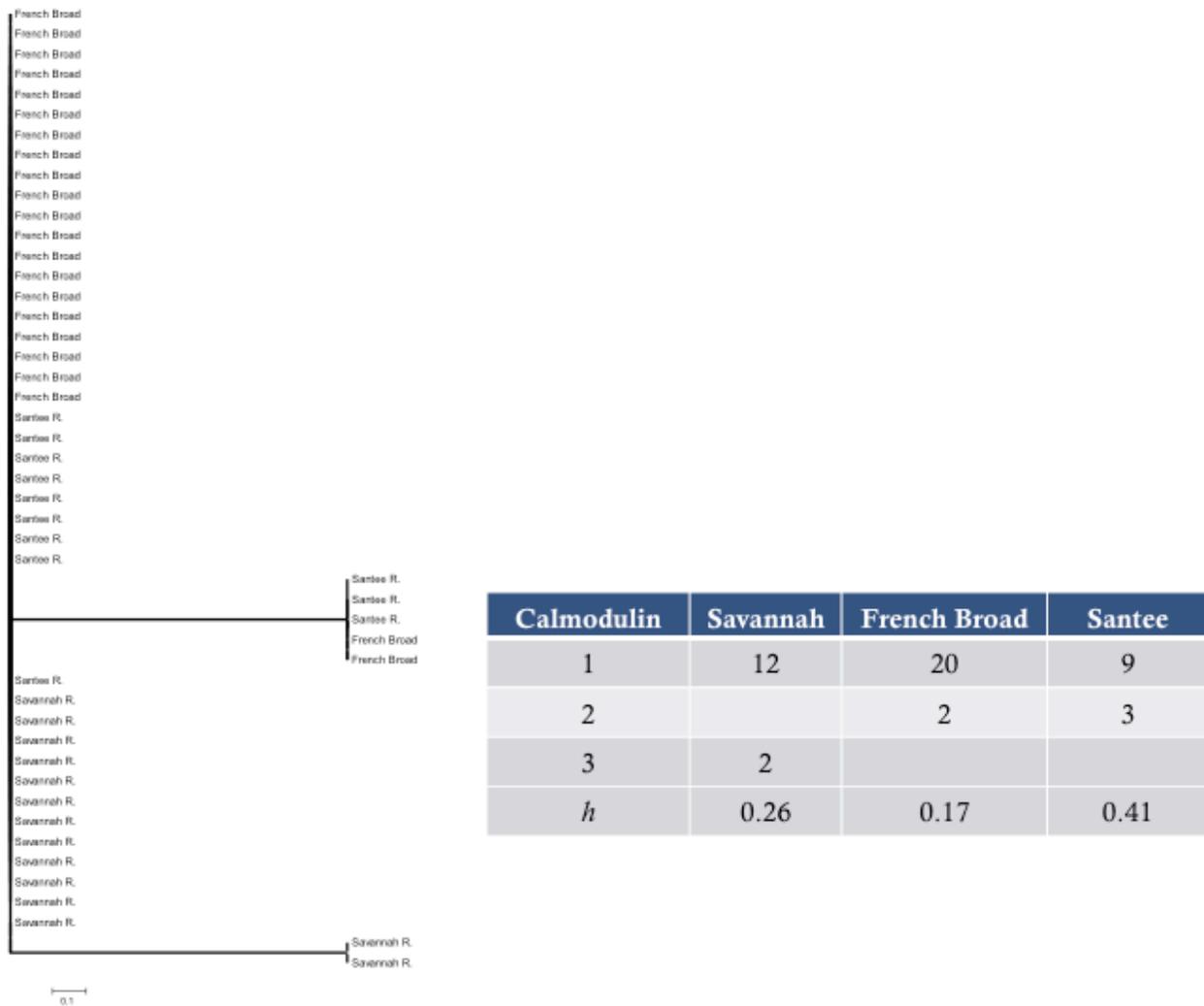


Figure 5. Neighbor-joining tree relating Calmodulin sequences collected from Warpaint Shiners (*Luxilus coccogenis*).

Table 2. Estimates of population differentiation based on allelic diversity at the mitochondrial ND2 and Calmodulin loci in two species of minnow. Differentiation is based on an Analysis of Molecular Variance that partitions genetic variation to components within versus between river drainages. Significant values (\*) are indicated ( $P < 0.05$ ).

Taxon	Pairwise Comparison	Among Drainage Variance	
		ND2	Calmodulin
<i>Notropis rubricroceus</i>	Savannah – French Broad	0.436*	0.565*
	Savannah-Santee	0.329*	0.523*
	Santee-French Broad	0.274*	0.519*
<i>Luxilus coccogenis</i>	Savannah – French Broad	0.593*	0.790*
	Savannah-Santee	0.880*	0.668*
	Santee-French Broad	0.107	0.737*

We have designed sets of hydrolysis probes that target species-specific alleles at the Actin and Calmodulin loci for five species of black bass. The Actin probe was most promising since only a single nucleotide change differentiates Alabama Bass from Redeye Bass. We have synthesized this probe and are actively developing amplification conditions that reliably differentiate these two species. Calmodulin probe design was complicated by a pair of closely linked polymorphisms that differentiate Redeye and Alabama Bass near the annealing site for the predicted hydrolysis probe. Molecular Beacon software cannot identify a suitable probe when two site changes are contained within the probe sequence. Instead, we have designed pairs of probes that contain each pair of diagnostic base changes (four possible combinations) within the annealing site. Once the Actin probe is completed and tested we will move on to Calmodulin probe synthesis.

Initial computer runs with sequences for the ITS region were problematic. Molecular Beacon software could not identify suitable probe sequences because of an extreme GC bias in the ITS

sequences (~75% GC). Synthesis of an ITS hydrolysis probe does not appear feasible due to prohibitive GC content. For the ITS locus we are turning to an alternative assay development method that uses species-specific PCR primers termed allele specific amplification. Recent developments have demonstrated that ‘deliberate’ base pair mismatches 2-3 bases from the 3’ end of an oligonucleotide has the capacity to raise the specificity of the primer assay (Liu et al. 2012). Although this application has been limited somewhat to plants, we are confident that a PCR-based assay can be developed for fishes. We are currently developing this assay.

In addition to ongoing research and survey work directed at redeye bass conservation, efforts have continued in the presentation and publication of results. Staff presented an invited talk at the Black Bass Diversity Symposium held at the 2013 Southern Division American Fisheries Society meeting. One manuscript was authored and two others co-authored for the Black Bass Diversity Symposium proceedings. A species profile was also written for publication in the proceedings, and a corresponding poster was co-authored.

## **Discussion**

The change in tributary collection results from 2004 – 2009/2010 indicates a continued spread of non-native bass and their alleles in redeye bass stream populations. This is disturbing in that it represents the potential for loss of pure populations through introgression. It also highlights the need for public education on the ramifications of such species introductions.

The introduced or native status of populations of redeye bass in the Saluda River of the Santee Basin has been in question for some time. The lack of divergence of Santee redeye from populations within the Savannah basin, and limited diversity within the Santee basin in comparison to the species presented here, supports that redeye bass were introduced from the Savannah. Even if

introduced, the fish from the Saluda River could still prove important to future conservation efforts directed at redeye bass. The Saluda River population could continue to represent an area not impacted by hybridization with Alabama bass, and thus be a source of pure individuals for conservation stocking efforts. Interestingly, field work has documented a range expansion within the Santee, with the fish now widespread in the Enoree River. Some of those fish were confirmed to be hybrids with Alabama Bass.

The funding of work last year to develop genetic and habitat baselines is a most positive development in our efforts to study and potentially conserve redeye bass populations in the Savannah basin. The associated new assay development is well underway and once completed will allow us to gain faster results more economically. This survey work will fill critical information gaps. Information gained will be used to identify and prioritize populations where conservation actions may have a positive impact.

### **Recommendations**

Complete development of new genetic assays. Implement those assays in development of baseline genetic and habitat data. Launch education/media campaign that targets movement of fish, and impacts on native species, black bass in particular. Continue to develop partnerships for education and funding of future work. Present findings at repeat presentation of 2013 native black bass symposium at the 2013 American Fisheries Society National Meeting.. Continue work to publish earlier and current results.

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**Job Title:** Redbreast Stocking Evaluation – Edisto River

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

A study to evaluate the contribution of stocked redbreast sunfish *Lepomis auritus* to the Edisto River fishery was initiated in 2010. Hatchery broodstocks were established with redbreast sunfish captured by electrofishing from the Edisto River. Fingerlings were produced, immersion marked with oxytetracycline (OTC), and stocked each year from 2010 to 2012. Approximately 275,000 marked fingerlings were released each year at multiple locations in an 11.12 mile section of the main stem of the Edisto River, bounded by SC Hwy 61 and US Hwy 17A. Subsamples for each year class of OTC marked redbreast were grown out for mark evaluation. The 2010 year class was well marked, and evaluations of age 1 wild caught fish from this year class (N=398) were completed. Size and condition of marked and unmarked fish were similar. Total proportion of marked fish collected from areas within the stocking zone was 14%. Stocking of the other year classes were not evaluated due to very faint marks in 2011, and the loss of most known marked fish during grow-out in 2012. Marking and stocking of fingerlings will continue with a 2013 year class.

### **Introduction**

Redbreast sunfish is a much sought after sport fish on the Edisto River. This is evidenced in collections made in 2004 that spanned a very high water event. Those collections suggest that once hydrologic conditions normalized, allowing for greater river access and angling, larger fish were quickly exploited and removed (Bulak 2005). The annual stocking of redbreast sunfish began in Edisto River in 1995. This was in response to public concerns that introduced flathead catfish were

negatively impacting the popular fishery. Records show approximately 13.7 million redbreast stocked in the river since 1995, with annual stocking ranging from 0.45-2.2 million.

The supplemental stocking of redbreast sunfish in Edisto River has never been evaluated. Collections of microtagged redbreast sunfish that were stocked in Little Pee Dee River from 1990 – 1992 suggested minimal contribution, though further sampling was recommended before drawing conclusions from the available data (Crochet and Sample 1993). Genetic survey of redbreast sunfish populations across five South Carolina drainages indicated Edisto river redbreast were markedly less diverse than redbreast populations from other drainages (Leitner 2006). This could be a result of lost diversity in the former hatchery population and its impact on the receiving population in the river, or could be an indication of bottleneck events occurring in the wild. To best manage this resource, we need a basic understanding of whether supplemental stocking is contributing to the redbreast sunfish population and fishery of the Edisto River. In the last year, stocking of the 2010 year class was evaluated and a 2012 year class was produced and stocked.

### **Materials and Methods**

Redbreast sunfish collected by Region 3 from the Edisto River in Fall 2011 were evaluated for OTC marks. These fish were collected from eight, 1-mile sampling reaches. Four contiguous river segments comprise the stocking zone. There are also two contiguous segments upstream, and two downstream of the stocking zone. Effort for each segment was standardized to 60 minutes pedal time of boat electrofishing. All otoliths from age 1 fish were processed according to standard procedures for OTC mark evaluation, and mark evaluations were conducted by two independent readers. Size (total length) and condition (relative weight) were compared for marked and unmarked

fish using the T-test. The proportion of marked fish collected was determined for each sampling segment, and for the study area as a whole.

## **Results**

Otoliths from 398 redbreast from the 2010 year class were evaluated for marks. Catch per unit effort (CPUE) by segment ranged from 14 – 85 fish/hr, and was generally higher for segments within the stocking zone and downstream. No marked fish were collected from segments upstream of the stocking zone. Marked fish comprised from 2-28% of fish from segments within the stock zone, 14% of total fish from the stock zone, and from 3-7% of fish from segments downstream of the stock zone (Table 1; Figure 1). Size (total length) and condition (relative weight) were similar for marked and unmarked fish collected (T-test; Table 2).

Table 1. Age 1+ redbreast collected by river segment from the Edisto River in Fall of 2011. N collected is for 1 hour of electrofishing in each segment.

River Segment	N Collected	N Marked	Proportion Marked
Upstream 2	19	0	0%
Upstream 1	24	0	0%
Stock 1	45	1	2%
Stock 2	14	1	7%
Stock 3	60	17	28%
Stock 4	83	10	12%
Downstream 1	85	3	3%
Downstream 2	45	3	7%

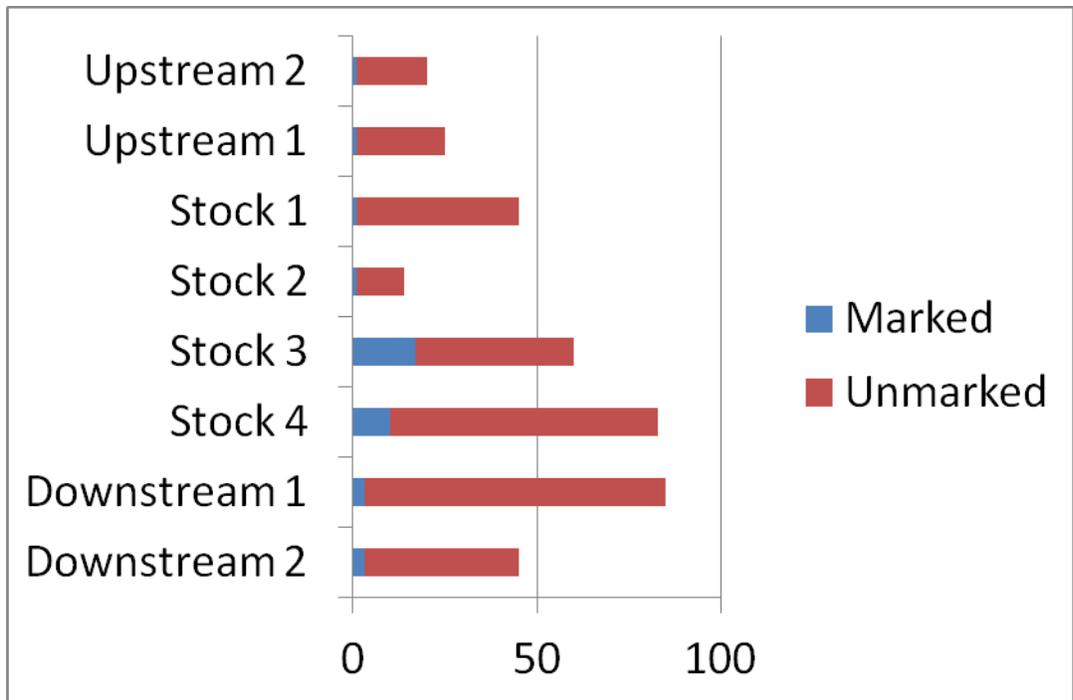


Figure 1. Marked and unmarked 2010 year class redbreast sunfish collected by boat electrofishing from the Edisto River at age 1+. Number collected is presented by 8 contiguous 1-mile river segments (2 upstream of the stocking zone, 4 within the stocking zone, and 2 downstream of the stocking zone). Catch represents 60 minutes of standardized pedal time in each river segment.

Table 2. Mean total length (tl) and relative weight (Wr) of marked and unmarked age 1+ redbreast collected from the Edisto River Fall of 2011.

Population Segment	N	Mean tl (sd)	Mean Wr (sd)
Marked	35	99 (16.0)	93.6 (8.7)
Unmarked	336	102 (16.2)	92.4 (7.1)

A blind mark evaluation was completed for marked fish from the 2011 year class. We had previously confirmed marks on a subsample of 2011 year class known marked fish, but marks were very faint. The blind evaluation included known unmarked fish as well, and confirmed that there was poor potential for identifying hatchery produced fish from the 2011 year class from the wild. Planned field collections of this year class were cancelled.

In 2012 a third year class of fish was produced, marked and stocked under the same protocol as used in 2010. Unfortunately, most known marked fish from this year class were lost to an apparent hatchery water quality issue during the grow-out period. One subset of fish that was not lost was held for possible evaluation in the continuing effort to equate marking techniques with successful mark events in redbreast sunfish. However, this subset of fish does not represent enough of the stocked fingerlings to warrant an assessment of the 2012 year class stocking at age 1+.. Continuing efforts will go into production, marking, stocking, and grow out of the 2013 year class.

## **Discussion**

There are no published assessments of redbreast stocking such as this one in the literature. This will ultimately be a valuable contribution to all of us and others that are managing redbreast populations. We are excited to be moving forward with assessments of the 2010 year class.

The successful marking of redbreast sunfish has been demonstrated (Leitner 2011), and is a vital step toward full implementation of this study. The results for the 2011 year class mark evaluations are a reminder however that OTC marking of *Lepomis spp* can be problematic. As with any study involving the OTC marking of fish, great care should be taken to adhere to section protocols during marking and stocking of subsequent year classes. As that still does not guarantee

that 100% of fish will be marked, a robust evaluation of known marked fish is essential to study success.

To evaluate OTC marks effectively a number of steps must be taken. A sufficient grow out period is required. For sunfish marked in the fall this period should span at least 6 months. A set of known unmarked fish from the same year class should also be grown out, to ensure availability of suitable size and age fish of the same species for development of blind OTC evaluation sets. These blind sets require a minimum of 30 fish after growout from each mark event, and from known unmarked fish. Multiple growouts of each group is ideal as it provides insurance against routine or catastrophic die offs in any one group, as impacted the evaluation of the 2012 year class. The above mentioned protocols are in place for the marking and growout of redbreast in 2013.

### **Recommendations**

Continue study. Abandon plans to collect and assess the 2012 year class from the wild. Mark and stock a 2013 year class of redbreast sunfish, following in place protocols. Ensure an extended grow out is allowed for a sufficient sample of fish from each mark event, and of known unmarked fish from the same year class. Following grow out, complete mark evaluations of the 2013 year class with a blind set of known marked and unmarked fish. Repeat marking and stocking assessment through at least the 2014 year class, or until at least 3 year class stocking evaluations are completed.

### **Literature Cited**

- Bulak, James S. 2005. Recruitment and growth of Edisto River redbreast sunfish. Study Completion Report. South Carolina Department of Natural Resources.
- Crochet, Daniel W. and Christopher W. Sample. 1993 Fisheries Investigations in Lakes and Streams – District VII. Study Completion Report F-31-4. South Carolina Department of Natural Resources.

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**Job Title:** Performance Comparison of Largemouth Bass Strains in Farm Ponds

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

We completed analysis of a historic genetic database of allele frequencies found in multiple filial generations of largemouth bass *Micropterus salmoides* produced in 28 farm ponds over a 12 year period. These ponds are clustered in the Piedmont and Coastal Plain regions of South Carolina. Analysis assessed selection for or against alleles typical of Florida bass *M. floridanus* over time. While 18 of 28 ponds did exhibit significant allelic change, selection for or against Florida alleles was not indicated in either geographic region.

### **Introduction**

South Carolina is located within the hybrid zone between the largemouth bass and Florida bass. Allozyme surveys have shown that South Carolina largemouth bass populations possess a combination of alleles typical of both subspecies. Further, an allelic cline exists where Florida alleles dominate the genome of those Coastal Plain populations surveyed, and the incidence of northern alleles increases as you move up a drainage (Bulak et al., 1995). In 1994 and 1995 a group of 36 farm ponds, clustered in the Piedmont and Coastal Plain regions of South Carolina, were stocked with largemouth bass from either of two genetic stocks. One stock was produced with broodfish collected from Lake Moultrie, a population whose genome is about 95% Florida. The other was produced with Lake Wateree broodfish, a population that is about 50% Florida. A major objective of this study was to follow the successive generations produced in these ponds, and assess whether selection in each region affects the frequencies of Florida and Northern alleles. To that end juveniles were collected from these ponds on an annual or semiannual basis from 1995 - 2005.

Genetic data was generated for each year class from each pond sampled, to track changes in the proportions of largemouth and Florida bass alleles over time. Sufficient genetic data for evaluation was produced from 28 ponds. In the last year analysis of this genetic database was completed.

## **Materials and Methods**

Filial generations were combined into three periods, where generations 1-3 = period A, 4-6 = period B, and 7-11 = period C. Using the software program GenePop, we statistically evaluated the change across periods at each of four loci for each pond population. We also calculated an overall Chi-square for allelic change in each pond across all four loci.

## **Results**

While 18 of 28 ponds did exhibit significant allelic change, selection for or against Florida alleles was not indicated in either geographic region. Of 12 Coastal Plain ponds evaluated for change across all loci, 2 exhibited an overall decrease and 3 an increase in Florida alleles. Three ponds had significant change in both directions, and 4 exhibited no change. Of 16 Piedmont ponds, 6 exhibited an increase in Florida alleles, 4 exhibited change in both directions, and 6 exhibited no change.

Results by individual locus are similar. Change in both directions was measured at each locus, and no change was measured more commonly than either an increase or decrease in Florida alleles.

## **Discussion**

Results indicate that the loci evaluated either are not under selection, or are not under selection that is strong enough to be measurable in the study period. The ponds evaluated in this study represent a cross section of privately owned small impoundments, all from 1 to 3 acres in

surface area. We strove to select manageable ponds that were typical of their geographic region, and that would have little potential for introduction of bass other than those we stocked. However, factors such as pond topography, in water habitats, and water quality certainly varied across ponds. Such factors associated with individual pond habitats may have confounded our ability to see any potential selective influence associated with Coastal Plain and Piedmont geographic regions on the genomes of largemouth bass populations in the ponds. Growth at age-1 and age-3 was also followed in this study, and while we did not see differences in growth associated with the Coastal Plain or Piedmont stocks of largemouth used, a common garden experiment using the same stocks did result in significant differences in growth (Leitner and Bulak 2008). This pond study indicates that pond-specific factors are most likely to influence the growth and abundance of largemouth bass in South Carolina ponds.

### **Recommendations**

Complete a final report for this study and consider publication of results. The protection of long term local adaptations is important to consider in the management of our freshwater fish species in the wild. We continue to recommend the use of local stocks of largemouth bass and other species when augmenting wild populations with fish produced in our hatcheries.

### **Literature Cited**

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Prepared By: Jean Leitner

Title: Fisheries Biologist

**Job Title:** Robust Redhorse Annual and Seasonal Movements within the Upper Santee River System

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

Seasonal movements of robust redhorse *Moxostoma robustum* were monitored with acoustic telemetry in the upper Santee-Cooper system during 2009 – 2013. During 2009 -2012 twenty-seven (27) robust redhorse were implanted with transmitters and monitored each year with a receiver array that consisted of at least 30 fixed receiver locations. Transmitter expulsion and/or tagging mortality was very high for robust redhorse; however, the movements of 12 fish were monitored for at least one year. Those fish had large annual ranges with most fish using the entire length of the Wateree River and the majority of the Congaree River. Three fish ventured down into the upper Santee River where they had access to Lake Marion and three fish moved above the Congaree River into the Broad and/or Saluda Rivers. All fish entered the tailrace below Wateree Dam each spring presumably to spawn.

### **Introduction**

Robust redhorse were stocked into the upper Santee River system each year during 2004 – 2011, and during 2013, in an effort to establish a genetically diverse naturally reproducing population. It was not known how these fish would utilize the multiple rivers and reservoirs that comprise the Santee-Cooper system or where they could be recaptured to monitor the population status. The objectives of this study were to: 1) document annual and seasonal use of river reaches within the upper Santee River system, and 2) use transmitter-implanted fish to locate spawning aggregations and population centers.

## **Materials and Methods**

### *Study Area*

Robust redhorse movements were monitored in the Santee-Cooper system. The Santee-Cooper system, situated in the Coastal Plain of South Carolina, consists of two large reservoirs (Lake Marion and Lake Moultrie) formed by dams on the Santee and Cooper rivers and tributary rivers that form the Santee River which flows into upper Lake Marion (Figure 1). Lake Marion is a partially wooded 44,000 ha impoundment on the Santee River with a maximum depth of 12 m at the dam, but overall the reservoir is shallow (1-3 m). Lake Moultrie is a 25,000 ha open water reservoir with a maximum depth of 21 m.

The upstream tributaries of Lake Marion include the Congaree, Wateree and Santee Rivers. The Congaree River originates in Columbia, SC at the confluence of the Saluda and Broad Rivers, and flows 85 km until it merges with the Wateree River to form the Santee River (Figure 1). Hypolimnetic releases from the Lake Murray Dam on the Saluda River provide cool water to 16 km of the lower Saluda River. The Wateree River originates below the Wateree Dam and flows roughly 122 km before merging with the Congaree River to form the Santee River. The Santee River flows 26 km before forming the headwaters of Lake Marion. Average annual discharge of the Congaree and Wateree Rivers are 267 m<sup>3</sup>/s and 225 m<sup>3</sup>/s, respectively (Bennett et al. 1993).

### *Field Methods*

We used ultrasonic telemetry to follow movements of robust redhorse throughout the system. During spring of 2009, 2011, and 2012 we attempted to collect robust redhorse, with boat-mounted electrofishing equipment from the upper Congaree and Wateree Rivers. During December 2012 we attempted to collect robust redhorse from the lower Wateree River. When captured

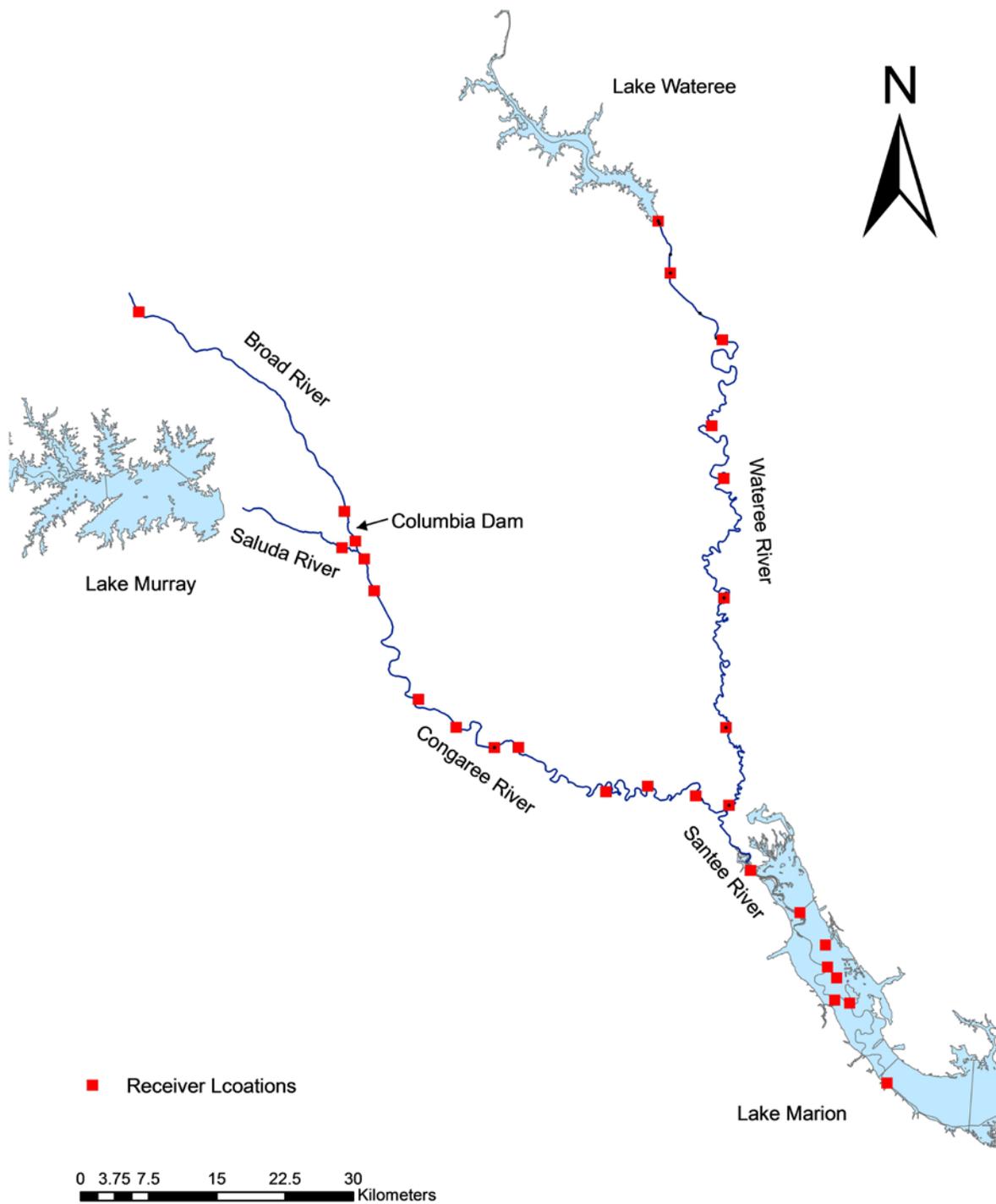


Figure 1. Receiver locations (VR2 and VR2W) in the upper Santee River system during 2009 – 2013.

robust redhorse were immediately placed on a large v-trough measuring board, or foam-lined cooler filled with river water, covered in wet towels, measured, and sexed, when possible. Ultrasonic transmitters (VEMCO Ltd., Nova Scotia; V16) were inserted through a 30 mm incision posterior to the right ventral fin. Incisions were closed with three interrupted absorbable sutures (2-0 Maxon; Tyco Health Care). No chemical anesthesia was used, fish were sufficiently narcotized from electrofishing for the short (3-4 minute) implantation procedure. After transmitter implantation fish were immediately released. All surgical tools and tags were disinfected with Benz-All® (Xttrium Laboratories, Chicago, IL) before surgery.

Ultrasonic transmitters measured 68 mm long, 16 mm in diameter, and weighed 24 g. Each transmitter operated at 69 kHz and was uniquely identifiable based on unique pulse periods between transmissions.

Robust redhorse were located between May 2009 and September 2013 with a receiver array consisting of at least 30 fixed receivers (VEMCO Ltd., Nova Scotia; VR2 and VR2W) positioned throughout the system (Figure 1). The receivers recorded the transmitter ID number, date and time whenever a fish passed within the receiver's detection range. Receivers were downloaded approximately once every four months. Manual tracking was occasionally conducted by boat, with a manual tracking receiver, to search for missing fish. Manual searches of the Wateree and Congaree Rivers occurred on 10 dates during fall 2012.

## **Results/Discussion**

Twenty-seven (27) robust redhorse (mean total length [TL] = 554 mm; range 469 – 615 mm TL) were implanted with transmitters between April 2009 and December 2012 (Table 1). Twenty-six (26) of those fish were captured from the Wateree River and one fish was captured from the

Congaree River. Twenty-three (23) of the fish were captured from the Wateree River 0.75 km below Wateree Dam from a shoal where aggregations of fish attempting to spawn are routinely encountered during spring.

Transmitter implanted robust redhorse experienced very high (48%) tagging mortality or perhaps transmitter expulsion. The cause of this mortality, or expulsion, is unknown, but may be related to the season of tagging. The majority (23 of 27) of fish were collected during spring from spawning aggregations below Wateree Dam and 52% of those fish apparently died or expelled their transmitters. Tagging actively spawning and recently spawned fish may have increased mortality and/or transmitter expulsion. Additionally fish in this area were subjected to frequent electrofishing sampling during routine SCDNR and Duke Energy fish sampling which may have caused additional stress that could have negatively influenced survival. High rates of mortality or transmitter expulsion for transmitter-implanted Robust Redhorse have been previously documented in a Georgia river (Ely 2012).

Of the 14 fish successfully implanted 8 were alive at the conclusion of the study, transmitters of 4 fish expired, and 2 fish apparently died of natural causes. Number of days tracked for fish that survived tagging averaged 565 d (range; 188 -837 d) and number of detections at receiver locations averaged 19,574 (range; 1,924 – 55,750) (Table 1); 12 fish were tracked for at least one year.

The robust redhorse tracked in this study exhibited large annual ranges with all fish utilizing at least 2 of the 5 rivers that comprise the upper Santee-system. All 14 transmitter-implanted fish used the Wateree Tailrace during the spring presumable to spawn. Each of the 12 fish that were tracked for at least one year traversed the entire Wateree River and utilized the lower Congaree River, 11 fish utilized the middle Congaree River, and 7 fish utilized the upper Congaree River (Figure 2). Three fish ventured above the upper Congaree River into the Broad and Saulda rivers,

with one fish entering both the Saluda and Broad rivers. None of the fish that entered the Broad River were detected above Columbia Dam. Three fish ventured down into the upper Santee River, where they were detected in the main river channel; however, they had access to the upper section of Lake Marion that was not instrumented with receivers.

Table 1. Date of transmitter implantation, transmitter ID, total length (TL,mm), tagging location, fate, days tracked, and total number of detections for robust redhorse implanted with transmitters and tracked in the Santee-Cooper system during 2009 – 2013. Fate codes are; TE (tag expired), TM (tagging mortality/transmitter expulsion), A (alive), and D (died).

Date	ID	TL	Location	Fate	D_tracked	Detections
4/30/2009	56800	491	Wateree River - upper	TE	813	55750
5/7/2009	56802	469	Wateree River - upper	TM		486
5/15/2009	56803	488	Wateree River - upper	TM		340
5/15/2009	56801	518	Wateree River - upper	TE	759	35901
5/20/2009	56799	507	Wateree River - upper	TM		6023
4/20/2011	47403	528	Wateree River - upper	A	837	36378
4/20/2011	47404	566	Wateree River - upper	TE	770	18254
4/20/2011	47405	572	Wateree River - upper	A	826	15434
4/20/2011	47406	576	Wateree River - upper	TM		277
4/20/2011	47407	569	Wateree River - upper	D	373	22974
4/20/2011	47408	576	Wateree River - upper	TE	749	38545
4/9/2012	30564	615	Wateree River - upper	TM		2347
4/9/2012	30562	587	Wateree River - upper	A	513	15880
4/9/2012	30560	585	Wateree River - upper	TM		1669
4/9/2012	30559	596	Wateree River - upper	D	391	8226
4/9/2012	30557	589	Wateree River - upper	A	513	3005
4/9/2012	30558	565	Wateree River - upper	TM		6
4/16/2012	30546	571	Wateree River - upper	TM		0
4/16/2012	30547	550	Wateree River - upper	TM		23
4/16/2012	30545	560	Wateree River - upper	TM		1667
4/16/2012	30549	580	Wateree River - upper	A	416	13522
4/16/2012	30548	575	Wateree River - upper	TM		397
4/16/2012	30550	499	Wateree River - upper	TM		182
4/19/2012	30556	588	Congaree River - upper	A	496	1924
12/18/2012	30551	557	Wateree River - lower	A	188	4408
12/18/2012	30554	567	Wateree River - lower	A	264	3834
12/18/2012	30552	505	Wateree River - lower	TM		0



During March of each year all transmitter-implanted Robust Redhorse entered the tailrace below Wateree Dam (Figure 3). During each year fish remained in the tailrace until late May or mid-June. Mean water temperature when fish entered the tailrace was 13.1°C (range; 11.4 – 14°C) and mean water temperature when fish exited the tailrace was 25.3°C (range; 23 – 27°C). Movements into the tailrace were presumably related to spawning activity. Spawning aggregations and fish in spawning condition were encountered in the Wateree River tailrace during spring 2012 and 2013. Robust Redhorse reportedly spawn during spring when water temperatures are between 18 -24°C (Hendricks 1998; Freeman and Freeman 2001).

### **Recommendations**

During 2014 a final report will be completed on the annual and seasonal movements of Robust Redhorse in the Santee-Cooper system.

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- Hendricks, A.S. 1998. The conservation and restoration of the robust redhorse, *Moxostoma robustum*, Volume 1. Report to the Federal Energy Regulatory Commission. Georgia Power Company, Atlanta, Georgia.

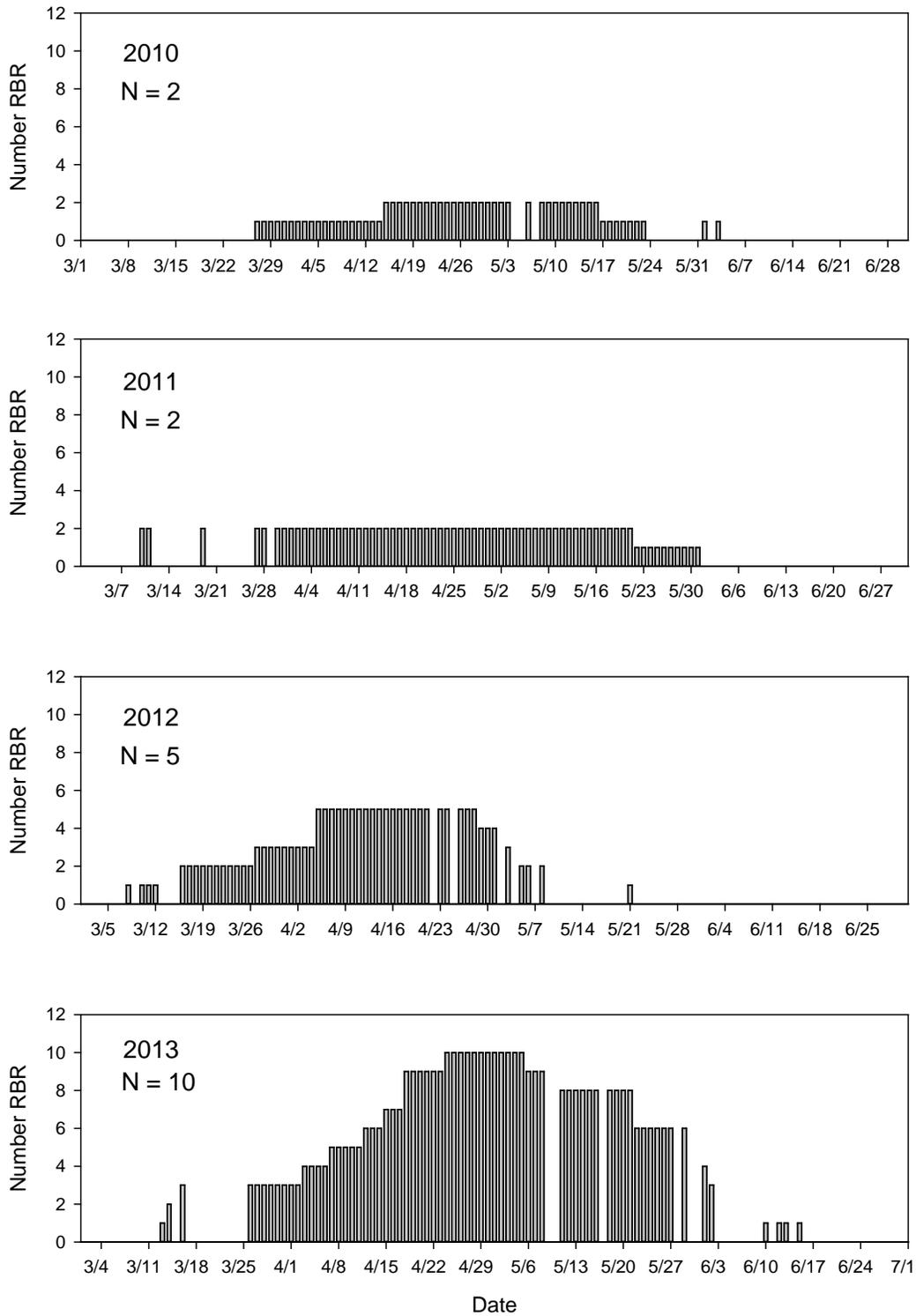


Figure 3. Number of transmitter-implanted Robust Redhorse in the Wateree Dam Tailrace by date during spring of each study year 2010 - 2013. “N” denotes the number of transmitter implanted Robust Redhorse alive each year.

**Job Title:** Assessment of condition, growth, contribution to fish community, and diet of striped bass, white perch, and American shad young-of-the-year in the Santee-Cooper lakes, South Carolina

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

Boat electrofishing was conducted at two Lake Marion sites during summer and fall 2012 to evaluate relative abundance and diet of key juvenile fish species. During summer and fall 2012 white perch *Morone americana* and American shad *Alosa sapidissima* were the most abundant species accounting for 45% and 33% of all young-of-year fish collected. Striped bass *Morone saxatilis* were the third most frequently encountered fish species comprising 15% of the total catch. Gizzard shad *Dorosoma cepedianum* juveniles, which were common in 2011, were rarely encountered during 2012. We continued our evaluation of the diet of juvenile striped bass, American shad and white perch. Dry weights were generated for 9,240 prey items identified in the stomach contents of juvenile fish. By weight American shad and white perch fed primarily on insects, and striped bass fed primarily on fish. Twenty-one (21) threadfin shad *Dorosoma petenense* stomachs were processed for diet contents. Every threadfin shad stomach contained algae, and more than 90% of stomachs contained benthic debris, sand and rotifers. Microcrustaceans were encountered in 57% of threadfin shad stomachs.

### **Introduction**

‘Fingerling mortality’ of striped bass is a key issue for the Santee-Cooper striped bass stakeholders and it has been a key issue of the DNR for many years. Many hypotheses have been generated to define the causes of either good or poor recruitment in a given year. These hypotheses include, but are not limited to, reduction in the adult spawning stock, competition with resident and

anadromous species, and reduced nutrient inflow due to drought. The Santee-Cooper Comprehensive study group of the DNR defined investigation of the ‘competition for resources’ hypotheses as its primary short-term goal. A strategy was needed to obtain key monitoring data on the species of interest. The objectives of this study are to, 1) define growth and condition of key juvenile species, 2) describe the diet of each species and 3) define the relative abundance of each key species.

## **Materials and Methods**

### *Growth, condition and relative abundance*

Young-of-year (YOY) American shad, blueback herring *Alosa aestivalis*, threadfin shad, white perch and striped bass were collected monthly from two Lake Marion sites with boat electrofishing gear. At each site night-time electrofishing was conducted for roughly 10 minutes at each of three transects. We attempted to collect all young-of-year (YOY) of the targeted species. Specimens were preserved on ice and measured (TL, mm) and weighed (mg) within 24 hours of collection.

### *Diet*

Up to 15 of each key species per site were preserved in 10% formalin on every sample date during 2009. Between 2010 and 2012 the stomach contents of preserved striped bass, American shad, and white perch specimens were examined under a dissecting microscope and identified to the lowest practical taxon. We continued our work on the diet of key species during 2013 when we updated our diet database to include dry weight of prey items so that diet composition by weight could be assessed. Weights for prey item were assigned, calculated, or directly measured. For larval insects and tessellated darters (the most frequently encountered fish in stomach samples) we

calculated weight using published length-weight relationships. A sample of adult insects (Midges and Mayflies) was collected from Lake Marion during summer 2013 and processed for dry weights. Those weights were then assigned to appropriate prey items in our data base. Tissue from unidentifiable fish was removed from diet samples, dried at 60°C for 48 h, and weighed.

During summer 2011 threadfin shad were retained for diet analysis. Contents from the foregut (esophagus and gizzard) were removed and stained with Eosin B during 2013. Three 1 ml subsamples were removed from the stained contents and placed on three individual Sedgewick-Rafter cells. The sample contents were reviewed under a compound microscope and identifiable prey items were enumerated along five horizontal transects of each Sedgewick-Rafter cell. In addition the proportion of algal cells and benthic material encountered was qualitatively assessed by percent. Frequency of occurrence was calculated as the proportion of fish stomachs that contained one or more individuals of a given food type.

## **Results/Discussion**

### *Relative abundance*

Young-of-year morones and clupeids were collected at night from two Lake Marion sites with boat electrofishing during July – December 2012. The “Big Water” site was located near I-95 on the Clarendon County side (34.5178, -80.4349) and the “Indian Bluff” site was located midway down the reservoir on the Orangeburg County side (33.4319, -80.3621). Three transects were sampled at each site on five different dates. Each site received approximately 0.5 h of electrofishing effort on each sample date. During 2012 thirty (30) transects were sampled with a total electrofishing effort of 5.0 h (Table 1).

Table 1. Number of transects sampled on each date and electrofishing effort (h) during nighttime electrofishing at two sites on Lake Marion, SC during 2012.

Date	Big Water		Indian Bluff		Total	
	Transects	Effort (h)	Transects	Effort (h)	Transects	Effort (h)
7/18/2012	3	0.50	3	0.50	6	1.00
8/30/2012	3	0.50	3	0.50	6	1.00
9/26/2012	3	0.50	3	0.50	6	1.00
11/15/2012	3	0.50	3	0.05	6	1.00
12/13/2012	3	0.50	3	0.05	6	1.00
Total	15	2.50	15	2.50	30	5.00

Overall white perch and American shad dominated the community representing 45% and 33% of all YOY fish collected during 2012, respectively (Figure 1). Striped bass and threadfin shad were next most commonly encountered species, accounting for 15% and 6%, respectively. Gizzard shad YOY were abundant in 2011; however, only two individuals were collected during 2012. Relative abundance of the target species varied by site and year. American shad were a larger component of the sample at the Big Water site during 2012, where they accounted for 44% of all fish collected, than the Indian Bluff site where they represented only 11% of all fish collected (Figure 1). In all years American shad have been at least twice as abundant at the Big Water site than the Indian Bluff site. During 2012 striped bass relative abundance was similar at the Big Water (14%) and Indian Bluff (18%) sites. Overall striped bass relative abundance during 2012 (15%) was higher than that observed during 2010 or 2011. Relative abundance of threadfin shad was higher at Big Water (9%) than Indian Bluff (0%) during 2012. Overall relative abundance of threadfin shad during 2012 was similar to that observed during 2010 and 2011, but less than that observed during 2009.

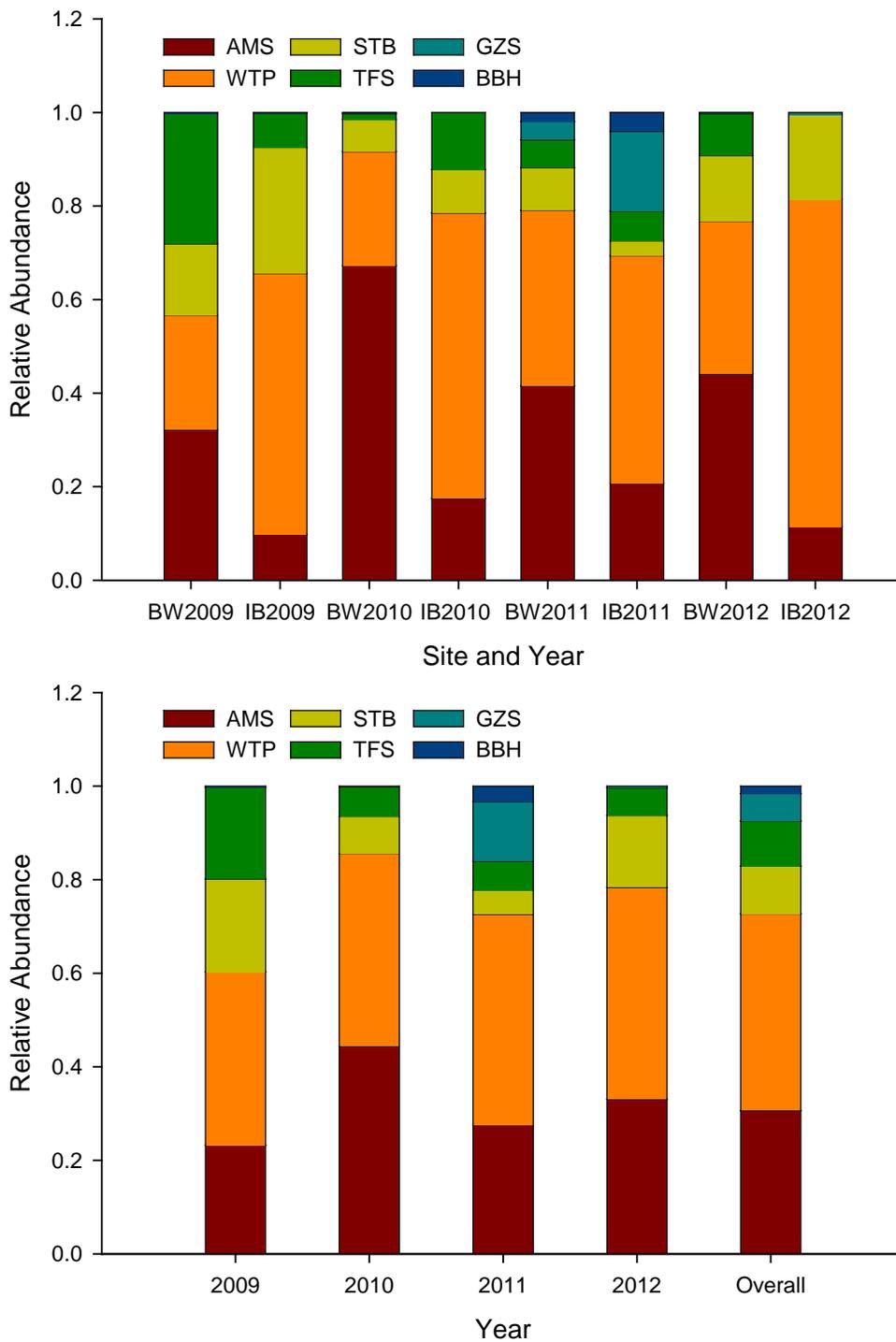


Figure 1. Relative abundance of young-of-the-year American shad (AMS), threadfin shad (TFS), striped bass (STB), gizzard shad (GZS), white perch (WTP), and blueback herring (BBH) collected from littoral areas at the Big Water (BW) and Indian Bluff (IB) sites, Lake Marion, South Carolina, during 2009-2012 (top panel). Overall relative abundance is given for each year (bottom panel).

## *Diet*

Weights were generated for 98% of the 9,463 prey items in our diet database which includes the stomach contents of 113 striped bass, 120 white perch and 69 American shad. Numerically the stomach contents of American shad were dominated by insects which accounted for 83% of the prey items encountered (Figure 2). Microcrustaceans and water mites (Chelicerata) each accounted for 8% of the items encountered while the remaining prey groups accounted for less than 1%. The most numerous items encountered in striped bass stomachs were microcrustaceans (78%) and insects (18%) while fish accounted for less than 2%. The most numerous items encountered in white perch were microcrustaceans (59%) and insects (40%). By weight insects accounted for over 99% of the diet of American shad (Figure 2). Although fish were rare (<2% of total prey items) in the stomach contents of striped bass they accounted for 90% of their diet by weight. By weight white perch diets were dominated by insects (81%), but microcrustaceans were also important (18%). Although the diet, by weight, of American shad and white perch consisted largely of insects the potential for competition for prey resources was diminished because American shad fed almost exclusively on adult insects while white perch fed primarily on larval insects.

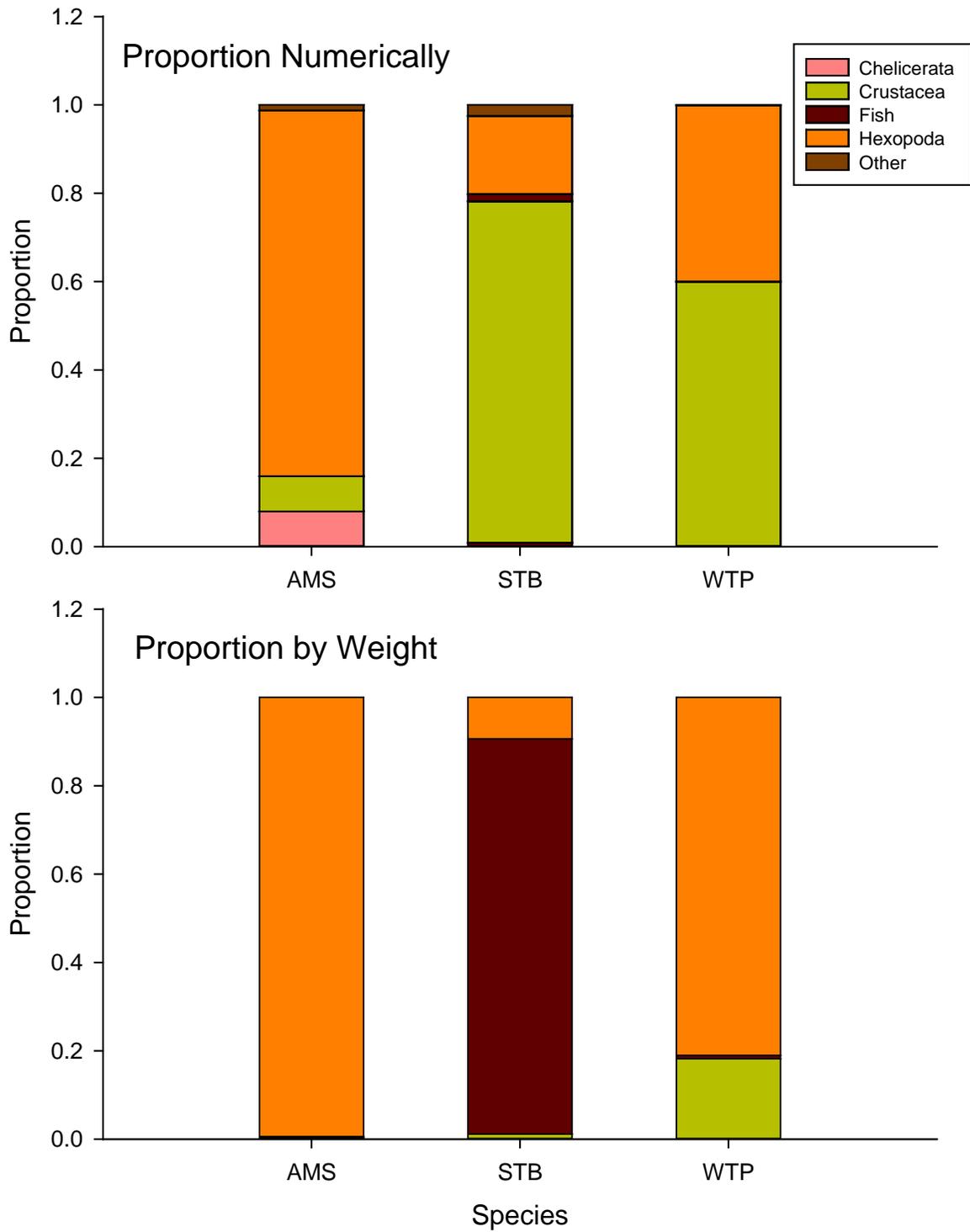


Figure 2. Proportion numerically (top panel) and by weight (bottom panel) of major prey items in the diets of young-of-the-year American shad (AMS), striped bass (STB), and white perch (WTP) collected from littoral areas of Lake Marion, South Carolina, during 2009.

During 2013, 21 threadfin shad (mean TL = 66 mm; range 56 - 84 mm TL) stomachs collected during 2011 were excised and examined for contents. All of the threadfin shad stomachs contained at least some items. A total of 5 different microcrustacean taxa, 3 taxa of loricate rotifers, 3 algal types as well as water mites (Hydracarina) were found in the dissected stomachs (Table 2). Algae and benthic material made up the bulk of the items encountered. Qualitatively, 51% (range; 24 – 83%) of the items identified in individual stomachs were algae and 29% (range: 10 – 75%) were benthic material. Algae, benthic material, sand, and rotifers were encountered in nearly all stomachs (Table 2). Microcrustacea (cladocerans and copepods) were common occurring in 57% of stomachs, while other items bryozoans (14%), water mites (10%) and insect fragments (5%) were rare.

### **Recommendations**

During 2014 we will combine juvenile fish data collected from Lake Marion with similar data collected from Lake Moultrie. Once a database has been constructed the data will be used to describe relative abundance, growth and condition of each species and evaluate spatial and temporal differences within the lakes. Additional threadfin shad diet samples collected from Lake Marion will be processed and the potential for resource competition among the key species assessed. Genetic samples collected from YOY striped bass during summer 2012 and 2013 will be processed to examine the contribution of stocked fish at our sample locations.

Table 2. Prey taxa encountered and frequency of occurrence (percent) of prey taxa in the stomachs of threadfin shad collected from Lake Marion, South Carolina during 2011.

Prey Group	Taxa	Frequency
Algae		100%
	Diatoms	
	Desmids	
	Filamentous	
Bryozoa	Bryozoa	14%
Crustacea		57%
	Cladocera	
	Daphnia	
	Latona	
	Bosminopsis	
	Copepoda	
	Calenoid	
	Cyclopoid	
Rotifera		95%
	Brachionus	
	Keratella	
	Monostyla	
Hydracarina		10%
Benthic debris		95%
Sand		91%
Insect		5%

**Job Title:** Trophic Resources for Larval Fish in Lake Marion

**Period Covered** July 1, 2012 – June 30, 2013

### **Summary**

We analyzed processes affecting phytoplankton dynamics in the main basin of Upper Lake Marion. The results from a model for potential impact of the Asiatic clam *Corbicula fluminea* on phytoplankton populations suggest that phytoplankton productivity is insufficient in some years to sustain the *Corbicula* population, which may thus depend on alternate food resources, such as allochthonous carbon imported from the extensive wetlands upstream.

### **Introduction**

In 2008, the South Carolina Department of Natural Resources (SCDNR) re-convened the Santee-Cooper Comprehensive Study Group to provide an update and overview of current conditions in the system and to guide and promote development of a scientific basis for management decisions about aquatic resources within the Santee-Cooper basin. The work reported here is part of the final phase of studies directed toward developing process-based models of food resources and other factors that may affect recruitment of key resident and anadromous fish species in the Santee-Cooper system.

These species, as identified by the Study Group, include striped bass, American shad, blueback herring, threadfin shad, and white perch. These key species have overlapping spawning seasons (April to June); they share nursery areas in Upper Lake Marion; and, in their larval stages, they feed on zooplankton as larvae.

Our general objectives were to assess current conditions in the lake, quantify trophic structure, and to model and evaluate processes that may influence trophic interactions, with

particular attention to the key fish species. A specific objective from the Study Group was to evaluate whether zooplankton abundance may limit the recruitment of key fish species. We focused on Upper Lake Marion, because of its importance as a nursery.

We have already reported on the structure of the food web, which is dominated in biomass by the Asiatic clam, *Corbicula fluminea*, and other molluscs in Upper Lake Marion (Taylor, 2012). We have also reported on zooplankton dynamics, including potential impacts of hydrologic processes, estimates of predation on zooplankton by larval fish (negligible) and by forage fish (potentially large), and an initial assessment of the effects of temperature and phytoplankton abundance on zooplankton dynamics (Taylor, 2011 and 2012).

Our main work during this reporting period entailed completing analyses of processes, including productivity, import, export, and feeding by *Corbicula*, affecting phytoplankton dynamics in the main basin of Upper Lake Marion during spring and summer. (The zooplankton biomass is so small, relative to phytoplankton biomass, that zooplankton feeding is negligible.) We also processed additional zooplankton samples from April-June 2012 for further analysis of zooplankton dynamics, and we also updated water quality and hydrology databases and analyses to incorporate results through 2012.

## **Materials and Methods**

### *Algal population dynamics*

We modeled growth of the algal population in the main basin of Upper Lake Marion (Figure 1) as the sum of rates of algal production, import, export, and consumption by *Corbicula*. Previously reported work on this project showed that zooplankton populations are too small to have a substantial impact on the phytoplankton. Basin volume was assumed to remain constant, and

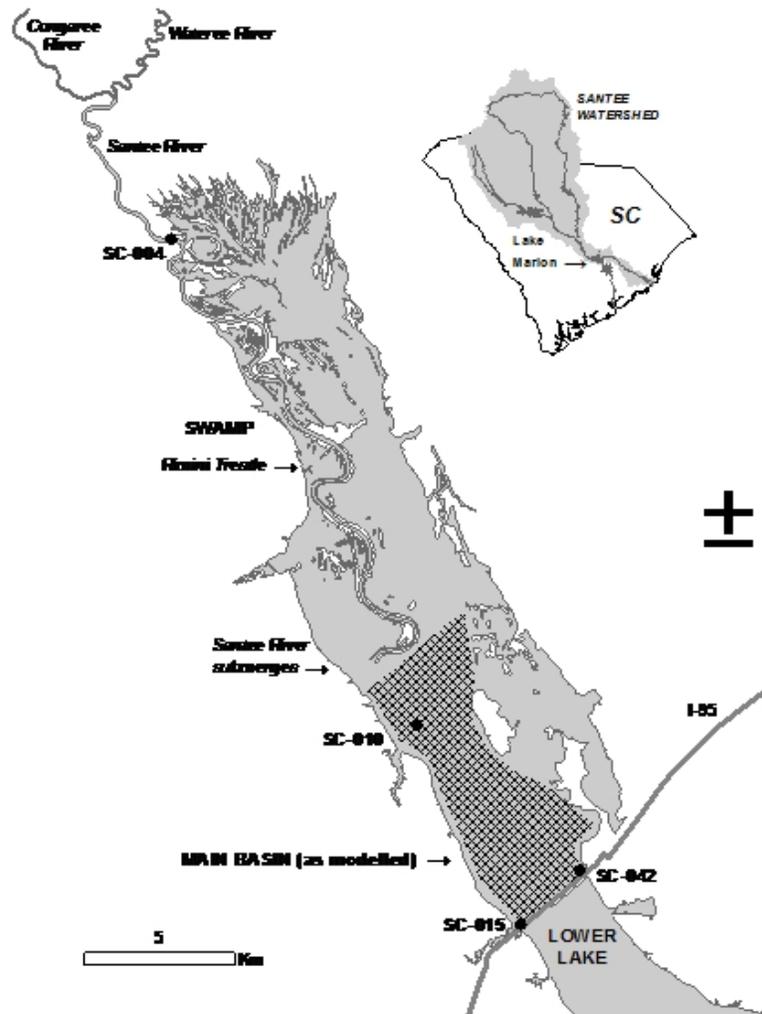


Figure 1. Upper region of Lake Marion. The Santee River flows along a defined channel through the uppermost part of Lake Marion, which is mainly forested swamp. At the lower end of this zone, the river submerges, and open water predominates. The map was derived from the National Hydrography Dataset for the Edisto-Santee Subregion (USGS, 2007). Filled circles show water quality stations.

hydrologic discharge to and from the basin were assumed to be equal. Algal productivity and consumption by *Corbicula* were assumed to be constant throughout the basin. Productivity, as used here, includes settling and other physiological losses. The algal concentration in water leaving the basin was assumed to be that same as the concentration within the basin. With variables as described in Table 1, growth of the algal population is

$$dA/dt = p_{alg} A + A_{in} D / V_{basin} - A D / V_{basin} - C/Z_{mean} \quad [\text{Eq. 1}]$$

$$= p_{alg} A - (A - A_{in}) D/V_{basin} - C/Z_{mean} . \quad [\text{Eq. 2}]$$

The quantity  $D/V_{basin}$  is the flushing rate of the basin. As shown In Eq. 2, this rate can be important to algal dynamics only if the influent algal concentration differs from the algal concentration in the main basin. If algal concentrations of influent water and the basin are identical, the term containing the flushing rate vanishes.

Table 1. Variables used in model of algal population dynamics.

<i>Symbol</i>	<i>Units</i>	<i>Description</i>
<i>A</i>	g dry mass/m <sup>3</sup>	Algal population of main basin
<i>A<sub>in</sub></i>	g dry mass/m <sup>3</sup>	Algal population of influent water
<i>C</i>	g dry mass/m <sup>2</sup> /day	Consumption rate of the <i>Corbicula</i> population
<i>D</i>	10 <sup>6</sup> m <sup>3</sup> /day	Discharge entering and leaving main basin
<i>p<sub>alg</sub></i>	g dry mass/g dry mass/day	Algal productivity
<i>t</i>	days	Time
<i>V<sub>basin</sub></i>	10 <sup>6</sup> m <sup>3</sup>	Volume of main basin
<i>Z<sub>mean</sub></i>	m	Mean depth of main basin

### *Flushing rates*

We estimated daily inflow rates to the main basin of Upper Lake Marion for 2001-2012, using daily mean discharge data from USGS stations in the Congaree River at Columbia and Wateree River at Camden (USGS 02169500 and USGS 02148000; USGS, 2013). These stations are 110 and 140 km upstream from Rimini Trestle; both rivers develop broad floodplains, which preclude good estimates of discharge downstream. There are no major tributaries entering below these stations.

According to Tufford and McKellar (1999), water passing the Camden and Columbia gages reaches Rimini Trestle in about 2 days. Under high flow conditions, water from the Rimini Trestle reaches Station SC-010 in 0.5 days and SC0-015 in 3 days (Patterson and Harvey, 1995). For computations, we assumed a 3-day lag.

We estimated the volume for the main basin of Upper Lake Marion using depths measured on ten evenly spaced, parallel transects across the lake in 2009 (n=50 sample points; Taylor, Bulak, and Morrison, manuscript). We then computed retention times and flushing rates, using combined discharge with a 3-day lag. We adjusted daily volume estimates according to water level in Lake Marion (USGS 02171000; USGS, 2013), but this effect was generally slight.

### *Algal abundance*

We used chlorophyll a data as a measure of algal abundance. Chlorophyll a was measured at 0.3 m depth at open water stations SC-010, SC-015, and SC-42 (Figure 1) at approximately monthly intervals. These data were provided by Santee Cooper Analytical and Biological Services; data for 2001-2006 are also available from STORET.

### *Consumption by Corbicula*

To model consumption, we considered estimates based on filtering rates and on energy requirements.

Filtering rates, which are expressed as the rate of clearance of phytoplankton from the water column, vary widely (e.g., Lauritsen, 1986; Cahoon and Owen, 1996). Lauritsen (1986) measured filtering rates for *Corbicula* from three locations in North Carolina under environmental conditions similar to those in Lake Marion, including spring and summer chlorophyll concentrations of <5 and 10-14 µg/L and water temperatures of 8, 20, and 31 °C. At “spring” phytoplankton concentrations and 20 °C,

$$FR = 3.534 SL^{1.723}, \quad [\text{Eq. 3}]$$

where FR is filtering rate in ml/hr/animal and SL is shell length in mm. At this phytoplankton concentration, filtering rates for animals of similar length were 73% lower at 8 °C and 5% higher at 31 °C. Lauritsen estimated that summer chlorophyll concentrations would cause a 64% reduction in filtering rates.

To estimate consumption for the Lake Marion population, we estimated average filtering rate as the sum of products of the size-specific filtering rates from Eq. 3 and average populations by size class from spring 2009 data multiplied by average depth of the water column. In spring 2009, the average population, based on 50 samples, was 424 animal/m<sup>2</sup> or 50 mg dry mass/m<sup>2</sup> (Taylor, Bulak, and Morrison, manuscript). To estimate consumption rates from the filtering rates, we assumed that chlorophyll a was 0.72% of dry algal biomass (Bicknell et al., 2001; the variability in this factor is large).

We estimated resource requirements for *Corbicula* using the consumption function for the zebra mussel *Dreissena polymorpha* from Schneider’s (1992) model in Fish Bioenergetics 3.0

(University of Wisconsin, Madison, WI), incorporating modifications made by Madenjian (1995). Consumption is computed as grams wet mass of phytoplankton per gram wet mass of mussel. For mussels, we assumed that dry mass was 15% of wet mass (Schneider, 1992). For phytoplankton, we assumed that dry mass was 25% of wet mass (Madenjian, 1995; published estimates range as low as 10%).

Madenjian applied the model to *Dreissena* ranging up to 0.8 mg wet mass per individual, equivalent to 0.12 mg dry mass per individual. We modeled an individual of this maximum size, setting the feeding parameter to its maximum ( $P=1$ ) or to a value yielding no growth ( $P=0.12$ ; value obtained numerically) to estimate algal consumption.

#### *Algal productivity*

We computed monthly estimates of algal productivity from a CE-QUAL-W2i water quality model for Lake Greenwood, an impoundment on the Saluda River upstream of Lake Marion (McKellar et al., 2008; Taylor et al., 2013). An excellent model for Lake Marion was built in the 1990s (Tufford and McKellar, 1999), but algal productivity was not reported in any published results, and the model is no longer available for further study. Although Lake Greenwood is a smaller impoundment, water depth of the selected segment (4 m) was similar to the average for Upper Lake Marion. Water temperature, total suspended solids, and total phosphorus in the model fell within ranges similar to those for open water stations in Upper Lake Marion. Algal productivity  $p$  (in 1/days) was computed from values for algal biomass (in mg/L) and instantaneous primary productivity (in mg/L/day); both were reported at 6-hr time intervals and 1-m depth intervals.

## **Results and Discussion**

Mean flushing rate of the main basin of Upper Lake Marion was typically 0.1-0.2 (retention times of 10 to 5 days) per cent during spring and summer months (Figure 2). The minimum was 0.08/day (retention time of 12.5 days). In 2003, however, the means exceeded 50% per day (retention time of 2 days) for April through July.

Chlorophyll a concentrations (Figure 3) were typically low (all medians and most of the 3<sup>rd</sup> quartiles <5 µg/L) from October through March, higher from April through September (most medians >5 µg/L, some 3<sup>rd</sup> quartiles >10 µg/L). Seasonal patterns and ranges were similar among the uplake station (SC-010) and the two downlake stations (SC-015 and SC-042).

Chlorophyll concentration varied inversely with discharge from the Santee River at the uplake station (Figure 4). The correlation was significant for all months combined ( $r^2=0.25$ ,  $p<<0.001$ ,  $n=98$ ) and for April through September ( $r^2=0.24$ ,  $p<0.001$ ,  $n=52$ ). Similar, but weaker correlations held for the downlake station SC-015. Only the correlation for all months combined was significant for downlake station SC-042.

During spring and summer, monthly median algal productivity  $p_{Alg}$  at the analog site in Lake Greenwood ranged generally between 0.1-0.3 day<sup>-1</sup> (Table 2). The differences in productivity between years were associated mainly with variation in suspended solids and temperature. Monthly stream discharge into Lake Greenwood was near or below normal for April to June of Year 1 (Taylor et al., 2013); discharge was well above normal for those months of Year 2.

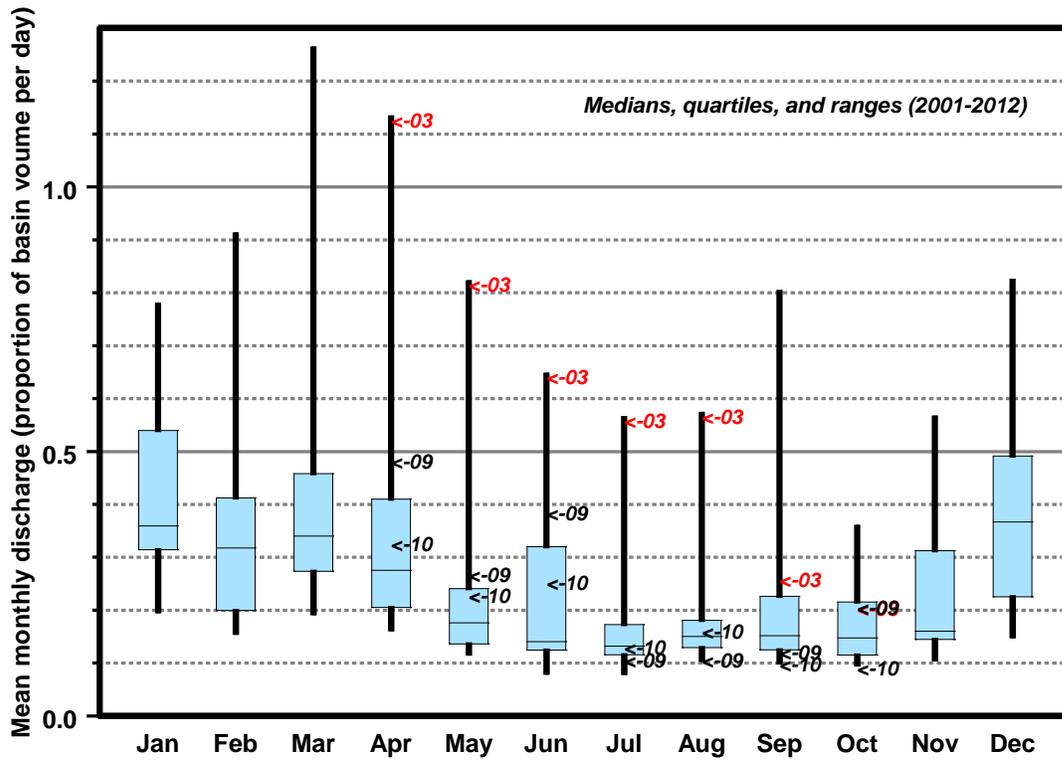


Figure 2. Mean discharge Congaree and Wateree rivers into Upper Lake Marion, 2001-2012. Means for April-October of 2003, an exceptionally wet year, and 2009 and 2010, the years of our benthic samples, are marked by arrows.

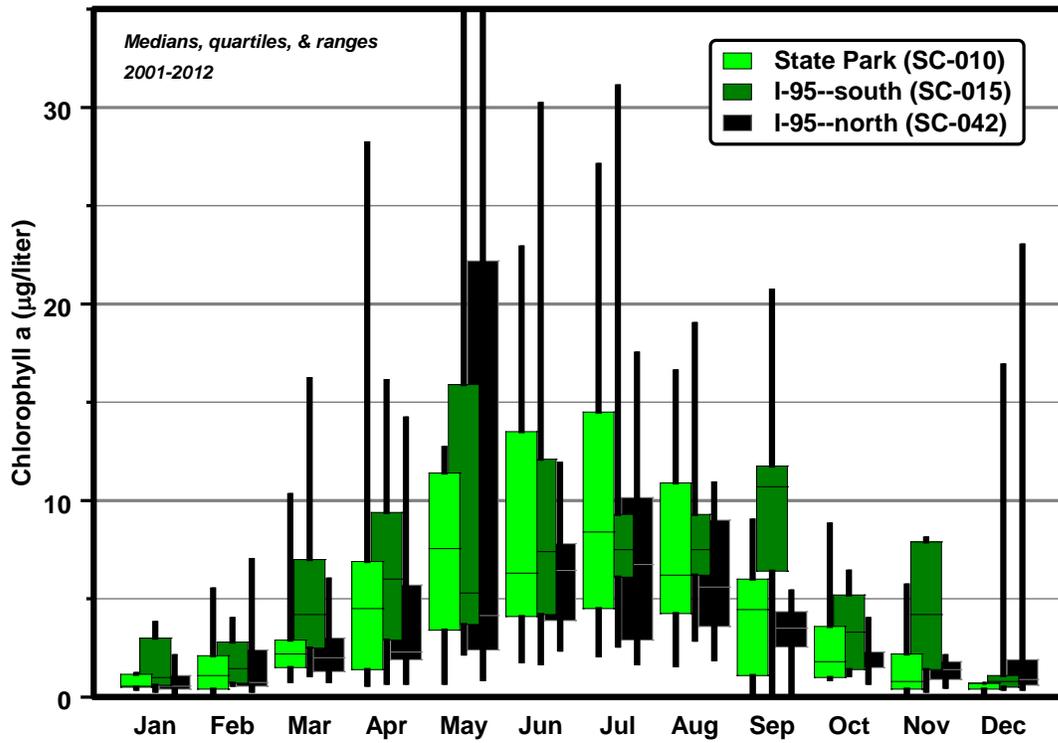


Figure 3. Chlorophyll a in Upper Lake Marion, 2001-2012. Monthly values are summarized for three stations; n of years for each station and month is 4-11.

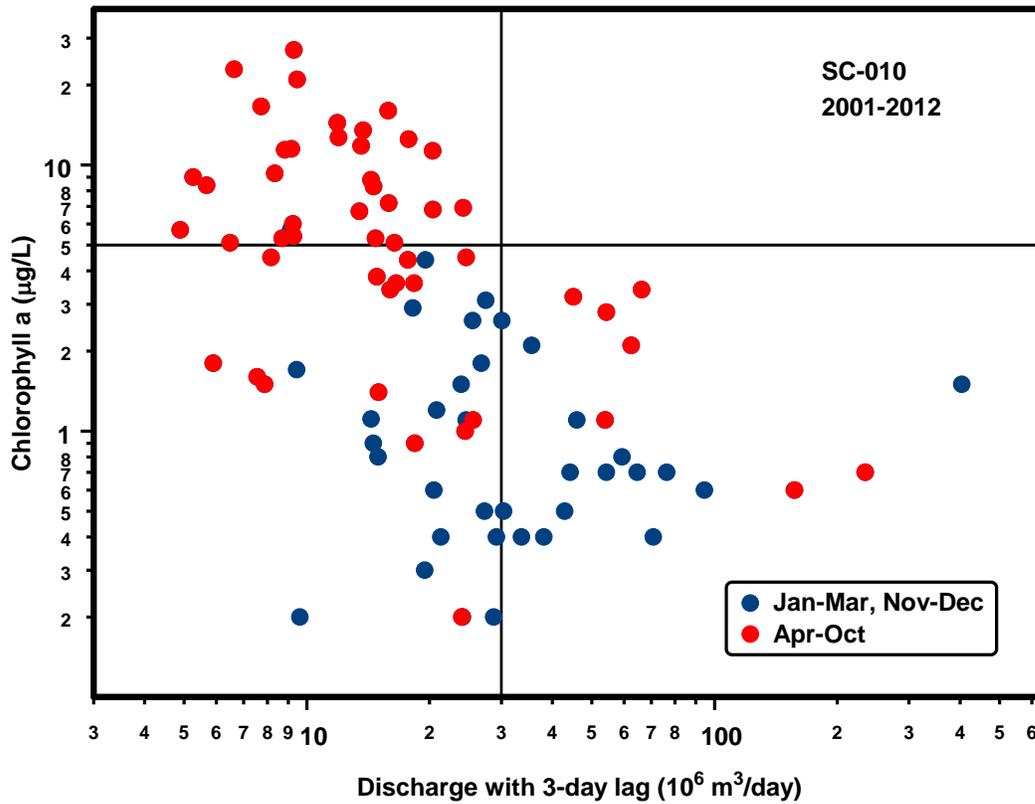


Figure 4. Chlorophyll a at station SC-010 in Upper Lake Marion, 2001-2012, as function of combined discharge from the Congaree and Wateree rivers. Discharge value was lagged by 3 days from the sampling date for chlorophyll a to account for travel time from the gages to the lake.

Table 2. Modeled spring and summer algal productivity.

<i>Month</i>	<i>Algal productivity (1/day)</i>			
	<i>Year 1</i>		<i>Year 2</i>	
	<i>Median</i>	<i>Range</i>	<i>Median</i>	<i>Range</i>
April	0.32	(0.15, 0.58)	0.08	(0.01, 0.18)
May	0.29	(0.13, 0.53)	0.10	(0.04, 0.41)
June	0.27	(0.14, 0.57)	0.13	(0.03, 0.39)
July	0.38	(0.02, 0.87)	0.16	(0.07, 0.28)
August	0.34	(0.18, 0.63)	0.26	(0.10, 0.48)
September	-0.01	(-0.03, 0.34)	0.11	(0.05, 0.21)

According to the bioenergetics model, daily consumption for an animal of 0.12 mg dry mass at 20 °C ranged from 0.6% per day at the maintenance feeding rate (P=0.12) to 4.9% per day at the maximum feeding rate (P=1.0); percentages were computed on a dry biomass basis. The filtering rates (Eq. 3) for the *Corbicula* population per m<sup>2</sup> of substrate was 6.4 m<sup>3</sup>/day. If chlorophyll a concentrations were unaffected by losses due to consumption, this filtering rate would provide the maintenance consumption requirement at chlorophyll a concentrations  $\geq 0.3$   $\mu\text{g/L}$ ; the maximum, at chlorophyll a concentrations  $\geq 2.7$   $\mu\text{g/L}$ .

We used Eq. 3 to estimate the minimum levels of algal productivity required to sustain consumption by the *Corbicula* population. When algal concentrations in the influent water and the lake are similar, the algal productivity required to sustain consumption is independent of the flushing rate. For chlorophyll concentrations of 5-10  $\mu\text{g/L}$ , productivity around 0.1/day will sustain maintenance consumption; productivity of 0.3-0.6/day will sustain moderate consumption, and productivity of 0.5-1/day will sustain maximum consumption (Figure 5, upper panel). When algal

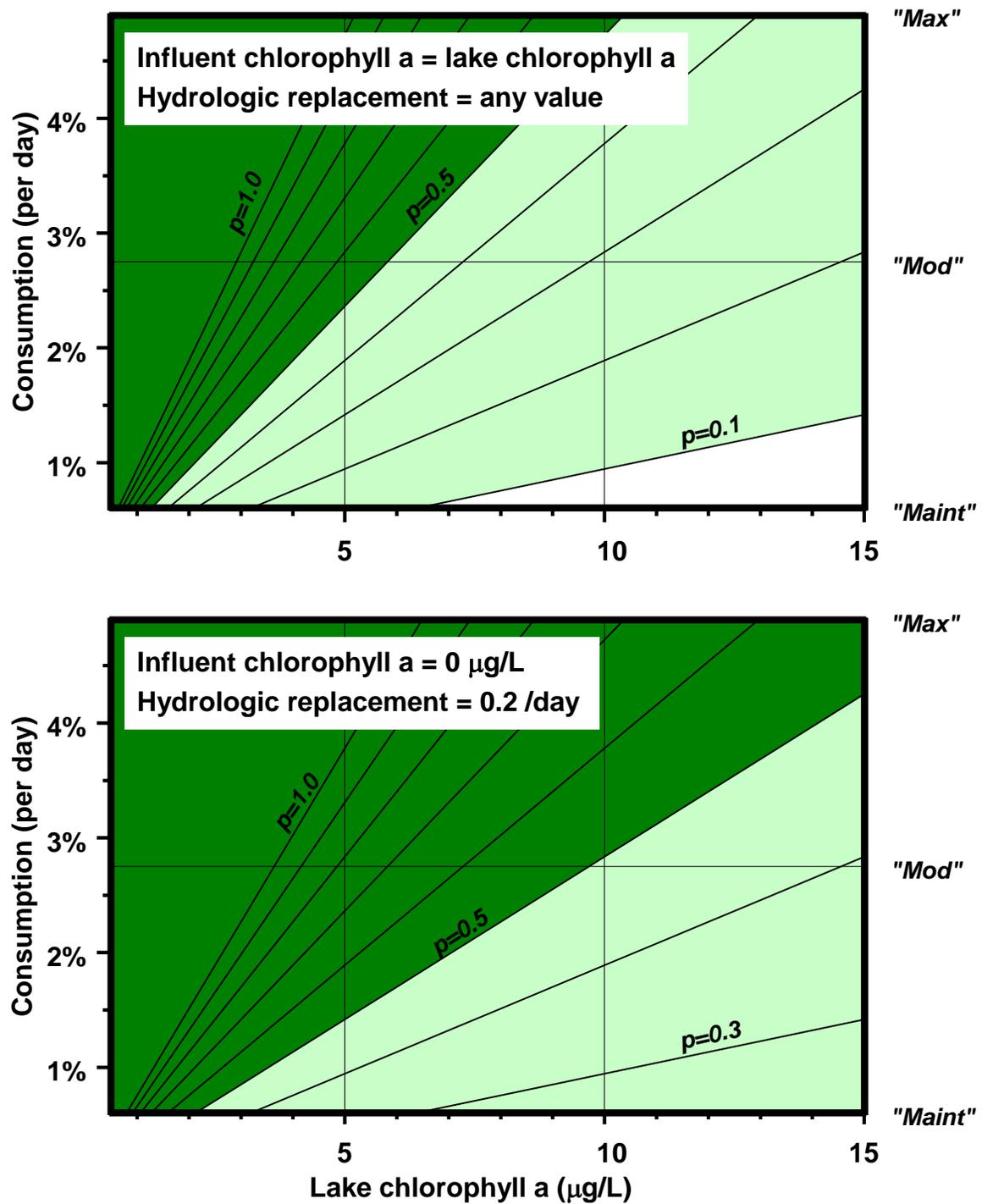


Figure 5. Phytoplankton productivity required to maintain algal populations in Upper Lake Marion, based on consumption by *Corbicula* population.

concentrations in the influent water are negligible, the algal productivity required to sustain consumption is increased by the hydrologic replacement rate. At the typical flushing rate of 0.2/day for Upper Lake Marion, productivity around 0.3/day will sustain maintenance consumption; productivity of 0.5-0.8/day will sustain moderate consumption, and productivity of 0.7-1.1/day will sustain maximum consumption (Figure 5, lower panel).

However, the estimates of algal productivity (Table 2) were typically only 0.1-0.3/day, levels that cannot sustain consumption rates much beyond the maintenance under typical conditions during spring and summer. We speculate that *Corbicula* may depend in part on detrital material of palustrine or terrestrial origin, rather than on planktonic algal production. This dependency may be influenced by discharge. High discharge from the Santee River to the lake inhibits development of phytoplankton populations (as in 2003) and probably brings greater quantities of detrital material.

The abundances of *Corbicula* are clearly large enough to impose substantial losses on the algal populations. The combination of rapid flushing, exacerbated by *Corbicula*, provides a plausible explanation for the relatively low abundances of phytoplankton.

We are continuing to explore how the food web of Lake Marion compares with other southeastern impoundments.

### **Recommendations**

Lake Marion's food web appears to differ substantially from food webs of Piedmont impoundments, such as Lake Norman, NC. The short hydrologic retention time, low phytoplankton abundances and productivity, and the large benthic component of the food web are major considerations for aquatic resource and fishery management in Lake Marion.

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