

# Virginia Largemouth Bass Populations Lack Geographic Pattern of Genetic Variation

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*Abstract:* The species largemouth bass *Micropterus salmoides* is comprised of two subspecies: northern largemouth bass *M.s. salmoides* and Florida largemouth bass *M.s. floridanus*. It is uncertain whether largemouth bass is native to the Atlantic slope and New drainages of Virginia. There exists a widely-held perception that Florida largemouth bass or F<sub>1</sub> northern x Florida hybrids provide more trophy catches than northern largemouth bass, which has led to widespread stocking of Florida largemouth bass into native northern and intergrade largemouth bass populations. Twenty-four Virginia populations of largemouth bass were screened for the frequencies of allozyme markers diagnostic for the two subspecies. The relative contributions of the Florida subspecies to the respective populations ranged from 0.32 in Occoquan Reservoir to 0.68 in Lake Robertson. No geographic pattern in genetic variation was seen. This finding may support the hypothesis that largemouth bass is a non-native species in the Atlantic slope and New drainages of Virginia; that is, lack of geographic stock structure may have been caused by stocking largemouth bass from varied sources. Alternatively, native geographic genetic structuring or that caused by stocking in the late 1880s to mid-1900s may have been modified by more recent stocking of Florida largemouth bass.

*Key words:* Largemouth bass, *Micropterus salmoides*, population genetics

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The largemouth bass species *Micropterus salmoides* is comprised of two subspecies: northern largemouth bass *M.s. salmoides* and Florida largemouth bass *M.s. floridanus* (Bailey and Hubbs 1949), although Kassler et al. (2002) have argued for elevation of the subspecies to species status. Both subspecies have been introduced far beyond their native ranges and are known to intergrade. By 1900, *M.s. salmoides* was widely distributed across the United States (MacCrimmon and Robbins 1975),

although as late as 1980, Lee et al. (1980) did not consider it a native species on the Atlantic slope north of South Carolina. Similarly, *M.s. floridanus* has been widely distributed throughout the southern United States and into sites farther north (Philipp et al. 1982, 1983), although Bailey and Hubbs (1949) reported the subspecies to be native to the Florida peninsula. Jenkins and Burkhead (1994) considered both subspecies as introduced to the Atlantic slope and New drainages of Virginia; the subspecies designation was supported and the geographic extent of the intergrade zone was delineated using isozyme markers (Philipp et al. 1982, 1983). Only limited research has refined understanding of the spatial extent of the intergrade zone (Hallerman et al. 1986, O'Bara et al. 1991), and it remains unclear how far the intergrade zone naturally extends northward along the coastal plain on the Atlantic coast of the United States.

Largemouth bass is a highly popular gamefish, and frequently is managed for trophy fisheries (Clepper 1975). It has been widely stocked both within and outside its native range (MacCrimmon and Robbins 1975). The widely-held perception that Florida largemouth bass or  $F_1$  northern x Florida hybrids outperform northern largemouth bass has led to widespread stocking of Florida largemouth bass into northern largemouth bass populations (e.g., Inman et al. 1976, Philipp et al. 1981, Maccina et al. 1988). However, the impacts of largemouth bass stockings on fishery performance and native diversity (e.g., Hoover et al. 1997) mostly remain uncharacterized. Jenkins and Burkhead (1994) suggest that historic stocking (early 1800s–mid 1900s) introduced the species. Stocking of Florida largemouth bass by the Virginia Department of Game and Inland Fisheries in the 1980s and 1990s was aimed at enhancing targeted sport fisheries. Against this background, the objectives of this study were to: (1) screen populations of largemouth bass in Virginia for the frequencies of isozyme markers diagnostic for the respective subspecies, (2) estimate the relative contributions of the subspecies to each population, (3) interpret geographic patterns of genetic variability, and (4) relate findings to management of Virginia largemouth bass for trophy fisheries.

## Methods

### Populations Sampled

Collections were made by electrofishing from 24 largemouth bass populations from seven rivers within three major watersheds (Table 1);  $N$  ranged from 17 to 60. Many of these populations received stockings of largemouth bass from the 1960s through the 1990s (Jenkins and Burkhead 1994; Virginia Department of Game and Inland Fisheries, unpublished stocking records). Fish were dissected in the field, and samples of muscle and liver tissues from each individual were placed on ice or dry ice. The samples were stored at  $-20$  C pending allozyme analysis.

### Data Collection and Analysis

Four sub-specific diagnostic isozymes (Phillip et. al. 1983)—aspartate aminotransferase (*AAT-B\**), isocitrate dehydrogenase (*IDH-B\**), malate dehydrogenase

**Table 1.** Locations and stocking histories of largemouth bass populations surveyed within rivers and watersheds in Virginia.

Collection site	N fish sampled	Stocking history
<b>Chesapeake Bay</b>		
Potomac River		
Burke Lake	30	Stocked from VDGIF hatcheries 1969-1975 <sup>a</sup>
Lake Frederick	30	No stocking records available
Ocoquan Reservoir	60	500 largemouth bass stocked in 1961
Shenandoah River	41	No stocking records available
York River		
Lake Anna	36	Northern, Florida largemouth bass stocked <sup>b</sup>
Beaverdam Swamp Reservoir	30	No records that largemouth bass ever were stocked
Lake Orange	30	VDGIF hatchery and Florida largemouth bass strains stocked <sup>c</sup>
Spring Branch	23	Unknown background, many sources
Walker-Coleman Reservoir	17	Unknown background, many sources
James River		
Briery Creek Lake	60	Northern, Florida largemouth bass stocked <sup>d</sup>
Lake Chesdin	59	Stocked 1968 <sup>e</sup>
Chickahominy River	60	Adjacent reservoir stocked <sup>f</sup>
Lake Cohoon	25	No records that largemouth bass ever were stocked
Lake Powhatan	40	No stocking records available
Lake Robertson	28	Stocked from Lake Merriweather, VA in 1971
Sandy River Reservoir	33	Stocked from VDGIF hatcheries 1994 <sup>g</sup>
<b>Albemarle Sound</b>		
Roanoke River		
Lake Burton	37	Florida (1976), VDGIF hatchery strains (1980, 1983) stocked <sup>h</sup>
Lake Conner	27	Florida largemouth bass stocked 1974 <sup>i</sup>
Smith Mountain Lake	53	1,000,000 of unknown background stocked 1961
Chowan River		
Nottoway River	28	Stocked with largemouth bass of unknown background <sup>j</sup>
<b>Mississippi Drainage</b>		
Ohio River		
Claytor Lake	29	No stocking records available
Flannagan Reservoir	57	Stocked in 1965, mid-1990s <sup>k</sup>
Tennessee River		
South Holston Lake	56	No stocking records available
Keokee Lake	25	No stocking records, but received Florida largemouth bass

a. Burke Lake stocked from Stephenville Virginia Department of Game and Inland Fisheries (VGDIF) hatchery (4,500 in 1969, 4,360 in 1972, 141 in 1974, and 5,000 in 1975) and from Front Royal VDGIF hatchery (250 in 1971).

b. Lake Anna stocked with northern largemouth bass in 1972 (357,820) and 1977 (17,308); Florida largemouth bass stocked in 1976 (18,650) and 1977 (43,639).

c. Lake Orange from Stephenville VGDIF hatchery (2,500 in 1969, 3,700 in 1971, 4,900 in 1972, 2,400 in 1974, and 1,350 in 1976) and from Charles City hatchery (4,500 in 1973 and 4,000 in 1976).

d. After rotenone treatment, Briery Creek Lake was stocked with 62,600 Florida largemouth bass and 17,500 northern largemouth bass fingerlings in 1986 and 65,400 and 22,800, respectively, in 1987 (Wilson and DiCenzo 2002).

e. Stocked in 1968 with 200,000 fish from McKinney National Fish Hatchery, North Carolina.

f. Chickahominy Reservoir stocked with 22,644 1.9-cm Florida largemouth bass in 1975 and with 51,000 largemouth bass fry of unspecified background in 1979.

g. Stocked with 20,000 fish from Front Royal and 22,479 fish from Stephenville VDGIF hatcheries, 1994.

h. Florida largemouth bass stocked in 1976 (800), Stephenville hatchery strain stocked in 1979 (7,500) and 1983 (3,850).

i. Florida largemouth bass stocked in 1974 (1147 fingerlings and 236 yearlings).

j. Nottoway River stocked with 1,350 largemouth bass in October and 4,300 (from Dinwiddie County) in November 1960.

k. Largemouth bass of unknown background stocked in 1965, likely of intergrade background in mid-1990s.

(*MDH-B\**), and superoxide dismutase (*SOD-A\**)—were screened. Liver tissue was used for all analyses except *MDH-B\**, for which white skeletal muscle tissue was used. Enzyme activities were observed by histochemical staining following electrophoresis through cellulose acetate gels (Hebert and Beaton 1993). Individual phenotypes observed on the surface of gels and were scored as presumptive genotypes. Population genetic statistics were estimated using Biosys-1 software (Swofford and Selander 1981, 1989). Relative contributions of subspecies in particular populations were estimated by averaging the frequencies of the diagnostic alleles across the *IDH-B\** and *AAT-B\** loci, which are fixed within the respective subspecies (Phillip et al. 1983). Allozyme frequencies at all four loci were used to estimate genetic distances among populations.

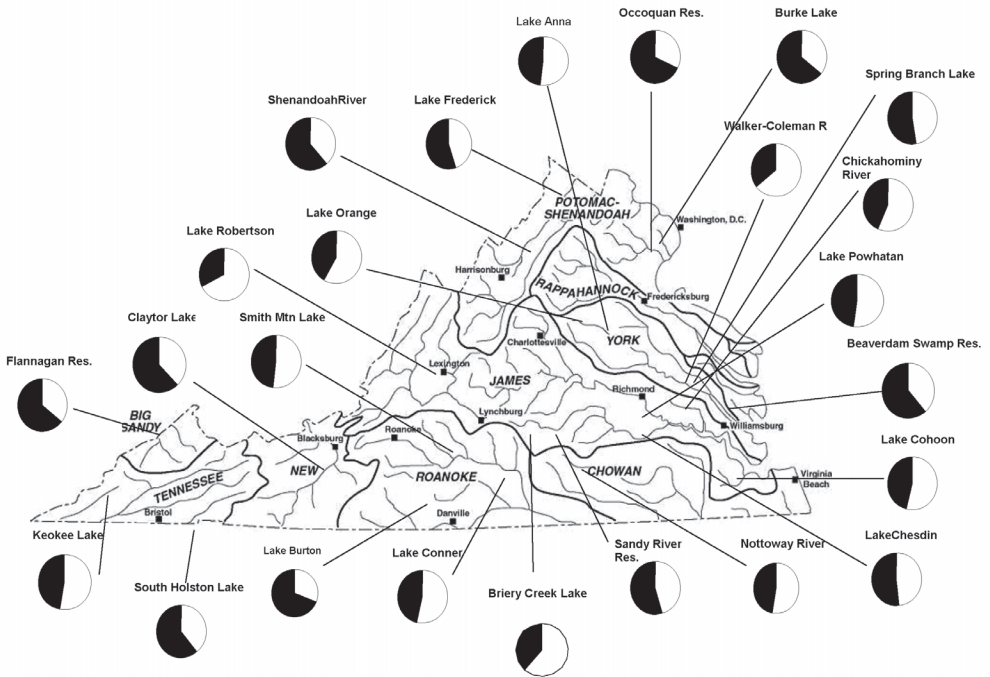
## Results

Both northern- and Florida-subspecific alleles were observed in all 24 populations surveyed (Table 2, Fig. 1). The relative contributions of the Florida subspecies

**Table 2.** Allele frequencies at four isozyme loci and estimated contribution of Florida-subspecific background<sup>a</sup> in 24 Virginia populations of largemouth bass.

Population	<i>MDH - B*</i>		<i>IDH - B*</i>		<i>SOD - A*</i>			<i>AAT - B*</i>				Percent Florida
	1	2	1	3	1	2	3	1	2	3	4	
Flannagan Reservoir	0.265	0.735	0.605	0.395	0.298	0.702	0.000	0.500	0.184	0.193	0.123	35.5
South Holston Lake	0.885	0.115	0.571	0.429	0.052	0.948	0.000	0.448	0.198	0.302	0.052	39.1
Nottoway River	0.411	0.589	0.482	0.518	0.446	0.554	0.000	0.214	0.250	0.304	0.232	52.7
Spring Branch Lake	0.217	0.783	0.381	0.619	0.333	0.667	0.000	0.405	0.262	0.190	0.143	47.6
Walker-Coleman	0.294	0.706	0.179	0.821	0.471	0.529	0.000	0.265	0.265	0.206	0.265	64.5
Chickahominy River	0.550	0.450	0.317	0.683	0.442	0.558	0.000	0.258	0.292	0.258	0.192	56.6
Lake Chesdin	0.611	0.389	0.483	0.517	0.373	0.627	0.000	0.212	0.339	0.288	0.161	48.3
Occoquan Reservoir	0.758	0.242	0.725	0.275	0.100	0.900	0.000	0.417	0.217	0.258	0.108	32.0
Lake Robertson	0.268	0.732	0.232	0.768	0.839	0.161	0.000	0.089	0.321	0.268	0.321	67.9
Shenandoah River	0.802	0.198	0.628	0.372	0.023	0.942	0.035	0.329	0.244	0.293	0.134	40.1
Claytor Lake	0.483	0.517	0.603	0.397	0.155	0.845	0.000	0.259	0.379	0.207	0.155	37.9
Briery Creek Lake	0.271	0.729	0.325	0.675	0.183	0.817	0.000	0.225	0.217	0.425	0.133	61.7
Smith Mt. Lake	0.519	0.481	0.406	0.594	0.349	0.651	0.000	0.358	0.189	0.264	0.189	52.3
Lake Anna	0.528	0.472	0.471	0.529	0.441	0.559	0.000	0.250	0.235	0.235	0.279	52.2
Burke Lake	0.267	0.733	0.667	0.333	0.633	0.367	0.000	0.400	0.200	0.250	0.150	36.7
Sandy River												
Reservoir	0.758	0.242	0.470	0.530	0.455	0.545	0.000	0.470	0.273	0.167	0.091	39.4
Lake Orange	0.350	0.650	0.483	0.517	0.617	0.383	0.000	0.086	0.224	0.397	0.293	60.4
Lake Conner	0.346	0.654	0.481	0.519	0.692	0.308	0.000	0.259	0.352	0.241	0.148	45.4
Lake Frederick	0.500	0.500	0.586	0.414	0.466	0.534	0.000	0.367	0.217	0.200	0.217	41.6
Beaverdam Swamp												
Reservoir	0.533	0.467	0.683	0.317	0.600	0.400	0.000	0.350	0.233	0.100	0.317	36.7
Lake Cohoon	0.480	0.520	0.400	0.600	0.560	0.440	0.000	0.200	0.180	0.340	0.280	61.0
Lake Powhatan	0.400	0.600	0.450	0.550	0.550	0.450	0.000	0.262	0.275	0.200	0.262	50.6
Lake Burton	0.514	0.486	0.757	0.243	0.608	0.392	0.000	0.265	0.294	0.221	0.221	34.3
Keokee Lake	0.500	0.500	0.520	0.480	0.480	0.520	0.000	0.360	0.060	0.060	0.520	53.0

<sup>a</sup> Relative contributions of subspecies in particular populations were estimated by averaging the frequencies of diagnostic alleles *IDH-B\* 3* and *AAT-B\* 3* and 4.



**Figure 1.** Pie diagrams showing the percentage of northern (black) and Florida (white) largemouth bass alleles in each population.

to the respective populations (Table 1) ranged from 0.32 in Ocoquan Reservoir to 0.68 in Lake Robertson.

Genetic variability metrics for the populations (Table 3) were relatively high because only variable loci were screened. Direct-count heterozygosities ranged from 0.372 in the Shenandoah River to 0.663 in Lake Powhatan. In four cases, observed heterozygosities exceeded Hardy-Weinberg expectations by 0.1 or more, perhaps a reflection of recent stocking with  $F_1$  hybrids.  $F$ -statistics quantifying departures of genotype frequencies from Hardy-Weinberg equilibrium (Table 4) showed that  $F_{IT}$ , the total departure from Hardy-Weinberg equilibrium in the total collection, was small.  $F_{IS}$ , the departure within populations, was negative, a somewhat unusual observation for natural populations. Negative values can occur due to disassortative mating (Wright 1969) or, in this case, to largemouth bass having been recently stocked into a divergent existing population and panmixia not yet having been achieved. Most of the negative contributions to the overall  $F_{IS}$  estimate came from one locus,  $AAT-B^*$ .  $F_{ST}$  was the largest of the fixation indices estimated, which is expected given that genotype frequencies differed among populations within the overall collection. Indeed,  $F_{ST}$  may have been elevated by stocking the respective populations from different source populations.

**Table 3.** Genetic variability metrics for in all populations.<sup>a</sup> Standard errors are shown in parentheses.

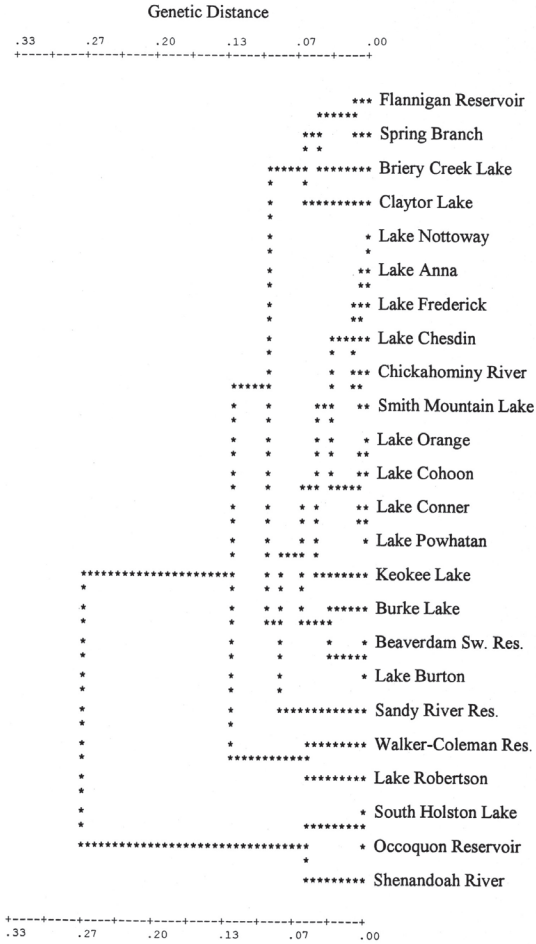
Population	Mean <i>N</i> per locus	Mean heterozygosity	
		Direct – count	HdyWbg expt <sup>b</sup>
Flannagan Reservoir	55.0 (2.0)	.487 (0.117)	.492 (0.062)
South Holston Lake	48.0 (0.0)	.474 (0.203)	.375 (0.128)
Nottoway River	28.0 (0.0)	.616 (0.129)	.566 (0.064)
Spring Branch Lake	21.5 (0.5)	.587 (0.130)	.504 (0.080)
Walker-Coleman	16.3 (0.8)	.589 (0.126)	.504 (0.099)
Chickahominy River	60.0 (0.0)	.608 (0.103)	.546 (0.070)
Lake Chesdin	56.8 (1.3)	.489 (0.154)	.548 (0.063)
Occoquan Reservoir	60.0 (0.0)	.408 (0.170)	.415 (0.109)
Lake Robertson	28.0 (0.0)	.473 (0.179)	.441 (0.099)
Shenandoah River	43.0 (0.0)	.372 (0.198)	.413 (0.133)
Claytor Lake	29.0 (0.0)	.552 (0.144)	.499 (0.096)
Briery Creek Lake	59.8 (0.3)	.472 (0.154)	.463 (0.087)
Smith Mt. Lake	52.8 (0.3)	.597 (0.092)	.547 (0.064)
Lake Anna	34.5 (0.5)	.590 (0.130)	.568 (0.064)
Burke Lake	30.0 (0.0)	.617 (0.069)	.512 (0.073)
Sandy River Reservoir	33.0 (0.0)	.492 (0.079)	.515 (0.063)
Lake Orange	29.8 (0.3)	.616 (0.128)	.541 (0.058)
Lake Conner	26.3 (0.3)	.577 (0.150)	.537 (0.070)
Lake Frederick	29.3 (0.3)	.613 (0.111)	.563 (0.060)
Beaverdam Swamp Reservoir	30.0 (0.0)	.583 (0.111)	.540 (0.063)
Lake Cohoon	25.0 (0.0)	.610 (0.108)	.563 (0.062)
Lake Powhatan	40.0 (0.0)	.663 (0.099)	.561 (0.065)
Lake Burton	36.3 (0.8)	.542 (0.077)	.530 (0.081)
Keokee Lake	25.0 (0.0)	.660 (0.026)	.533 (0.024)

a. A locus was considered polymorphic if more than one allele was detected. Mean number of alleles for all loci and populations was 2.5 ( $\pm 0.5$ ).

b. Unbiased estimate (Nei 1978).

**Table 4.** Summary of *F*-statistics across loci.

Locus	$F_{IS}$	$F_{IT}$	$F_{ST}$
<i>MDH</i> – <i>B</i> *	0.003	0.133	0.131
<i>IDH</i> – <i>B</i> *	-0.088	0.037	0.115
<i>SOD</i> – <i>A</i> *	0.033	0.196	0.168
<i>AAT</i> – <i>B</i> *	-0.249	-0.196	0.042
Mean	-0.101	0.016	0.106



**Figure 2.** Phenetic tree showing Nei (1978) genetic distance relationships of populations clustered using the UPGMA method.

Nei's (1978) unbiased genetic distances among populations showed no geographic patterning. Genetic distances among 12 pairs of populations were zero. Only three such pairings were among populations within the same river (the James), and three were among James and York river populations. Genetic distances among populations within rivers were of similar magnitude as genetic distances among rivers. Mississippi drainage populations collectively were most divergent from others. A phenetic tree of Nei's (1978) genetic distance relationships among populations (Fig. 2) exhibited populations clustered in ways that did not reflect hierarchical geographic organization within watersheds. For example, Mississippi drainage populations—South Holston Lake, Claytor Lake, and Flannigan Reservoir—all grouped within clusters of Atlantic slope drainage populations. Albemarle Sound populations were interspersed with Chesapeake Bay populations. Hence, largemouth bass popu-

**Table 5.** Genotypic variance components and  $F_{XY}$  statistics across all loci.

Comparison		Variance component	$F_{XY}$
X	Y		
Population	River	0.19676	0.088
Population	Watershed	0.22557	0.099
Population	Total	0.20738	0.092
River	Watershed	0.02881	0.013
River	Total	0.01062	0.005
Watershed	Total	-0.01819	-0.008

**Table 6.** Contingency  $\chi^2$  analysis of population genetic differentiation overall and within watersheds.

	$\chi^2$	d.f.	$P$
Overall	1676.349	184	0.00000
Chesapeake Watershed	1099.225	120	0.00000
Potomac River	292.887	24	0.00000
York River	78.048	24	0.00000
James River	213.563	36	0.00000
Albemarle Watershed	59.279	18	0.00000
Roanoke River	54.847	12	0.00000
Chowan River <sup>a</sup>	—	—	—
Mississippi Watershed	195.095	18	0.00000
Ohio River	23.352	6	0.00069
Tennessee River	114.550	6	0.00000

a. There was only one population in the Chowan River; hence, no analysis was performed.

lations in Virginia do not show the hierarchical pattern of inter-population relatedness expected of natural populations. Likewise, hierarchical analysis of population differentiation using Wright's (1978)  $F$ -statistics (Table 5) showed that the variance among populations within watersheds was greater than that among rivers within watersheds. Both of these findings are consistent with the pattern expected for populations established by stocking from different sources. Genotypic heterogeneity among populations was demonstrated by highly significant results for contingency  $\chi^2$  tests for populations overall, within watershed, and within rivers (Table 6).

## Discussion

Variation at four isozyme loci distinguishing the northern and Florida subspecies showed no geographic pattern of genetic variation among 24 largemouth bass



populations in Virginia. This observation might be explained by two hypotheses: (1) largemouth bass is a non-native species in most of Virginia, and lack of geographic stock structure is the consequence of stocking largemouth bass from different sources, or (2) native geographic genetic structuring once existed, but was obliterated by past stocking practices.

Jenkins and Burkhead (1994) regard largemouth bass as introduced into the Atlantic slope and New River (Ohio) drainages in Virginia, and tentatively as native in the Virginia portion of the Tennessee and Big Sandy drainages. The northern limit of native largemouth bass on the Atlantic slope is uncertain. Hubbs and Bailey (1940) regarded the species as native to Virginia, but Hubbs and Lagler (1958) regarded it as native "to North Carolina and possibly farther north." Jenkins and Burkhead (1994) cited angling publications and agency reports to build the case that largemouth bass were introduced into Virginia from the Carolinas. First collection records of largemouth bass in Virginia drainages were: Potomac, 1876; James, Dismal Swamp, and Chowan, 1888; York, 1897; New, 1928; Roanoke, 1935; Rappahannock, 1951; and Pee Dee, 1983. During the 1990s, the Virginia Department of Game and Inland Fisheries stocked impoundments with largemouth bass from a variety of sources (Table 1). Hence, Virginia Atlantic slope largemouth bass populations likely were established with intergrade founders, and the proportion of Florida-subspecific background was increased by subsequent stocking. In particular, we note that the Florida-subspecific contribution to the Lake Anna population was 52.2% in our study, higher than the 46.2% observed by Philipp et al. (1982), presumably due to stocking in the 1990s. Our observation of a lack of a geographic pattern for genetic variability in largemouth bass supports the hypothesis that largemouth bass is not a native species in the Atlantic slope and New drainages in Virginia, as geographic genetic patterning would not be expected among populations recently founded by stocking from a variety of sources.

An alternative hypothesis is that largemouth bass is native to most or all drainages of Virginia and that natural patterns of differentiation were obliterated by later stocking of reservoirs with Florida largemouth bass. Stocking of Florida largemouth bass into native northern largemouth populations has led to introgressed populations in many systems (Philipp et al. 1982), including Lake of Egypt, Illinois; Lake D'Arbonne, Louisiana; DeGray Reservoir, Arkansas; Ross Barnett and Sardis reservoirs, Mississippi; and likely, Deep Creek Reservoir, Maryland. Stocking has altered patterns of genetic differentiation in some drainages for other managed species, including brook trout in the southern Appalachians (McCracken et al. 1993) and Atlantic salmon in Norway (Hindar et al. 1991) and Spain (Moran et al. 2005). We note, however, that stocking into established populations does not necessarily obliterate native patterns of genetic differentiation. For example, despite a history of stocking, native stock structure can still be discerned in some drainages for brook trout in the southern Appalachians (Guffey 1990) and Atlantic salmon in North America (King et al. 2001, Cordes et al. 2005), Denmark (Nielsen et al. 1997), and Spain (Blanco et al. 2005).

We note that the two hypotheses discussed above are not strictly mutually ex-

clusive. Introgression of introduced genotypes into native background may have occurred in watersheds (notably, the Tennessee) where largemouth bass is native, while all other Virginia largemouth bass populations may be introduced. Geographic genetic patterning established by historic stocking may have been affected by later stocking of Florida largemouth bass. To more fully characterize patterns of genetic variation, we suggest sampling additional river populations, old ponds, and small impoundments that were not directly influenced by stocking of reservoir populations during the 1990s, as well as likely source areas for late 19th–early 20th century and more recent stockings. Use of additional genetic markers would sharpen characterization of structure among largemouth bass populations.

### Management Implications

Many anglers and managers raise the issue of whether stocking of Florida largemouth bass increases yield or trophy yield in a largemouth bass fishery. This study showed that the 24 Virginia populations surveyed averaged 47% Florida and 53% northern alleles. To advocates of stocking pure Florida-subspecies largemouth bass, we point out that diagnostic allele frequencies are already near equal. There may be rationale for stocking  $F_1$  Florida x northern largemouth bass for the narrow benefit of increased hybrid vigor in the one generation stocked, although the effectiveness and cost-effectiveness of the approach have yet to be demonstrated. We note that genetic composition of populations in Virginia reservoirs resembles those in the natural intergrade zone, where catches of trophy individuals are frequent. Further, Virginia lakes producing trophy bass (e.g., Briery Creek Lake, Wilson and DiCenzo 2002) tend to exhibit favorable habitat and forage base rather than particular frequencies of Florida-subspecific alleles. We suggest that a combination of harvest regulation, forage manipulation, and habitat manipulation would be more effective than the stocking of Florida largemouth bass or the  $F_1$  hybrid for maximizing the potential for trophy largemouth bass fisheries in Virginia.

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