# Biochemical Genetics of Crappie in Georgia

**by**

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# BIOCHEMICAL GENETICS OF CRAPPIE IN GEORGIA


## ABSTRACT

Isozyme variation at 42 loci was examined for black crappie, *Pomoxis nigromaculatus*, populations in Clarks Hill Reservoir, upper and lower Walter F. George Reservoir, Lake Blackshear, Satilla River, Ogeechee River, Lake Sinclair, Lake Seminole, Lake Tobesofkee, Lake Nottely, Lake Lanier, Lake Allatoona and Carters Lake, and for white crappie, *P. annularis*, in Lake Blackshear. As has been found in other Southeastern black and white crappie populations, isozyme variation was minimal. All Southeastern populations of black crappie and white crappie examined, including Georgia crappie, are closely related. However, several unique rare alleles were detected in Georgia populations that have not been observed in populations in other states. No $F_1$ hybrids between black and white crappie were found in any populations. In 7 of 13 populations sampled, however, hybrid derived individuals were found indicating past hybridization and introgression of the black and white crappie genomes. Although black crappie populations in Georgia are closely related, they can be divided into management subsets based on presence or absence of rare alleles or white crappie alleles.


## INTRODUCTION

Biochemical genetic variation within black crappie and white crappie was minimal among populations in Texas, Arkansas, Tennessee and Alabama (Maceina and Greenbaum 1988, Dunham et al. 1994). Thirteen diagnostic isozyme loci have been identified which distinguish the two species (Buck and Hooe 1986, Maceina and Greenbaum 1988, Dunham et al. 1994). The primary source of biochemical genetic variation in crappie is generated by hybridization between the two species (Dunham et al.

1994, Smith et al. 1994). Hybridization occurs in both hatchery and natural populations in reservoirs.

The $F_1$ hybrids are fertile and are able to backcross with the parent species. As much as 41% of a crappie population may consist of $F_1$, $F_n$ and backcross crappie (Dunham et al. 1994). Although the hybrids are fertile, the number of $F_n$ and backcross crappies was less than expected based on the number of $F_1$ parents in the system. This indicates that the $F_1$ hybrids have reduced reproductive capacity when in competition with the parent species. The backcross hybrids on Weiss Lake had a greater frequency of alleles in black crappie than in white crappie indicating either a greater tendency of the hybrids to backcross with black crappie or a selective advantage for black crappie alleles.

If the explanation for the increased frequency of black crappie alleles in hybrid derived individuals is the tendency to backcross to that parent, it may be related to the appearance of the $F_1$ hybrids. The appearance, meristics and morphology of the $F_1$ hybrids is virtually identical to black crappie. The appearance and color of centrarchids affects their ability to mate in both intra- and interspecific pairings (Childers 1967, Dunham and Childers 1980).

Black crappie also exhibit variation in color pattern. One color variant is the blacknose trait. A distinct black line extends from the tip of the snout to the insertion of the first dorsal spine. Isozyme allele frequencies of this color morph are not different from the normal morph. The blacknose trait is a result of a dominant allele at a single locus (Dunham, unpublished).

The meristics traditionally used to distinguish black, white and hybrid crappie are not effective. The dorsal fin ray count overlaps between the species (Smith 1992) and appears to be inherited by the hybrids in a dominant fashion, the black crappie genes for

this trait being dominant. Conversely, the nape length of the white crappie is dominant. The overlap in these characteristics leads to frequent misidentification of crappie. Overlap in these measurements is not surprising since meristic traits can be environmentally influenced (Dunham et al. 1991). Biochemical identification of crappie is more accurate than meristic identification.

The growth rate of $F_1$ hybrid crappie is faster than that of parents in both small ponds in Illinois (Buck and Hooe 1986) and reservoirs in Alabama (Smith et al. 1994). The $F_1$ hybrids enter the creel faster than their parents, and the use of $F_1$ hybrids might have significant management implications.

The objectives of this study were to survey the biochemical variation of crappie in Georgia and determine if hybridization occurs between black and white crappie populations in Georgia.

## MATERIALS AND METHODS

Crappie populations were collected by fisheries biologists of the Georgia Department of Natural Resources. Samples were collected in all Georgia river basins except the St. Marys, Suwannee, Ochlocknee, and Tallapoosa (Figure 1). Available file data showed no stocking of crappie into any of the study sites. A possibility of undocumented stocking of crappie exists for all streams selected, however. Samples were frozen and sent to Auburn University for electrophoretic analysis.

Samples were analyzed using horizontal starch gel electrophoresis according to procedures of Steiner and Joslyn (1979), Philipp et al. (1983) and Norgren et al. (1986). Nomenclature was modified from that of Norgren et al. (1986). Alleles were assigned numbers reflecting their relative mobilities (distance traveled on the gel) with the largest numbers indicating the furthest migration on the gel.

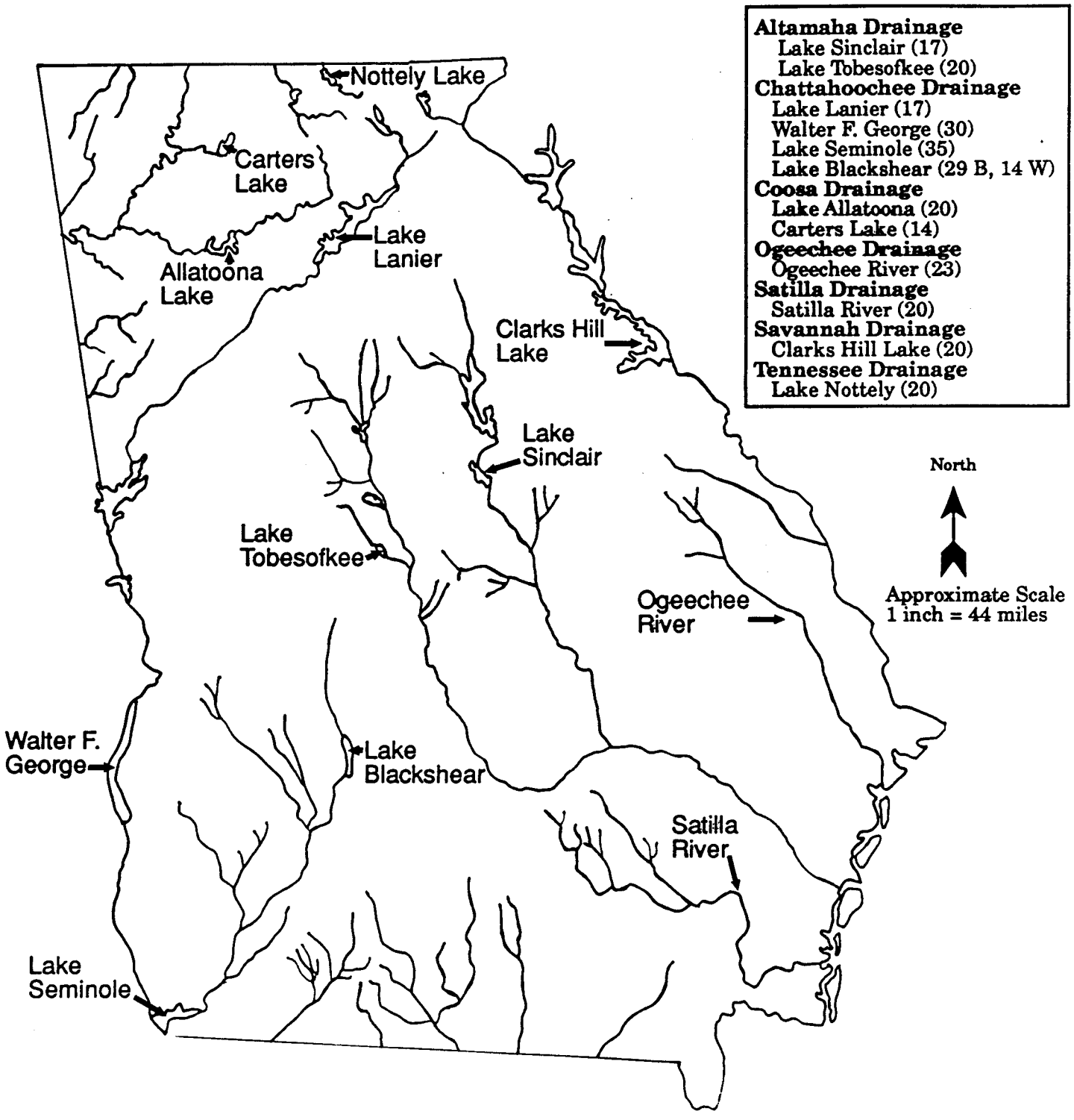


Figure 1. Collection sites of black and white crappie in Georgia. Drainage and numbers of fish collected at each site are shown in the box. Both black (B) and white (W) crappie were collected from Lake Blackshear.

Forty-two loci were examined. Loci evaluated were AAT-A, B; ADH-B; AK-B; APH-B, C; CBP-A, B, C, D; CK-A, B, C; EST-B, C, D; F-1,6-A, B; FUM-A, B; AGP-A, B; GPI-A, B; G2D-A, B; HK-B; IDH-A, B; LDH-A, B, C; MDH-A, B; ME-A, B; PEP-A, B; 6PG-A; PGM-A; SDH-B and SOD-A.

Genotypes, allele frequencies, percentage of loci polymorphic, and mean heterozygosities were determined. A locus was defined as polymorphic if it had at least two alleles. Mean heterozygosity is calculated by averaging the percentage of heterozygous genotypes at individual loci for individual fish within a population. These variables are measures of relative genetic variation between populations. Genetic relationships among the populations were calculated using Rogers' (1972) genetic similarity (S). Dendrograms of these relationships were generated. The higher the value for S, the more the two populations are related.

## RESULTS AND DISCUSSION

### Intraspecific Variation

As was found in previous studies in other states (Maceina and Greenbaum 1988, Dunham et al. 1994), intraspecific isozyme variation was minimal for both black crappie and white crappie in Georgia. Mean heterozygosities were low, except for white crappie in Lake Blackshear, even when including heterozygosity from hybridization (Table 1). When excluding hybridization, the mean heterozygosity for white crappie from Lake Blackshear was near zero. If genetic variation from hybridization is excluded, black crappie from Blackshear and Carters Lake had no intraspecific variation. Six of the remaining populations had only one intraspecific polymorphic locus, three populations had two polymorphic loci and three (Sinclair, Seminole and Tobesofkee) had three polymorphic loci.

Table 1. Mean number alleles per locus, number of intraspecific and interspecific polymorphic loci, percent total loci polymorphic, percentage of individuals $F_n$ or backcross, and mean heterozygosity for Georgia populations of crappie. All populations were identified in the field as black crappie, except for a population of white crappie marked Blackshear$^w$.

| Weinberg Population | N | Alleles per locus | Number of polymorphic loci: interspecific | intraspecific | polymorphic | % loci $\%F_n$ | Mean heterozygosity: Direct Count | Hardy expected |
|---|---|---|---|---|---|---|---|---|
| Clarks Hill | 20 | 1.0 | 0 | 1 | 2.4 | 0 | .001 | .001 |
| Walter F. George (U) | 15 | 1.0 | 0 | 2 | 4.8 | 0 | .009 | .012 |
| Blackshear | 29 | 1.1 | 5 | 0 | 12.0 | 17 | .014 | .015 |
| Walter F George (L) | 15 | 1.0 | 1 | 2 | 7.2 | 7 | .009 | .008 |
| Blackshear$^w$ | 14 | 1.3 | 9 | 1 | 24.0 | 36 | .055 | .104 |
| Satilla | 20 | 1.1 | 3 | 1 | 9.6 | 25 | .008 | .007 |
| Ogeechee | 23 | 1.1 | 1 | 2 | 7.2 | 13 | .009 | .009 |
| Sinclair | 17 | 1.1 | 1 | 3 | 9.6 | 15 | .015 | .013 |
| Seminole | 35 | 1.1 | 1 | 3 | 9.6 | 40 | .017 | .021 |
| Tobesofkee | 20 | 1.1 | 0 | 3 | 7.2 | 0 | .009 | .013 |
| Nottley | 20 | 1.0 | 0 | 1 | 2.4 | 0 | .000 | .002 |
| Lanier | 17 | 1.0 | 0 | 1 | 2.4 | 0 | .004 | .004 |
| Allatoona | 20 | 1.0 | 0 | 1 | 2.4 | 0 | .001 | .008 |
| Carters | 14 | 1.3 | 9 | 0 | 21.0 | 14 | .005 | .051 |

Seminole populations of black crappie may have a fourth polymorphic locus. The majority of the intraspecific variation was unique variation only found in Georgia and not previously found in other states.

Hybridization

Hybridization between black and white crappie in Georgia was frequent in some populations (Table 1), as had been observed in previous studies. High levels of hybridization were observed in Lake Blackshear, Lake Seminole and the Satilla River. All nine loci polymorphic for the Carters Lake crappie population, and all five loci polymorphic for the Lake Blackshear black crappie population, were a result of hybridization with white crappie. Nine of ten polymorphic loci for white crappie in Lake Blackshear were a result of hybridization with black crappie. Low levels of introgression of white crappie alleles into black crappie populations were found in Carters Lake, Ogeechee River, Lake Sinclair, Lake Lanier and Walter F. George populations. There was no evidence of introgression of white crappie alleles in the remaining six black crappie populations.

Unique Alleles

Georgia populations of crappie were similar to other Southeastern crappie because of their lack of isozyme variation (Table 2). Georgia populations were different from other Southeastern populations, however, since a large number of unique rare alleles were observed that had not been detected in other states. The only populations in which at least one new allele was not observed were Lake Blackshear and Carters Lake. Black crappie in Carters Lake did have a rare allele only seen previously in Douglas Reservoir, Tennessee. New alleles were found at the GPI-B, LDH-A, MDH-B and PEP-B loci. Additionally those populations had a rare allele at ME-A that had only been observed

Table 2. Allele frequencies at polymorphic loci in populations of crappie from Georgia. White crappie are marked with a [w]. Weiss Lake fish were collected during another study.

| | Population | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Locus allele | Weiss Lake | Clarks Hill | Walter F. George (U) | Blackshear | Walter F. George (L) | Blackshear[w] | Satilla | Ogeechee | Sinclair | Seminole | Tobe-sofkee | Nottley | Lanier | Allatoona | Carters |
| AAT–A (N) | 18 | 20 | 14 | 12 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 19 | 19 | 21 | 14 |
| A | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| B | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| AAT–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 17 | 19 | 35 | 20 | 19 | 20 | 21 | 14 |
| A | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .964 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| B | .000 | .000 | .000 | .000 | .000 | .036 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| ADH–B (N) | 18 | 20 | 15 | 30 | 15 | 9 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .000 | 1.000 | 1.000 | .975 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .929 |
| B | 1.000 | .000 | .000 | .000 | .000 | 1.000 | .000 | .000 | .025 | .000 | .000 | .000 | .000 | .000 | .071 |
| APH–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | 1.000 | .000 | .000 | .000 | .000 | .857 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .036 |
| B | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .143 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .964 |
| APH–C (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 18 | 35 | 20 | 20 | 10 | 21 | 14 |
| A | 1.000 | .000 | .000 | .000 | .000 | .929 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| B | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .071 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| CBP–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 10 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | .967 | 1.000 | .250 | .975 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .929 |
| B | 1.000 | .000 | .000 | .033 | .000 | .750 | .025 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| CK–A (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | .983 | 1.000 | .000 | .975 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .929 |
| B | 1.000 | .000 | .000 | .017 | .000 | 1.000 | .025 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| EST–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 10 | 15 | 20 | 20 | 20 | 21 | 14 |
| A | 1.000 | .000 | .000 | .000 | .000 | .786 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| B | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .214 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| EST–C (N) | 18 | 20 | 15 | 22 | 15 | 14 | 20 | 15 | 8 | 32 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .000 | 1.000 | 1.000 | 1.000 | .938 | 1.000 | 1.000 | 1.000 | 1.000 | .857 |
| B | 1.000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| D | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .063 | .000 | .000 | .000 | .000 | .071 |

Table 2 (continued). Allele frequencies at polymorphic loci in populations of crappie from Georgia. White crappie are marked with a [w]. Weiss Lake fish were collected during another study.

| Locus allele | Population | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Weiss Lake | Clarks Hill | Walter F. George (U) | Blackshear | Walter F. George (L) | Blackshear[w] | Satilla | Ogeechee | Sinclair | Seminole | Tobe-sofkee | Nottley | Lanier | Allatoona | Carters |
| FUM–A (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 19 | 13 |
| A | 1.000 | .000 | .000 | .000 | .000 | .750 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| B | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .250 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| FUM–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 19 | 13 |
| A | 1.000 | .000 | .000 | .000 | .000 | .750 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| B | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .250 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| GPI–A (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | .917 | .967 | .214 | .975 | .978 | 1.000 | .800 | 1.000 | 1.000 | 1.000 | 1.000 | .929 |
| B | 1.000 | .000 | .000 | .083 | .033 | .786 | .025 | .022 | .000 | .200 | .000 | .000 | .000 | .000 | .071 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| GPI–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | .967 | 1.000 | .933 | .250 | .925 | .957 | .950 | .986 | .900 | 1.000 | .925 | 1.000 | .929 |
| B | 1.000 | .000 | .000 | .000 | .000 | .750 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| D | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| E | .000 | .000 | .033 | .000 | .007 | .000 | .075 | .043 | .050 | .014 | .100 | .000 | .075 | .000 | .000 |
| IDH–A (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| B | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| IDH–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| B | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |

Table 2 (continued). Allele frequencies at polymorphic loci in populations of crappie from Georgia. White crappie are marked with a [w]. Weiss Lake fish were collected during another study.

| Locus allele | Population | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Weiss Lake | Clarks Hill | Walter F. George (U) | Blackshear | Walter F. George (L) | Blackshear[w] | Satilla | Ogeechee | Sinclair | Seminole | Tobe-sofkee | Nottley | Lanier | Allatoona | Carters |
| LDH–A (N) | 18 | 20 | 15 | 24 | 15 | 14 | 19 | 17 | 19 | 35 | 19 | 19 | 20 | 21 | 14 |
| A | 1.000 | .975 | 1.000 | 1.000 | .933 | 1.000 | 1.000 | .912 | .816 | 1.000 | .947 | 1.000 | 1.000 | 1.000 | 1.000 |
| B | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| D | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| E | .000 | .025 | .000 | .000 | .067 | .000 | .000 | .088 | .184 | .000 | .053 | .000 | .000 | .000 | .000 |
| MDH–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | .967 | 1.000 | .250 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .950 | 1.000 | .857 | .929 |
| B | 1.000 | .000 | .000 | .033 | .000 | .750 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| D | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .050 | .000 | .143 | .000 |
| ME–A (N) | 18 | 20 | 15 | 25 | 15 | 12 | 20 | 23 | 20 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | 1.000 | 1.000 | .733 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .757 | .875 | 1.000 | 1.000 | 1.000 | 1.000 |
| B | .000 | .000 | .267 | .000 | .000 | .000 | .000 | .000 | .000 | .243 | .125 | .000 | .000 | .000 | .000 |
| PEP–B (N) | 18 | 20 | 15 | 30 | 15 | 14 | 20 | 23 | 10 | 35 | 2 | 020 | 20 | 21 | 14 |
| A | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .014 | .000 | .000 | .000 | .000 | .000 |
| B | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .950 | .986 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |
| C | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| D | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 |
| E | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .050 | .000 | .000 | .000 | .000 | .000 | .000 |
| PGM–A (N) | 18 | 20 | 15 | 30 | 14 | 14 | 20 | 23 | 10 | 35 | 20 | 20 | 20 | 21 | 14 |
| A | 1.000 | .000 | .000 | .050 | .000 | .786 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .071 |
| B | .000 | 1.000 | 1.000 | .950 | 1.000 | .214 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .929 |
| SDH–B (N) | 18 | 8 | 15 | 18 | 15 | 9 | 20 | 23 | 10 | 35 | 20 | 15 | 19 | 21 | 14 |
| A | .000 | 1.000 | 1.000 | 1.000 | 1.000 | .000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | .964 |
| B | 1.000 | .000 | 1.000 | .000 | .000 | 1.000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .000 | .036 |

previously in Douglas and Cherokee Reservoirs, Tennessee. Upper Lake Walter F. George, Seminole and Lake Tobesofkee populations were distinguished by having a relatively high frequency of this ME-A allele. Upper and lower Walter F. George, Satilla River, Ogeechee River, Lake Sinclair, Lake Seminole, Lake Tobesofkee and Lake Lanier populations all had a GPI-B allele at low frequency which is only found in Georgia. Clarks Hill, lower Walter F. George, Ogeechee River, Lake Tobesofkee and Lake Sinclair had a unique LDH-A allele.

Lake Nottely and Allatoona populations had a unique MDH-B allele only found in Georgia. Sinclair and Seminole had a rare PEP-B allele only found in Georgia.

Relatedness of Crappie

All black crappie in the Southeast are closely related, including those from Georgia, and all white crappie in the Southeast are closely related, including those from Georgia (Figures 2 and 3). All populations of black crappie were closely related within Georgia. As indicated earlier, however, several low frequency alleles were found that were unique to Georgia populations that had not been found in other states. Although closely related, Georgia populations are different from other Southeastern populations and outside populations should not be introduced to Georgia.

Although all populations in Georgia were genetically similar, upper and lower Walter F. George, Satilla River, Ogeechee River, Lake Sinclair, Lake Seminole, Lake Tobesofkee, and Lake Lanier populations could be classified as a subset based on detection of the rare GPI-B allele and possession of the majority of rare alleles at other loci. A second subset might be considered as Nottely and Allatoona populations based on possession of a rare MDH-B allele and no white crappie alleles. Carters and Blackshear populations had no rare alleles and the highest percentage of hybrid derived individuals.

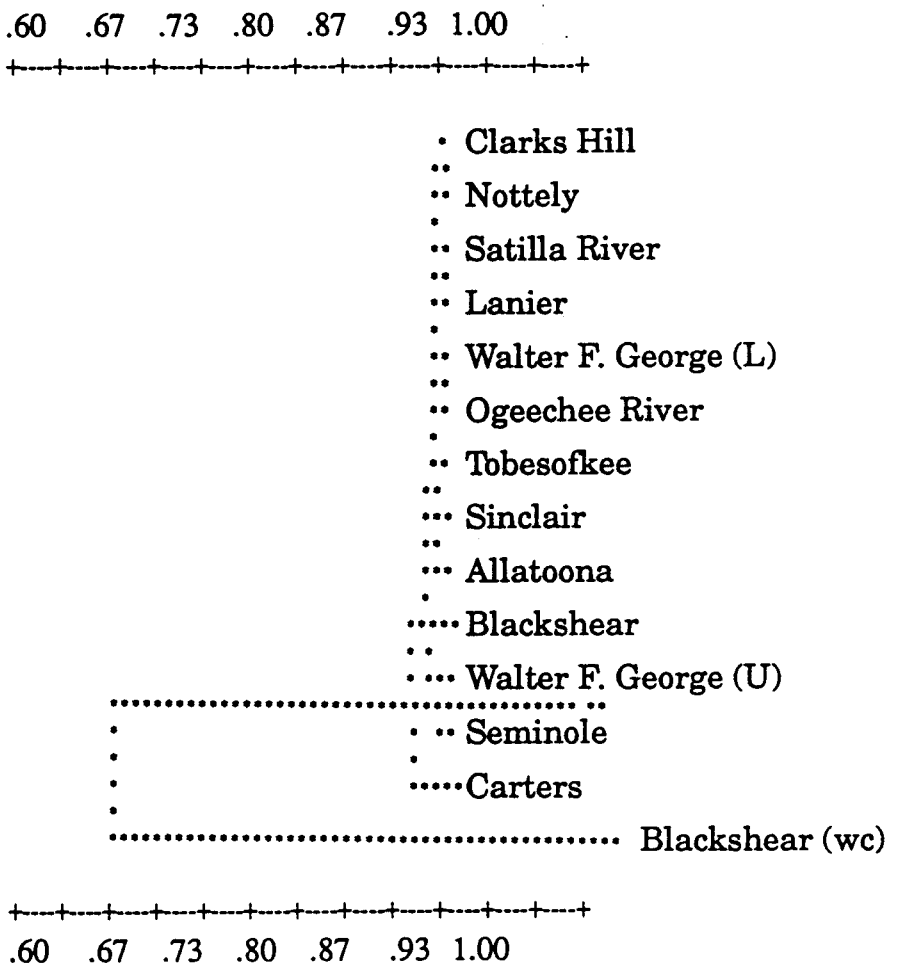


Figure 2. Genetic similarity (Rogers 1972) of crappie in Georgia. All populations are black crappie, except for Blackshear (wc) which is white crappie.

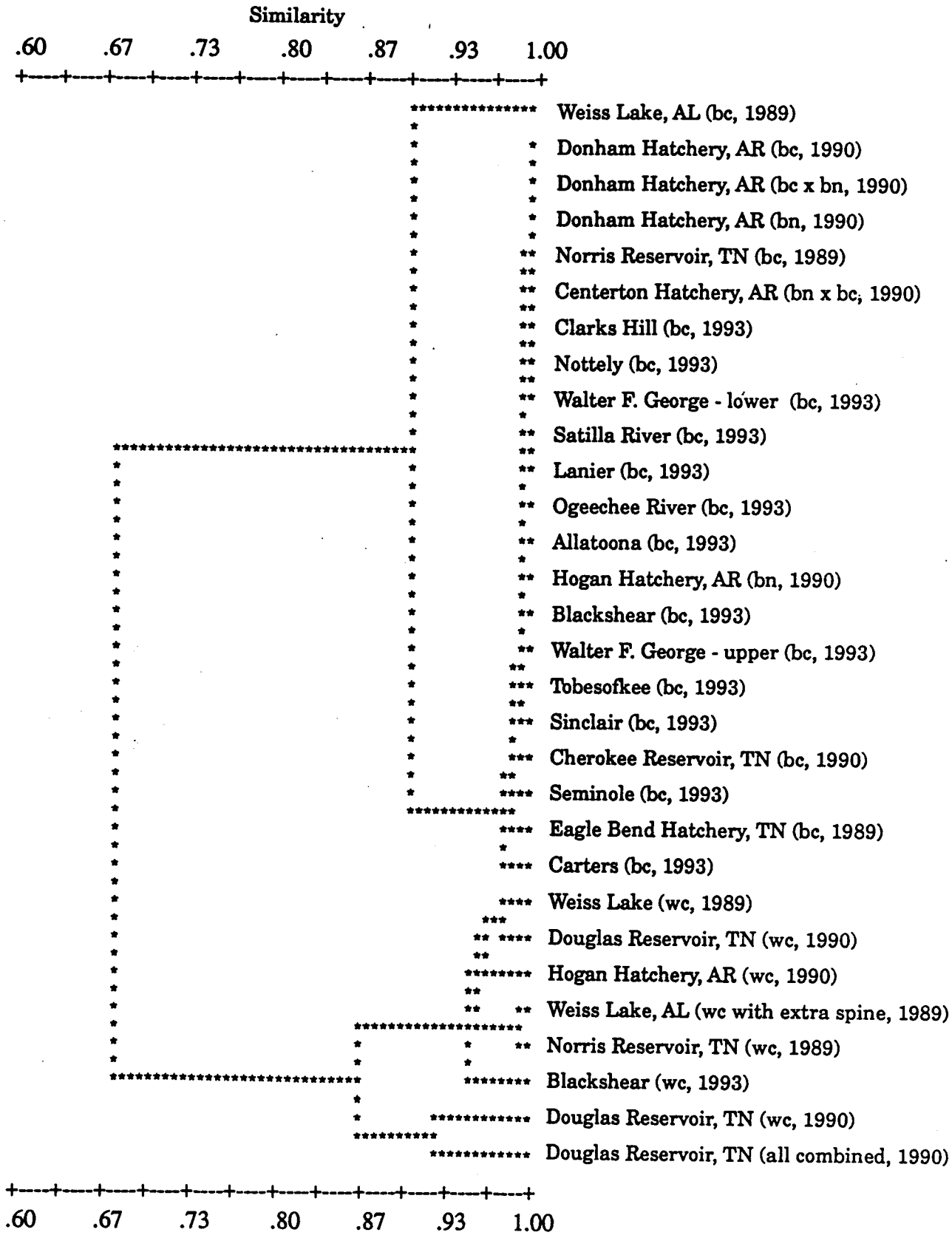


Figure 3. Genetic similarity (Rogers 1972) of crappie in the Southeastern United States. Populations examined during this study are marked 1993. bc = black crappie, wc = white crappie, bn = blacknose crappie.

## RECOMMENDATIONS

l. Because Georgia populations possessed several unique rare alleles not found in other states, black crappie from outside Georgia should not be introduced.

2. Upper Walter F. George, Satilla River, Ogeechee River, Lake Sinclair, Lake Seminole, Lake Tobesofkee, and Lake Lanier populations could be classified as a subset for management based on sharing a rare GPI-B allele and possession of the majority of rare alleles at other loci. A second subset might be Nottely and Allatoona populations based on possession of a rare MDH-B allele and no white crappie alleles. Carters and Blackshear populations had no rare alleles and the highest percentage of hybrid derived individuals, and should be considered a third management subset.

3. Hybridization was detected in seven of 13 populations. Since $F_1$ hybrid crappie grow faster than parent species, utilization of $F_1$ hybrid crappie could be recommended to enhance crappie fishing in these six reservoirs where some degree of hybridization has already occurred.

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