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EVIDENCE FOR A GENETICALLY UNIQUE WALLEYE POPULATION IN THE UPPER TOMBIGBEE RIVER SYSTEM OF NORTHEASTERN MISSISSIPPI

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Abstract – Electrophoretic evaluation of walleye from several areas of the upper Tombigbee River system in northeastern Mississippi revealed no heterozygosity at any of the presumptive loci examined (skeletal muscle malate dehydrogenase and myogen, liver isocitrate dehydrogenase, and serum albumin), in contrast to widespread genetic heterogeneity observed in all other studies involving the species. This unique genetic character may be typical of walleye throughout the Gulf Coast drainages of Mississippi and Alabama. The genetic integrity of walleye in the Tombigbee River system is threatened by invasion of Mississippi River strain walleye through the Tennessee-Tombigbee Waterway. Genetic traits of Tennessee River walleye should be confirmed, and the invasion of these fish into the Tombigbee River system should be monitored. A captive breeding/transplantation program may be the only feasible method of preserving the genetically unique walleye of the upper Tombigbee River system.

INTRODUCTION

Walleye *Stizostedion vitreum vitreum* is one of the most important sportfish species in the United States and Canada. Because of their importance, they have been widely cultured and stocked both within and outside their native range (Hackney and Holbrook 1978; Laarman 1978). The natural range of the species extends from northwestern Canada to the southeastern United States (Radforth 1944; Barila 1980). Walleye have been reported from the Tombigbee River system in Mississippi and Alabama, in the Alabama River system of Alabama and Georgia (Brown 1962; Schultz 1971; Mettee et al. 1987; Boschung 1989), and the Coosa River system in northwestern Georgia (Spencer 1986; Beisser 1987; 1989). However, Colby et al. (1979) and Barila (1980) have indicated that populations of walleye in Atlantic drainage areas of the southeastern United States are probably introduced. Conversely, the former fish may be part of a distinct Gulf Coast strain of walleye postulated to exist from the extreme western portion of the Florida panhandle to the Pearl River, Mississippi (Hackney and Holbrook 1978). This strain may be different from the Mississippi River strain to the north in that it does not establish in reservoirs, populations do not reach high abundance even in preferred habitat, and individuals do not reach large sizes (Brown 1962; Hackney and Holbrook 1978). Wingo (1982) demonstrated some genetic differences between walleye of the Upper Tombigbee River system and fish from Iowa, New York, and Pennsylvania. If a unique Gulf Coast strain of walleye indeed exists, the creation of the Tennessee-Tombigbee Waterway (TTW) linking the Tennessee River with the Tombigbee River may allow passage of Mississippi River strain walleye into areas previously occupied exclusively by the Gulf Coast strain. The objective of the present study was to clarify the genetic traits of walleye from the Upper Tombigbee River system in Mississippi, in order to define baseline criteria for future evaluations of the genetic integrity of walleye in this area.

METHODS

All site numbers for collections are as described by Boschung (1989). Walleye (n=27) were collected from the Luxapallila River, Lowndes County, during the spring spawning season of 1985. All fish in this sample were collected within 5 km of the confluence with the Tombigbee River (near sites 157, 158, and 161), and are thought to represent Tombigbee River fish on a spawning run up the tributary stream (C.A. Schultz, Mississippi Department of Wildlife Conservation; personal communication). Additional samples were collected from the same area in spring 1988 (one fish) and spring 1989 (one fish); Yellow Creek, a Luxapallila River tributary (near site 167; one fish, spring 1985); the Buttahatchie River at Caledonia, Monroe County (near site 235; one fish, February 1989), and Sipsey Creek, a Buttahatchie River tributary (near site 242; two fish, April 1989). All fish were collected with gill nets or hoop nets, immediately frozen, and shipped to the Wildlife Genetics Laboratory at Texas A&M University for electrophoretic analyses. Liver and white muscle tissue samples were excised from each fish, and stored at –90 C pending electrophoretic analysis.

Subsamples of white skeletal muscle were thawed and homogenized in 0.5-1.0 mL grinding buffer (.01M Tris-0.001M EDTA, pH 6.8), and centrifuged (800 x gravity) at room temperature for 5 minutes. Liver samples were thawed, but not ground or centrifuged. Electrophoretic analyses were limited to protein systems demonstrated to be polymorphic in previous studies of the species (Uthe and Ryder 1970; Clayton et al. 1974; Terre 1985). Muscle and liver supernatants were subjected to starch gel electrophoresis (Selander et al. 1971), using N-(3-aminopropyl) morpholine-citrate buffer pH 6.1 (Clayton and Tretiak 1972). Malate dehydrogenase (MDH, ISN[1] 1.1.1.37) and isocitrate dehydrogenase (IDH, ISN[1] 1.1.1.42) were stained with specific enzyme stains from Harris and Hopkinson (1976). Vertical-slab polyacrylamide-gel electrophoresis (Hoefer Scientific Instruments 1980), with gel formulations from Davis (1964), was utilized to visualize muscle myogen (MYO) proteins (Uthe and Ryder 1970) and a general serum albumin (ALB) (Terre 1985). Muscle supernatant was mixed with an equal volume of layering solution (60% sucrose in distilled water), applied to a 12% acrylamide gel in 10-µl aliquots, and subjected to electrophoresis for 3,000 volt-

[1] International standard number (IUBNC 1984).

hours at 40 mA per gel. General proteins were stained with a 0.04%/5% Coomassie Brilliant Blue Green/perchloric acid solution, and destained with a 15%/10% ethanol/acetic acid solution.

RESULTS AND DISCUSSION

The walleye examined in this study were unique in that no heterozygosity was observed at any of the presumptive loci examined. This genetic fixation is in contrast to a significant amount of variability that has been observed at these loci in most other genetic studies of walleye (Table 1). While some of the variability currently evident in most walleye populations is probably a result of the widespread stocking of the species, considerable variability has been reported in populations across Canada (Uthe and Ryder 1970; Clayton et al. 1974) where stocking has probably impacted natural genetic structure less than populations in the United States. Murphy and Lee (1986) found that walleye from four to six sites in Minnesota were homozygous for the MYO-A[1] allele, but heterozygosity was observed in the same fish for the other three loci. No other cases of genetic fixation in walleye have been reported in the literature.

Genetic characteristics of walleye examined in this study are quite distinct from walleye in the Cumberland River segment of Dale Hollow Reservoir, Tennessee (Dryden et al. 1988), which presently show relatively high frequencies of genes that do not occur in the Tombigbee populations (Table 1). No specific information exists on the genetic characteristics of Tennessee River walleye, but they most likely bear some resemblance to walleye from the Cumberland River area since these rivers are adjacent Ohio River tributaries. A long history of stocking walleyes from northern populations into the reservoirs of the central Appalachian states would make it impossible to determine the genetic makeup of native Tennessee River walleye (Dryden et al. 1988). Assuming a genetic similarity between Tennessee River walleye and Cumberland River walleye, and assuming that the genetic fixation observed in this limited study is representative of all walleye in the Tombigbee River system, it should be possible to genetically trace any future invasion of the Tombigbee drainage by Tennessee River walleye through the TTW. Genetic characteristics of Tennessee River walleye should be verified as soon as possible to facilitate these comparisons.

The uniquely uniform genetic makeup of walleye examined in the present study seemingly invalidates the assumption that walleye were transplanted into the upper Tombigbee River system. Transplantation during modern times from any other area of North America likely would have introduced fish with much more genetic diversity than that observed in the present study. My results imply that walleye in the Tombigbee River drainage indeed represent a unique population of the species that has been isolated from other populations for a considerable period of time. The depauperate genetic nature of walleye observed in the present study may be the result of a genetic bottleneck, possibly linked to a limited stream capture event at some point in the past. This unique genetic character may be typical of walleye throughout the Gulf Coast drainages of Mississippi, Alabama, and Georgia; and it may be linked to the unique thermal tolerance traits reported for walleye from this area (Colby et al. 1979). More research is needed to verify the genetic characteristics of walleye throughout the suspected range of the Gulf Coast strain. The unique population described in this study, and other such populations that may be identified, may represent the last walleye populations in the United States that have not been impacted by the cross-stocking that has been so common in the management of this species. As such, they should be afforded protection from introgression with other strains to the maximum extent possible. Walleye populations in the upper Tombigbee River system should be monitored regularly to detect any invasion of walleye from the Mississippi River watershed through the TTW. If Tennessee River fish do indeed invade the Tombigbee River, a captive breeding/transplantation program may be the only feasible method of preserving the genetically unique walleye of the upper Tombigbee River system.

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Table 1. Gene frequencies for four presumptive loci for Mississippi walleye investigated in the present study, and frequencies reported for the same loci for walleye from other areas of North America.

Locus	Allele	MS[1]	TN[2]	TX[3]	VA[4]	PA[4]	KS[4]	NE[4]	MN[5]	Canada
MDH-B	1	0.00	0.01	0.00	<0.01	0.00	0.07	0.04	<0.05	0.00-0.62[6]
	2	0.00	0.86	0.43	0.55	0.80	0.84	0.54	0.31-0.69	0.07-0.70
	3	1.00	0.13	0.57	0.45	0.20	0.09	0.42	0.31-0.69	0.17-0.65
IDH-A	1	0.00	0.42	0.62	–	–	–	–	0.37-0.58	–
	2	1.00	0.58	0.38	–	–	–	–	0.42-0.63	–
MYO-A	1	1.00	0.52	0.91	0.53	0.65	0.88	0.85	0.83-1.00	0.38-0.84[7]
	2	0.00	0.48	0.09	0.47	0.35	0.12	0.15	0.00-0.17	0.06-0.62
ALB-A	1	1.00	0.09	0.82	–	–	–	–	0.10-0.92	–
	2	0.00	0.91	0.18	–	–	–	–	0.08-0.90	–

References: [1]Present study; [2]Dryden et al. 1988; [3]Terre 1985; [4]Murphy 1981; [5]Murphy and Lee 1986 (range reported for 6 lakes and rivers); [6]Clayton et al. 1974 (range reported for 19 lakes and rivers); [7]Uthe and Ryder 1970 (range reported for 5 lakes).