

GENETIC STRUCTURE AND SYSTEMATICS OF  
SMALLMOUTH BASS: ZOOGEOGRAPHY  
AND IMPLICATIONS FOR  
CONSERVATION

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## TABLE OF CONTENTS

Chapter	Page
I. ABSTRACT .....	1
II. INTRODUCTION .....	2
III. METHODS .....	5
IV. RESULTS .....	8
V. DISCUSSION .....	13
Zoogeography .....	13
Anthropogenic effects .....	18
VI. CONCLUSIONS .....	20
LITERATURE CITED .....	22
APPENDIXES .....	43
APPENDIX I--COLLECTION LOCALITIES .....	43
APPENDIX II--ALLELE FREQUENCIES .....	47

## LIST OF TABLES

Table	Page
I. Localities and genetic variability .....	27
II. Proteins, loci, tissues, and analytical systems .....	30
III. Hierarchical analysis of genetic variation .....	31

## LIST OF FIGURES

Figure	Page
I. Map of species range and collection localities .....	32
II. UPGMA dendrogram of genetic distances .....	33
III. Allele frequency distributions at <i>sMEP-1</i> * .....	34
IV. Allele frequency distributions at <i>GPI-B</i> * .....	35
V. Allele frequency distributions at <i>PEPS</i> * .....	36
VI. Allele frequency distributions at <i>TPI-1</i> * .....	37
VII. Allele frequency distributions at <i>GPI-A</i> * .....	38
VIII. Allele frequency distributions at <i>SOD</i> * .....	39
IX. Consensus cladogram .....	40
X. UPGMA dendrogram of native and introduced populations .....	41
XI. Map of pre-pleistocene drainage patterns .....	42

## ABSTRACT

Smallmouth bass populations were sampled at 62 localities encompassing the majority of the native range of the species. Allozyme variation revealed high within-population genetic diversity ( $H_T = 0.068$ ) and high heterogeneity among populations ( $F_{ST} = 0.401$ ). Phenetic and phylogenetic analyses indicated that the most divergent populations of smallmouth bass are those near the southwestern periphery of the geographic range of the species: the Neosho smallmouth bass in western Arkansas River tributaries of the Ozark Highlands and the Ouachita smallmouth bass in the Little and Ouachita river drainages of the Ouachita Highlands. Smallmouth bass from the remainder of the Ozark Highlands were genetically intermediate between southwestern forms and samples from the Upper Mississippi River and Ohio River drainages. The physiographic history of the western Ozarks and Ouachita Highlands, high genetic variability within southwestern forms, and the distribution of the *PEPS\*-106* allele suggest that the Neosho and Ouachita forms represent evolutionarily old historic entities that contain a significant portion of the genetic diversity of the species. The hatchery stock in Oklahoma is genetically divergent from both native forms within the state. In the interest of preserving genetic diversity and the options that divergent native stocks represent for future management, stock transfers of non-native smallmouth bass into the native range in Oklahoma should be avoided.

## INTRODUCTION

Fundamental to the management of fisheries resources should be a concern for the conservation and maintenance of patterns of genetic diversity within and among native populations (Nelson and Soule 1987). Genetic surveys of exploited fisheries typically reveal significant geographic variation in genetic structure (Aspinwall 1974; Philipp et al.

1983; Koppelman and Philipp 1986; Stahl 1987; Altukhov and Salmenkova 1987; Leary et al. 1987; Krueger et al. 1989). When fisheries are exploited without regard for genetic structure, differential fishing pressure can cause elimination of unique subpopulations (Brown et al. 1981). Ironically, subpopulations with the most desirable properties (e.g., rapid growth and high catchability) for the fishery and for future enhancement programs may be at the greatest risk (Thorpe and Koonce 1981). In addition, exploited fisheries are often the focus of enhancement through artificial propagation programs. Introductions of non-native stocks disrupt natural patterns of genetic variation and can result in the permanent loss of genetically divergent forms and the options they represent for future management (Nelson and Soule 1987, Echelle 1991). Through outbreeding depression, congeneric hybridization, and introduction of parasites, stock transfers have the potential to reduce the fitness of populations that they were intended to enhance (Whitmore 1983; Altukhov and Salmenkova 1987; Stahl 1987; Philipp and Whitt 1991).

The smallmouth bass (*Micropterus dolomieu*) is a highly prized sportfish that is endemic to the perennial high-gradient streams of much of eastern United States and southern Canada. It has been stocked within and outside its native range, resulting in numerous naturalized populations (Stroud and Clepper 1975). Currently, the smallmouth bass comprises two nominal subspecies (Hubbs and Bailey 1940), a widespread northern form (*M. d. dolomieu*) and a geographically restricted southwestern form, the Neosho smallmouth bass (*M. d. velox*). The northern form is native to the area from the Missouri River basin northward and east of the Mississippi River (stippled area, Fig. 1). Except for populations in the northward flowing tributaries of the Missouri River, the northern form does not occur within the Interior Highlands (Ozark and Ouachita highlands). The Neosho subspecies is restricted to direct tributaries of the Arkansas River in the extreme

western and southern Ozarks. Hubbs and Bailey (1940) tentatively designated the remaining Ozark populations (principally in the White and Black river basins) and those in the Ouachita Highlands (Little and Ouachita river basins) as intergrades between the two nominal subspecies.

The two nominal subspecies are distinguished by a slight modal difference in number of soft dorsal fin-rays, the Neosho form having fewer than the northern form (13 vs 14; Hubbs and Bailey 1940). Other distinguishing characters of the Neosho form include a straighter predorsal contour, a more slender appearance, a higher frequency of occurrence of glossohyal teeth, and the young having broader vertical markings that tend to form hollow rhomboid shapes (Hubbs and Bailey 1940). Hubbs and Bailey (1940) concluded that at least 80% of 640 individuals could be correctly identified as one or the other of the two subspecies on the basis of the dorsal fin-ray count alone. They also suggested that anthropogenic stocking of smallmouth bass may have affected natural geographic patterns. Bailey (1956) rejected recognition of the Neosho subspecies because of a lack of fixed morphologic differences. Hubbs and Lagler (1958) later defended subspecific recognition for the Neosho form. More recently, Hoyt (1974) agreed with Bailey's (1956) conclusion and indicated that as a result of stocking of "intergrade" forms from the White River by the Arkansas Game and Fish Commission, meristic counts were not the same as reported by Hubbs and Bailey (1940) for Neosho smallmouth bass in several streams in the Arkansas River drainage.

Smallmouth bass of unknown origin were stocked in streams and reservoirs of eastern Oklahoma from the late 1960s into the 1980s without establishment of significant reservoir fisheries (J. Smith, pers. comm.). Similar stock transfers have been made throughout Arkansas (stocking records; Arkansas Game and Fish Commission). Recently,



stocks of smallmouth bass from reservoirs in the Cumberland River drainage in Tennessee have been used to establish high-quality reservoir fisheries at several sites in central Oklahoma that are outside the native range of the species. Extending this stocking program to eastern Oklahoma reservoirs associated with native stream populations is very popular among anglers because native smallmouth bass fisheries have not developed in these reservoirs (J. Smith pers. comm.).

Philipp et al. (1979) characterized presumptive gene loci, tissue specificity, and timing of isozyme expression during embryogenesis in smallmouth bass, laying the framework for allozyme studies with this species. Subsequently, smallmouth bass have been the subject of a number of genetic investigations that principally dealt with hybridization among congeners (Whitmore and Butler 1982; Whitmore 1983; Whitmore and Hellier 1988; Morizot et al. 1991; Koppelman 1994). The result has been the designation of diagnostic loci among spotted bass (*M. punctulatus*), largemouth bass (*M. salmoides*) and smallmouth bass. These studies have dealt primarily with the northern smallmouth bass, and, excepting a study by Koppelman (1994), have not dealt with genetic variability in native smallmouth bass populations.

The basic genetic information required to manage populations of smallmouth bass has been lacking. Morphological and meristic differences among conspecific populations indicate genetic differentiation is likely but inadequately defined for effective management. Hatchery propagation has resulted in range extensions and numerous interbasin transfers having unknown consequences for genetic diversity. In addition, contemporary angling demands can only exacerbate the situation. In this study, I use an allozyme survey to describe genetic variation in native populations of the species. My purposes were 1) to identify and delimit the geographic range of genetically distinct native forms 2) to interpret

genetic patterns in a historical zoogeographic context, 3) to gain insight into the effects of historic and potential stock transfers, and 4) to formulate management options compatible with the conservation of genetic resources.

## **METHODS**

I obtained samples of smallmouth bass from 62 localities (Fig. 1) as follows: 56 stream localities within the native range (sites 1-56), a natural lake in Canada (site 57), Byron Fish Hatchery in Oklahoma (site 58), three Oklahoma reservoirs outside the native range of the species (sites 59-61), and one Oklahoma reservoir within the native range (site 62). Table 1 shows the regional and taxonomic distribution of these 62 populations; detailed locality descriptions are provided in Appendix I. To simplify the analysis, samples 45 and 46, and 54 were analyzed as Black and Missouri river samples, respectively (Table 1). These samples were effectively indistinguishable from those within the respective rivers.

Field collections of approximately 20 individuals each were made by electrofishing, seining, and angling as conditions warranted. From each individual, eye, liver, and epaxial muscle tissues were excised, placed in separate cryo-vials, and stored in liquid nitrogen (-190 °C) for transport to the laboratory. Collections provided by state agency personnel were shipped frozen on dry ice (-95 °C). These included samples from Wisconsin, West Virginia, Tennessee, Kentucky, and Canada, and Oklahoma samples from Broken Bow Reservoir, Black Fork of the Poteau River, Lake Murray, Lake Texoma, and Skiatook Reservoir. A sample of largemouth bass, from a farm pond in Payne Co., Oklahoma, was used as the outgroup in the phylogenetic analysis. Additional samples of spotted bass (Illinois River, Cherokee Co., Oklahoma) and redeye bass (*M. coosae*) from (Alabama River, Walker Co., Georgia) were used to test the monophyly of

smallmouth bass populations.

In the laboratory, tissues were stored at  $-65^{\circ}\text{C}$ . A portion of each tissue sample was then homogenized in distilled water and centrifuged (4,000 X g). Supernatants were subjected to standard methods of horizontal starch-gel electrophoresis (Murphy et al. 1990). Initially, electrophoresis was performed on seven individuals from each of 62 populations of smallmouth bass in a search for polymorphic loci. Loci that were invariant in this screening were not assayed in subsequent runs with additional specimens.

Analytical systems and staining procedures follow Philipp et al. (1983), Murphy et al. (1990), and Richardson et al. (1986) with minor modifications (Table 2).

Genetic analyses were conducted with BIOSYS1 (Swofford and Selander 1981). Chi-square goodness-of-fit tests (with Levene's correction for small sample sizes) and the fixation index ( $F_{IS}$ ) were used to examine deviations from Hardy-Weinberg expectations for genotypic frequencies. Average heterozygosity per individual ( $H$ ) was computed from allele frequencies (Table 1). A locus was considered polymorphic ( $P$ ) if the frequency of the most common allele did not exceed 0.95 (Tables 1 and 2). The standardized variance ( $F_{ST}$ ) was calculated as the mean value over all polymorphic loci. Total gene diversity ( $H_T$ ) was calculated by summing the total limiting variance over all polymorphic loci and dividing by the total number of loci assayed. Calculations of  $F_{ST}$  and  $H_T$  are based only on native populations (i.e., sites 12 and 58-62 were excluded).

Hierarchical analyses of genic diversity (Nei 1977; Wright 1978) among native stream populations were performed on 55 samples in four different designs. Total gene diversity ( $H_T =$  Wright's limiting variance) was partitioned into the proportion due to differences among localities ( $F_{LS}$ ) and the proportion due to within-locality variation ( $H_L/H_T = 1 - F_{LS}$ ).  $F_{LS}$  was further partitioned into the proportions associated with each

level of the hierarchy (Table 3). This type of analysis is comparable to a nested analysis-of-variance in that significance levels are not computed as indicators of biologically important effects (= levels); instead, the proportionate distribution of variance explained by the various effects (levels) is used to indicate relative importance (Sokal and Rolf 1969). I used four levels, with localities (level 4) nested within drainages, drainages (level 3) nested within a variable level 2, and level 2 nested within the species as a whole (or total, level 1); e.g., (Species (Region(Drainage(Locality)))) after Table 1. In all designs, the categories in levels 4, 3 and 1 do not change; however, the number and composition of categories in level 2 allow evaluation of genetic variation associated with taxonomic designations, regional biogeographic scale, and two additional groupings as follows: Hierarchy I nests drainages within taxonomic categories (Table 1), Hierarchy II nests drainages within biogeographic regions (Regions; Table 1), Hierarchy III is the same as II except the Missouri drainage is included in a group (formerly Region III) comprising all other samples of the northern subspecies (Ohio and Mississippi drainages; Table 1), Hierarchy IV differs from III only in that the western Arkansas River drainage is elevated from within Ozark Highlands (Region II; Table 1) to an equivalent group, resulting in four groups (formerly three) at level 2 in the hierarchy, including each of the two nominal subspecies, the remaining Ozark Highland samples (White and Black drainages), and the Ouachita Highlands.

The chord distance (D) of Cavalli-Sforza and Edwards (1967) was computed as the measure of genetic distance rather than the more commonly reported Rogers' (1972) or Nei's (1972, 1978) distances because 1) Rogers' and Nei's distances are biased by within taxon heterozygosity (Swofford and Olsen 1990), 2) the rate of increase in Cavalli-Sforza and Edwards chord distance under random drift is independent of the initial gene

frequencies, providing a realistic assumption about the nature of evolutionary change in gene frequencies (Swofford and Olsen 1990), and 3) this metric appears more appropriate for use in phylogenetic analysis (Rogers 1986). Genetic distances were summarized with cluster analysis using the unweighted-paired-group-method with arithmetic-averaging (UPGMA).

I used a three-step approach in a search for the shortest (most parsimonious) tree of phylogenetic relationships among smallmouth bass populations. First, I used the results of phenetic and gene diversity analyses as a basis for reducing the number of terminal nodes. All locality samples within the Interior Highlands were pooled by drainage basin into single samples. The six samples of native populations from outside the Interior Highlands were treated individually because of the large geographic distances separating them from each other and from all other samples. The matrix of pairwise genetic distances (D) was subjected to the distance-Wagner procedure in BIOSYS1 (multiple addition criterion, MAXTREE = 30). The procedure provided an objective set of phylogenetic topologies (hypotheses of relationship) which were then evaluated for allele frequency parsimony with the FREQPARS program (Swofford and Berlocher 1987). Outgroups for this analysis were one sample each of largemouth bass, spotted bass and redeye bass.

## **RESULTS**

Nineteen polymorphic loci were detected in the initial survey of 33 loci in seven specimens from each of 62 populations. Nine of 397 Chi-square tests indicated deviations from Hardy-Weinberg expectation ( $P \leq 0.05$ ), half the number expected due to sampling error alone ( $397 \times 0.05 = 19.8$ ). The fixation index ( $F_{IS} = 0.002$ ) also gave no indication of any trend toward deviation from Hardy-Weinberg expectations. Total genic diversity for the 56 native populations (1-11 and 13-57) was  $H_T = 0.068$ . The standardized

variance ( $F_{ST} = 0.401$ ) indicated a "very great" degree of genetic heterogeneity (Hartl 1981) among samples (Localities; Table 1). Average genetic variability across samples of the northern subspecies from Iowa, Tennessee, Wisconsin, Kentucky, and West Virginia ( $\bar{H} = 0.020$ ,  $\bar{P} = 6.7$ ) was lower than the average for any single drainage within the Ozark ( $\bar{H}_D = 0.032-0.048$ ,  $\bar{P}_D = 10.2-17.6$ ) or Ouachita ( $\bar{H}_D = 0.045-0.049$ ,  $\bar{P}_D = 12.9-15.6$ ) highlands (Table 1). Removing the six outlying samples (47-49, 55-57) resulted in only a slight reduction in genetic variance ( $F_{ST} = 0.381$ ).

The hierarchical analysis indicated that neither traditional taxonomic designations (level 2, analysis I, Table 3) nor regional physiography (level 2, analysis II, Table 3) are effective descriptors of the high degree of among-locality genetic variation within the smallmouth bass (38.3% of  $H_T$ ). Rather, locality groupings based on drainage flow patterns are more informative (level 2, analyses III, IV, Table 3). In Hierarchy I, genetic differences among taxonomic groups (*M. d. dolomieu*, *M. d. velox*, and intergrades) accounted for 0.0 % of the genic diversity within the species. In Hierarchy II, differences between populations in the Ozark and Ouachita biogeographic regions (Regions; Table 1) accounted for 11% of the genic diversity among localities; however, twice as much genic diversity (22 %) was explained by drainages within regions. Hierarchy III is the same as II except the Missouri drainage is nested in a group that conforms to the range of the northern subspecies (Missouri, Ohio, and Mississippi drainages; Table 1). In this hierarchy, differences among groups and among drainages within groups explained similar proportions of the total genic diversity (17 and 16.2 %, respectively). Hierarchy IV differs from III only in that the Arkansas drainage samples are elevated from within Ozark Highlands (Region II; Table 1) to a separate group of equal rank, resulting in groupings of drainages into four groups: the two nominal subspecies, the remaining Ozark Highland

samples (White and Black river drainages), and the Ouachita Highlands. In this hierarchy, differences among the four groups accounted for 25% of total genic diversity, whereas differences among drainages within these groups accounted for only 8.2%.

The major features of the UPGMA dendrogram are as follows: There are four readily identifiable groups separated by relatively large genetic distances (Fig. 2). One group consists of the Little River samples (1-7) and sample 12 from the Black Fork of the Poteau River (Arkansas River drainage). The second group comprises the samples from the Ouachita River drainage (8-11). The third group is a cluster of all samples from the western Arkansas River drainage (13-28). The fourth group comprises a heterogeneous grouping of localities from the Black, White, and Mississippi rivers (29-46), a cluster from the Ohio River Basin (Tennessee, Kentucky, West Virginia) and Canada (47-49,57) and a cluster from the Missouri and upper Mississippi rivers basins (50-56).

Individual allele distributions at six loci support some of the above interpretations. Within the Ouachita Highlands, *sMEP-1\*86* and *GPI-B\*183* were unique to the four Ouachita River samples (8-11) (Figs. 3 and 4). Ouachita Highland localities (1-11; Little and Ouachita river drainages) were nearly fixed for a unique combination of *sMEP-1\** alleles (*\*115, \*107, \*92, \*86*). Mobility differences among allele products at *sMEP-1\** were minor and difficult to resolve. Side-by-side comparisons on different gel types indicated that *sMEP-1\*107* (common in Ouachita River drainage samples) was present at low frequencies (0.026-0.071) in populations from tributaries of the Arkansas River, and that the otherwise common *sMEP\*100* was rare (0.025-0.075) in Ouachita Highland samples. High frequencies of *PEPS\*106* (>0.5; Fig. 5) and *TPI-1\*140* (>0.75; Fig. 6) support the separation of Ouachita uplift populations (Little and Ouachita rivers) from all except western Arkansas River drainage (13-28) smallmouth bass. *GPI-A\*90* occurred

exclusively in samples from the western Arkansas River drainage (Fig. 7). *PEPS\**, *TPI-I\**, and *SOD\** showed tendencies toward clinal variation from the southern portion of the Western Interior Highlands eastward and northward (Figs. 5-8). No unique shared alleles were detected among the six reference samples encompassing the majority of the native range of the northern subspecies (localities 47-49, 55-57).

The distance-Wagner procedure produced 12 phylogenetic topologies (total lengths 1.561-1.587), each of which was subjected to the FREQPARS allele-frequency-parsimony analysis. FREQPARS tree lengths ranged from 57.821 to 58.583. The difference (0.762) in terms of total allele frequency change between the longest and shortest trees (0.38) was negligible. We therefore developed a strict consensus topology reflecting the common features of all 12 trees (Fig. 9). The major features of the consensus tree are the following: 1) the smallmouth bass is a monophyletic species; 2) samples from the Little River and Ouachita River drainages clustered as a monophyletic Ouachita Highlands group ("Ouachita smallmouth bass"); 3) samples from within the range of the Neosho smallmouth bass (Neosho River and other western Ozark tributaries of the Arkansas River) clustered as a monophyletic group; and 4) the remaining samples formed a polytomy that included samples from the White, Black, Missouri, Ohio and upper Mississippi rivers.

To further examine relationships among the three major clusters shown in the consensus cladogram (Fig. 9), I computed FREQPARS tree lengths for three alternative topologies, one conforming with the shortest distance-Wagner tree (Tree I, Fig. 9); one in which the Neosho and Ouachita forms were the monophyletic sister-group to all other smallmouth bass (Tree II, Fig. 9), and one in which the Neosho form was sister to all other smallmouth bass (Tree III, Fig. 9). Otherwise, the topologies of these three trees were



constrained to be identical to that of the shortest tree derived from the distance-Wagner procedure. FREQPARS tree lengths for the two rearrangements (57.851 and 57.928) were shorter than those for 11 of the 12 trees used in the consensus cladogram shown in Fig. 9, and were only slightly longer than the shortest distance-Wagner tree (length = 57.821). Allele frequency parsimony effectively does not discriminate among the tested topologies. However, one potential synapomorphy, the *PEPS\*106* allele, supports the possibility that the Neosho and Ouachita smallmouth basses share a common ancestor that is not shared with other populations of smallmouth bass. *PEPS\*106* occurred at low (0.05) to high (1.00) frequencies in all samples of the Neosho and Ouachita smallmouth bass. Otherwise, this allele occurred only at low to moderate frequencies (0.023 - 0.143) in four samples from the upper White River, possibly as a result of gene flow from nearby populations of Neosho smallmouth bass.

The sample from Byron Hatchery and those from introduced populations of smallmouth bass in Oklahoma (Skiatook Reservoir, Lake Texoma, and Lake Murray) clustered with samples from eastern North America (localities 47-49; Fig. 10). The sample of 16 fish from Broken Bow Reservoir apparently was a mixture of native fish and stock from the Byron Fish Hatchery that was introduced into the reservoir in 1993. This sample had the highest heterozygosity detected in this study ( $H = 0.09$ ). The Chi-square test for the diagnostic locus *sMEP-1\** indicated a significant deficiency of heterozygotes (Chi-square = 9.006,  $df = 1$ ,  $P < 0.003$ ). Six individuals exhibited the *SOD\*-145* allele; this allele was otherwise not present in the Little River drainage, but was common (0.262) in the Byron Hatchery stock. The same individuals also were *TPI-1\*100* homozygotes, a genotype that is characteristic of Byron Hatchery stock but extremely rare in the Ouachita Highlands. Only 10 (62.5%) of the specimens examined from Broken Bow Reservoir had

genotypes typical of the Ouachita smallmouth bass.

## **DISCUSSION**

The smallmouth bass includes genetically distinct forms in both the Ouachita Highlands, and the western Arkansas River drainage of the Ozark Highlands. These populations exhibit the highest heterozygosities within the species even though they occupy the smallest and most isolated basins surveyed. Populations in other Ozark river basins, the White, Black, and Missouri, are genetically intermediate between the southwestern forms and populations to the north and east. The samples from northern and eastern United States were relatively homogeneous and had the lowest heterozygosities detected in this study. These patterns of genetic variation do not conform well with the previously recognized subspecies and areas of intergradation (Hubbs and Bailey 1940). Like much of the zoogeography of North American fishes (Hocutt and Wiley 1986), these patterns may best be understood in light of Pre-pleistocene drainage patterns and subsequent glacier-mediated vicariant events of the Pleistocene (Wiley and Mayden 1985; Mayden 1988a).

### **Zoogeography**

The Central Highlands is a once continuous highland region that dates at least to the Eocene (40 mya) and now comprises two uplifted areas separated by the Mississippi River, the Eastern Highlands, and the Interior (Ozark and Ouachita) Highlands. Prior to pleistocene glacial advances (2.5 mya), the region from Canada south approximately to the Missouri and Ohio river basins, was geomorphically similar to the present remnants of the Central Highlands (Thornbury 1965) and had an aquatic fauna well-adapted to clear, high-gradient streams (Wiley and Mayden 1985; Cross et al. 1986; Mayden 1987a;

Mayden 1987b; Mayden 1988a). Cross et al. (1986) indicated that this Central Highland fauna probably extended well out into the present High Plains physiographic province of Kansas and Oklahoma, and possibly to the Rocky Mountains.

Glacial advances had major effects on the Central Highland area through erosion and deposition of vast amounts of glacial till. Subsequently, stream habitats were unsuitable for reinvasion by many highland forms (but not smallmouth bass). This degradation was not uniform across the ice fronts, and a number of small refugia were not physically affected by ice movement (Thornbury 1965; Wiley and Mayden 1985). The largest of these "driftless" zones occurred along the Wisconsin-Iowa border with numerous smaller ones east of the Mississippi River. On the plains, the Kansan glaciation (1.8-0.8 mya) diverted eastward-flowing streams south into the Ancestral Plains Stream (Figure 11) and to an independent confluence with the Gulf of Mexico via the Trinity River Basin (Metcalf 1966; Cross et al. 1986). During successive glacial advances, the channel of the Mississippi River changed a number of times and eventually stabilized into the wide lowland floodplain that now separates the Eastern and Interior highlands. Prior to the Sangamonian Interglacial (0.4-0.1 mya), the Arkansas River cut westerly and separated the Interior Highlands into the Ozark and Ouachita highlands (Quinn 1958) and ultimately captured much of the Ancestral Plains Stream. Farther to the south, the Ancestral Red River cut north and captured the western portion of the old Ouachita River near the headwaters of the current Little Missouri River in southwestern Arkansas (Mayden 1985), subsequent westward cutting captured eastward flowing basins on the High Plains.

Until recently, most hypotheses to account for contemporary fish distributions in the Central Highlands have focused on centers of origin and multiple dispersal events

(dispersal over barriers or stream captures) or have relied on recent community level interactions (competition, predation etc.) and responses to abiotic factors (Mayden 1987a, 1987b). However, Wiley and Mayden (1985) proposed a "Pre-pleistocene" explanation for current fish distributions. In essence, the hypothesis states that the highland ichthyofaunas of central North America are remnants of a once continuous fauna that was modified by the glacier-mediated vicariant events described above.

Mayden (1988a) tested the pre-pleistocene hypothesis using parsimony analysis to generate a cladogram of drainage basin relationships, with the presence or absence of members of seven monophyletic species-groups as independent basin characters. The results did in general supported the Pre-pleistocene hypothesis. The most important aspects of this analysis relative to genetic pattern observed in smallmouth bass are that 1) the faunas of the western Arkansas tributaries and Ouachita Highland rivers are the most derived, and 2) the fauna in western Arkansas tributaries is sister to the Ouachita Highland fauna rather than to the adjacent White River fauna.

The relationship between the faunas of the southwestern Ozarks and the Ouachita Highlands requires a riverine connection for which geomorphic support has not been previously demonstrated. However, structural geologic trends and the altitudinal gradient in the eastern one-third of Oklahoma are oriented northeast to southwest (Gould 1927), and suggest the possibility of a southwestern confluence between the ancestral Neosho River and an ancestral Ouachita Highlands river (Figure 11). Correspondingly, a broad valley extends from the current area of confluence between the Arkansas, Neosho, and Canadian drainages southwesterly to the Muddy Boggy River headwaters in the Red River Basin. The existing divide between the Arkansas River and Red River basins is less than 7 meters at its lowest point, which occurs near the town of Kiowa, Pittsburg Co., Oklahoma

(U.S. Geological Survey, 1:24,000 Topographic Map Series: Kiowa quadrangle).

Underlying this valley are beds of sand and gravel of plio-pleistocene age (Snider 1914), suggesting the possibility of a larger river system than the present headwaters of Muddy Boggy River.

Patterns of genetic variation observed in smallmouth bass are only in partial agreement with the Pre-pleistocene hypothesis. Populations throughout the range of the northern subspecies (excluding the Interior Highlands) were not genetically distinct and, therefore, could not be correlated to historical geologic events. The relatively high homogeneity of these populations is supported by a separate investigation focusing on northern and eastern populations of smallmouth bass, in which little genetic variability was detected in both restriction-fragment-length-polymorphisms of mitochondrial-DNA and allozyme data (Jim Ludden, Illinois Natural History Survey; pers. comm.). The low genetic variability observed in these populations suggests a recent origin relative to the distinctive southwestern forms. During the Wisconsin Glaciation (20,000 years ago), ice would have precluded smallmouth bass from much of the native range of the northern subspecies, and the previous Illinoian Glaciation would have been much more severe east of the Mississippi River (Thornbury 1965). Reinvasions of the northern areas by small founder populations may account for both the low heterozygosities and the relative lack of genetic divergence among the samples we examined from populations outside the southwestern Interior Highlands. Similarly, Seeb et al. (1987) proposed reinvasions from small founder populations to explain their failure to observe appreciable genetic variability in northern pike (*Esox lucius*) populations.

Until the Sangamonian Interglacial (0.4-0.1 mya), all drainage from the Ozark highlands flowed more or less directly into the Mississippi River (Cross et al. 1986;

Mayden 1988a), except for the Neosho River Basin, which is now confluent with the Arkansas River in northeastern Oklahoma (Quinn 1958; Metcalf 1966). The inferred presence of the common ancestor for the *Etheostoma craigini-pallididorsum* species-group, the distributions of *Luxilus cardinalis* and *Nocomis asper* (Mayden 1988a, 1988b) and geomorphic features, strongly indicate an integrated basin along the western edge of the Interior Highlands that would have comprised portions of the current Neosho, Verdigris, Arkansas, Canadian, Muddy Boggy, Red, and Ouachita rivers. This basin would have allowed the independent evolution of a southwestern clade of smallmouth bass that is now represented by populations in the western Arkansas, Little, and Ouachita river basins. The *PEPS\*106* allele provides the best allozyme evidence for such a clade, as this allele is distributed as a potential synapomorphy that would unite the Neosho and Ouachita populations of smallmouth bass (Figure 5). The subsequent capture of the ancestral Neosho River by the Arkansas River allowed the independent evolution of Neosho and Ouachita Highlands populations as indicated by the allele distributions for *sMEP-1\** (Figure 3).

Subsequent climatic warming associated with the receding glaciers may have reduced gene flow by way of the large lowland rivers that now effectively isolate Interior Highland populations. The geographic distributions of three alleles, *SIDHP-1\*76,90* and *PEPS\*106* suggest a potential interbasin exchange between populations in the headwaters of the White River (29-33) and adjacent western populations in the Arkansas River (16-18, 22). If Buth and Mayden (1981) and Distler (1968) are correct, similar types of faunal exchanges within the Interior Highlands may have occurred during the evolution of the *Luxilus zonatus* species group and among subspecies of *Etheostoma spectabile*.

## **Anthropogenic effects**

The native range of the smallmouth bass has been significantly extended and interbasin transfers have occurred as the result of intensive culture initiated as early as 1904 (Lee et al. 1980; Stroud and Clepper 1975). The exact nature and source of stocks for most of this early activity is undocumented, although a number of authors of regional works have noted the prolific stocking of smallmouth bass (Hubbs and Bailey 1938; Hubbs and Bailey 1940; Pflieger 1975; Trautman 1981; Robison and Buchanan 1988). Specifically, Hoyt (1974) indicates that stocks from the White River were transferred to western Arkansas River tributaries. Stocking records from the Arkansas Game and Fish Commission and the Oklahoma Department of Wildlife Conservation indicate frequent stockings of smallmouth bass from the National Hatchery System in their respective states up until the late 1980's.

Populations in the Black Fork of the Poteau River (site 12), although within the native range of the species, probably represent an artificial introduction. I am aware of no collection records of smallmouth bass from within the basin prior to a 1966 stocking of 553 fingerling smallmouth bass by the Oklahoma Department Wildlife Conservation (stocking records provided by Gene Gilliland; parent stocks are unknown). However, a number of early collection records of stream-dwelling spotted and largemouth bass have been reported from the basin (Hubbs and Bailey 1940, Robison and Buchanan 1988). The genetic structure of my sample from the Poteau River is best explained by an introduction of fish from the Little River. Smallmouth bass also are not native to the Kiamichi River drainage, which separates the Poteau drainage (Arkansas River drainage) from the Little River drainage in southeastern Oklahoma. Interviews with local individuals support the recent establishment of the Poteau River population.

Generally, it is difficult to determine the effects of early stocking on the natural pattern of variation because the source of hatchery populations usually cannot be known with certainty. Currently, smallmouth bass from the Cumberland River drainage in Tennessee are the only stock under culture in Oklahoma (Byron State Hatchery). Correspondingly, the genetic structure of the hatchery population is similar to that reported in this study for populations from the Ohio River Basin. Skiatook Reservoir and Lake Texoma populations were founded in 1981 and 1990, respectively, from these hatchery stocks and are genetically very similar to the Byron Hatchery sample (Fig. 10). Lake Murray was stocked with a previous hatchery stock of unknown origin. The Lake Murray sample clustered just outside of the other introduced reservoir populations from Oklahoma. The possibility of a mixed ancestry is indicated by its relatively high genetic variability ( $H = 0.039$ ,  $P = 12.1$ ) which is somewhat greater than that of other reservoir or Ohio River Basin populations (Table 1). The origin of parental stocks probably will never be known with certainty but *TPI-1\*140*, *PEPS\*106* and *SIDHP-1\*76* alleles were detected at low frequencies, indicating some parental forms of Ozark origin.

The most heterogeneous sample that I examined was from Broken Bow Reservoir. Prior to collection of this sample, Broken Bow Reservoir received one stocking of smallmouth bass from the Byron State Fish Hatchery. Fish were stocked as fingerlings in the late spring of 1993 and the relatively small sample ( $N = 16$ ) I examined from Broken Bow Reservoir was made in the fall of that year. Although the sample from Broken Bow Reservoir clusters within the Ouachita Highlands group, it is well separated from all other Little River populations. As judged by the occurrences of *SOD\*145*, *sMEP-1\*100,111*, and *TPI-1\*100*, 37.5% of the sample (6 individuals) were recruited from the hatchery stock released in 1993. The sample we examined was taken in the immediate area of



release so the percentage recruited from hatchery stock is likely a maximum value. Additional sampling is required to determine the ultimate effect on the native population. Further stockings of this type should be avoided, given the genetic distinctness of the Ouachita smallmouth bass, and the likelihood of genetic interaction with introduced, non-native stock.

Introductions of non-native stocks of smallmouth bass are not the only threat to the genetic integrity of Neosho and Ouachita smallmouth bass. These two forms, although genetically diverse, inhabit relatively restricted ranges that, since the 1930's, have been fragmented by impoundments. Although some native populations do persist, significant fisheries never developed, indicating that smallmouth bass may be ill-equipped for long-term survival in these modified habitats. The dams forming these reservoirs restrict gene flow to the downstream direction. In only three instances would upstream connections between any pair of populations we sampled be physically possible. Range fragmentation on this scale may significantly reduce effective population size, increasing the potential for reduced genetic variability and local extinctions. To avoid such effects periodic exchange of individuals across these artificial barriers may become necessary.

## **Conclusions**

Smallmouth bass from the southwestern Interior Highlands comprise two genetically distinct forms, one from Arkansas River tributaries draining the southern and western Ozark Highlands (Neosho smallmouth bass) and one from the Ouachita Highlands in southeastern Oklahoma and southwestern Arkansas ("Ouachita" smallmouth bass). These two forms are genetically divergent from each other. Further, they are not simply genetically depauperate, peripheral isolates of the more wide-ranging form. Rather, they

appear to be the most genetically distinct populations of the species. The Neosho and Ouachita smallmouth bass apparently represent evolutionarily old historic entities that contain significant portions of the total genic diversity of the species. Populations in the central Ozarks (White and Black rivers) are genetically intermediate between the southwestern populations (Neosho and Ouachita smallmouth bass) and populations representing the remainder of the species. These latter populations occupy the majority of the species range but exhibit the least amount of genetic variability. Reduced variability may result from post-Pleistocene reinvasion of this area from glacial refugia. Stock transfers of non-native smallmouth bass into the southwestern Interior Highlands should be avoided. This will help avoid losses of genetic diversity and will preserve future management options represented by the existence of these genetically divergent native stocks.

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Table 1. Locality, drainage basin, sample size (N), percentage of polymorphic loci (P), expected heterozygosity per individual (H) and standard errors (S.E.), and mean variability ( $\bar{H}_D$  and  $\bar{P}_D$ ) within drainages at 33 loci for 62 samples of smallmouth bass. Taxon designations follow Hubbs and Bailey (1940). Locality numbers correspond to Figure 1 and Appendix I.

Collection Locality No.	Major River Stream (State) Basin	Sample Size N	Genetic Variability			
			P	H	S. E.	
REGION I: Ouachita Highlands						
<i>"Intergrades"</i>						
1	Black Fk. (OK)	Little	19	15.2	0.051	0.023
2	Little R. (OK)	Little	20	15.2	0.050	0.023
3	Glover R. (OK)	Little	18	12.1	0.043	0.021
4	Mountain Fk. (OK)	Little	19	21.2	0.054	0.022
5	Buffalo Cr. (OK)	Little	20	15.2	0.044	0.020
6	Rolling Fk. (AR)	Little	15	15.2	0.045	0.020
7	Cossatot R. (AR)	Little	19	15.2	0.054	0.022
				$\bar{P}_D=15.6$	$\bar{H}_D=0.049$	0.005
8	Ouachita R. (AR)	Ouachita	20	9.1	0.040	0.025
9	Caddo R. (AR)	Ouachita	20	15.2	0.049	0.023
10	Little Missouri R. (AR)	Ouachita	20	15.2	0.045	0.025
11	North Fk. Saline R. (AR)	Ouachita	20	12.1	0.047	0.024
				$\bar{P}_D=12.9$	$\bar{H}_D=0.045$	0.004
†12	Black Fk. Poteau R. (OK)	Arkansas	12	9.1	0.022	0.014
REGION II: Ozark Highlands						
<i>Micropterus dolomieu velox</i>						
13	White Oak Cr. (MO)	Arkansas	22	15.2	0.040	0.014
14	Shoal Cr. (MO)	Arkansas	20	24.2	0.062	0.021
15	Fivemile Cr. (OK)	Arkansas	20	9.1	0.022	0.009
16	Big Sugar Cr. (MO)	Arkansas	33	15.2	0.042	0.014
17	Spavinaw Cr. (OK)	Arkansas	41	24.2	0.059	0.017
18	Saline Cr. (OK)	Arkansas	19	18.2	0.046	0.017
19	Spring Cr. (OK)	Arkansas	19	18.2	0.043	0.017
20	Fouteenmile Cr. (OK)	Arkansas	20	15.2	0.025	0.010
21	Flint Cr. (OK)	Arkansas	11	15.2	0.049	0.016
22	Illinois R. (OK)	Arkansas	37	21.2	0.054	0.017
23	Baron Fork (OK)	Arkansas	21	18.2	0.050	0.018
24	Sallisaw Cr. (OK)	Arkansas	20	15.2	0.031	0.016
25	Little Lee Cr. (OK)	Arkansas	22	18.2	0.054	0.019
26	Frog Bayou (AR)	Arkansas	21	15.2	0.062	0.028
27	Little Mulberry R. (AR)	Arkansas	20	21.2	0.077	0.030
28	Big Piney Cr. (AR)	Arkansas	21	18.2	0.051	0.020
				$\bar{P}_D=17.6$	$\bar{H}_D=0.048$	0.014



Table 1 continued.

Locality	Stream (State)	Major River	N	P	H	S. E.
REGION II: Ozark Highlands						
<i>"Intergrades"</i>						
29	White R. (AR)	White	21	3.0	0.029	0.015
30	West Fk. (AR)	White	21	12.1	0.037	0.016
31	War Eagle (AR)	White	7	15.2	0.040	0.018
32	Kings R. (AR)	White	23	9.1	0.034	0.015
33	Flat Cr. (MO)	White	20	9.1	0.031	0.015
34	James R. (MO)	White	22	9.1	0.031	0.011
35	Bull Cr. (MO)	White	22	12.1	0.029	0.013
36	Beaver Cr. (MO)	White	29	9.1	0.030	0.016
37	North Fk. (MO)	White	22	15.2	0.030	0.014
38	Crooked Cr. (AR)	White	21	6.1	0.027	0.015
39	Buffalo R. (AR)	White	27	12.1	0.031	0.014
				$\bar{P}_D=10.2$	$\bar{H}_D=0.032$	0.004
40	Strawberry R. (AR)	Black	18	15.2	0.051	0.021
41	Eleven Point R. (MO)	Black	21	9.1	0.031	0.017
42	Current R. (MO)	Black	22	15.2	0.055	0.023
43	Jacks Fk. (MO)	Black	20	15.2	0.044	0.020
44	West Fk. (MO)	Black	21	15.2	0.040	0.018
45	St. Francis R. (MO)	†† St. Francis	19	21.2	0.062	0.025
46	Whitewater R. (MO)	†† Whitewater	20	12.1	0.031	0.016
				$\bar{P}_D=14.7$	$\bar{H}_D=0.045$	0.012
<i>Micropterus dolomieu dolomieu</i>						
50	Pomme de Terre R. (MO)	Missouri	21	9.1	0.034	0.016
51	Niangua R. (MO)	Missouri	21	6.1	0.029	0.018
52	Gasconade R. (MO)	Missouri	22	15.2	0.046	0.019
53	Big Piney R. (MO)	Missouri	21	18.2	0.050	0.020
54	Huzzah Cr. (MO)	††† Merimac	21	15.2	0.035	0.015
				$\bar{P}_D=12.8$	$\bar{H}_D=0.039$	0.009
Region III: Reference Collections						
<i>M. d. dolomieu</i>						
47	Clinch R. (TN)	Ohio	23	6.1	0.015	0.012
48	Elkhorn Cr. (KY)	Ohio	25	3.0	0.015	0.013
49	New R. (WV)	Ohio	24	6.1	0.011	0.008
55	Maquoketa R. (IA)	Upper Mississippi	36	6.1	0.026	0.019
56	Pecatonica R. (WI)	Upper Mississippi	22	12.1	0.032	0.017
				$\bar{P}_D=6.7$	$\bar{H}=0.020$	0.009
57	Fourteen Isle Lake, Canada	-----	5	3.0	0.010	0.010

Table 1 continued.

Locality	Stream (State)	Major River	N	P	H	S. E.
		Reservoir Samples				
58	Byron State Hatchery, (OK)	-----	21	6.1	0.024	0.013
59	Skiatook Reservoir, (OK)	-----	19	9.1	0.021	0.014
60	Lake Murray, (OK)	-----	20	12.1	0.039	0.016
61	Lake Texoma, (OK)	-----	20	6.1	0.012	0.009
62	Broken Bow Reservoir, (OK)	-----	16	21.2	0.090	0.033

† Sample no. 12 is believed to represent a naturalized population.

†† The St. Francis and Whiterwater river samples were treated as tributaries of the Black River in the hierarchical analysis of genic diversity

††† The Merimac River sample was treated as a tributaries of the Missouri River in the hierarchical analysis of genic diversity

Table 2. Protein designations, putative loci, tissues, and electrophoretic buffer systems used to assay genetic population structure of smallmouth bass. Locus abbreviations follow Shaklee et al. (1990) and Protein names and numbers follow the International Union of Biochemistry (1984). † Designates a polymorphic locus.

Protein	Locus	Tissue	Analytical system <sup>1</sup>
Adenylate kinase (EC 2.7.4.3)	<i>AK*</i>	Muscle	EDTA
Alcohol dehydrogenase (EC 1.1.1.1)	† <i>ADH*</i>	Liver	EDTA
Aspartate aminotransferase (EC 2.6.1.1)	† <i>sAAT-1*</i>	Liver	EDTA
Creatine kinase (EC 2.7.3.2)	<i>CK-A*</i>	Eye	TC
	<i>CK-B*</i>	EYE	TC
	<i>CK-C*</i>	EYE	TC
Fructose-Bisphosphatase (EC 3.1.3.11)	<i>FBP-1*</i>	Muscle	TC
	<i>FBP-2*</i>	Liver	TC
Fumarate hydratase (EC 4.2.1.1)	<i>FH*</i>	Muscle	TC
Glucose dehydrogenase (EC 1.1.1.47)	† <i>GDH*</i>	Liver	TC
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	<i>GAPDH-1*</i>	Eye	TC
Glucose-6-phosphate isomerase (EC 5.3.1.9)	† <i>GPI-A*</i>	Eye	EDTA
	† <i>GPI-B*</i>	Muscle	EDTA
Isocitrate dehydrogenase (EC 1.1.1.42)	† <i>sIDHP-1*</i>	Liver	TC
	<i>mIDHP-1*</i>	Muscle	TC
L-Lactate dehydrogenase (EC 1.1.1.27)	<i>LDH-A*</i>	Eye	EDTA
	<i>LDH-B*</i>	Eye	EDTA
	<i>LDH-C*</i>	Eye	EDTA
Malate dehydrogenase (EC 1.1.1.37)	† <i>sMDH-A*</i>	Muscle	EDTA
	† <i>sMDH-B*</i>	Muscle	EDTA
Malic enzyme (NADP+) (EC 1.1.1.40)	† <i>sMEP-1*</i>	Muscle	TC
Mannose-6-phosphate isomerase (EC 5.3.1.8)	<i>MPI-1*</i>	Muscle	TC
	<i>MPI-2*</i>	Liver	TC
Tripeptide aminopeptidase (EC 3.4.-.-)	† <i>PEPB*</i>	Eye	TC
Peptidase-C (EC 3.4.-.-)	† <i>PEPC*</i>	Liver	EDTA
Dipeptidase (EC 3.4.-.-)	† <i>PEPA*</i>	Eye	TC
Peptidase-S (EC 3.4.-.-)	† <i>PEPS*</i>	Liver	TC
General protein	† <i>PROT-1*</i>	Muscle	EDTA
	<i>PROT-2*</i>	Muscle	EDTA
Phosphogluconate dehydrogenase (EC 1.1.1.44)	† <i>PGDH*</i>	Liver	TC
Phosphoglucomutase (EC 5.4.2.2)	† <i>PGM*</i>	Muscle	EDTA
Superoxide dismutase (EC 1.15.1.1)	† <i>SOD*</i>	Liver	EDTA
Triosephosphate isomerase (EC 5.3.1.1)	† <i>TPI-1*</i>	Muscle	TC
Xanthine dehydrogenase-like	† <i>XDHI*</i>	Liver	EDTA

<sup>1</sup>TC. The gels were 11.6% starch (w/v) in 0.0175 M citrate, pH 6.7. Both buffer chambers consisted of 500 ml of 0.075M Tris/0.025M citrate, pH 6.7. Electrophoresis was conducted at a constant 45 mA for 14 hours at 6°C.

EDTA. The gels were 11.4% starch (w/v) in 0.045 M Tris/0.025 M borate/0.001 M EDTA, pH 8.6. The cathodal buffer chamber consisted of 500 ml 0.180 M Tris/0.1 M borate/0.004 M EDTA, pH 8.6 and the anodal chamber consisted of 0.129 M Tris/0.071 M borate/0.003 M EDTA, pH 8.6. Electrophoresis was conducted at a constant 35 mA for 10 hours at 6°C.

Table 3. Variance components ( $F_{XY}$ ) and distribution of genic diversity in four separate hierarchical analyses (I-IV) of genetic variation. The hierarchies were set up as follows: I corresponds to the Taxon and Drainage nestings in Table 1. II follows the Region and Drainage nestings in Table 1. III differs from II only in that Missouri drainage collections are nested within Region III rather than with the Ozark region. IV differs from III in that Arkansas River collections are elevated from Region II to its own Region IV.

Comparison	Symbol	Hierarchical Analyzes			
		I	II	III	IV
Locality - Drainage	$F_{LD}$	0.076	0.076	0.076	0.076
Locality- (Taxon, Region, or Group)	$F_{L(R,G)}$	0.383	0.307	0.263	0.177
Locality- Species	$F_{LS}$	0.383	0.383	0.383	0.383
Drainage-(Taxon, Region, or Group)	$F_{DT(R,G)}$	0.332	0.249	0.202	0.110
Drainage-Species	$F_{DS}$	0.332	0.332	0.332	0.332
(Taxa, Region, or Group)-Species	$F_{T(R,G)S}$	0.000	0.110	0.162	0.250

Total genic diversity ( $H_T$ )=0.068

Source of Genetic Variation		Gene Diversity (%)			
		I	II	III	IV
Within localities	$1-F_{LS}$	61.7	61.7	61.7	61.7
Among localities	$F_{LS}$	38.3	38.3	38.3	38.3
Among Taxa, Regions, or Groups	$F_{T(R,G)S}$	0.0	11.0	16.2	25.0
Among Drainages					
within Taxa, Regions, or Groups	$(F_{LS}-F_{T(R,G)})-(F_{LS}-F_{DS})$	33.2	22.2	17.0	8.2
Among Localities within Drainages	$F_{LS}-F_{DS}$	5.1	5.1	5.1	5.1

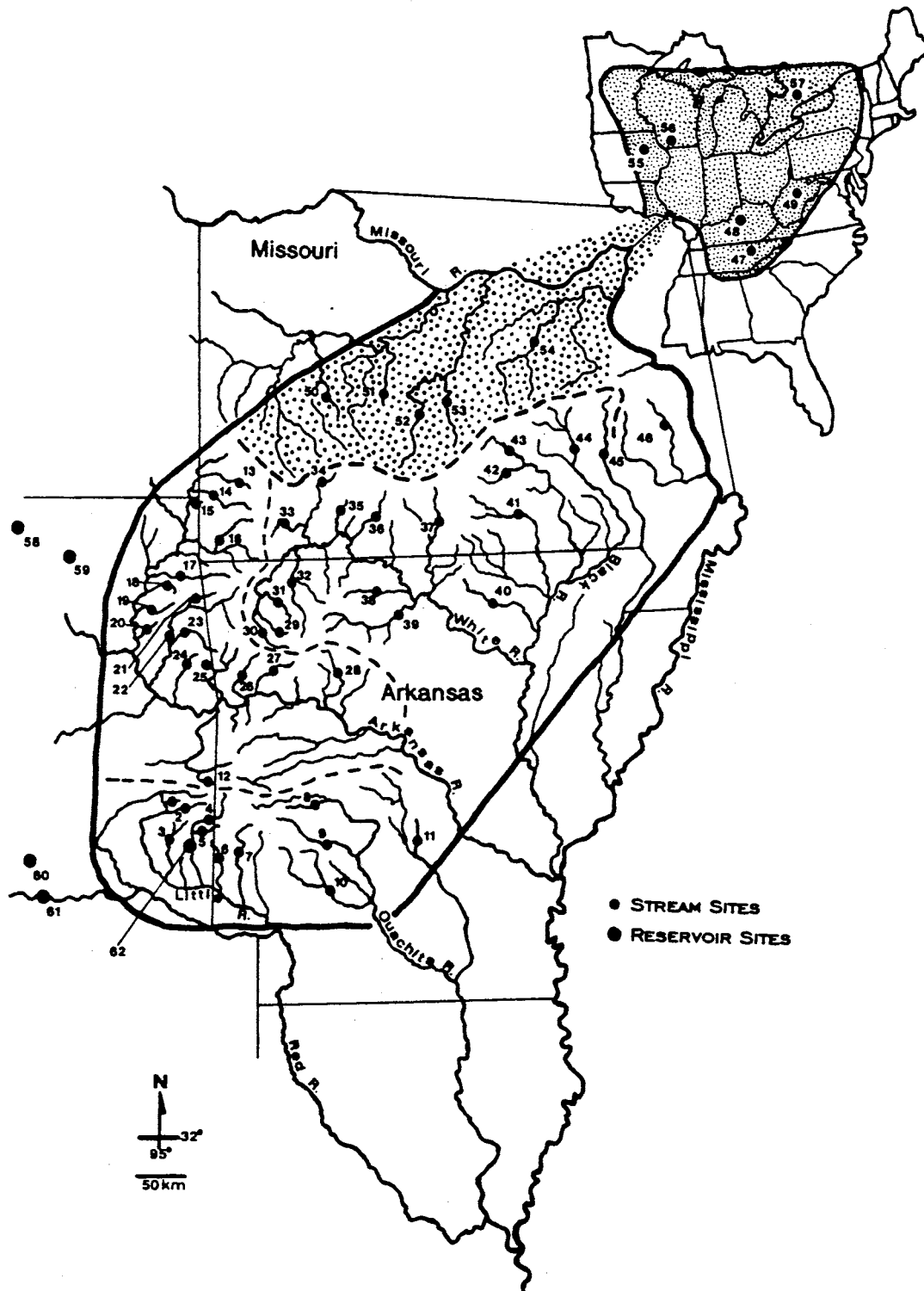


Figure 1. Collection localities plotted on a map of the native range of the smallmouth bass (*Micropterus dolomieu*) delimited by the heavy-line. Stippled area delimits the range of *M. d. dolomieu*. The dashed lines follow drainage basin boundaries and delimit the range of *M. d. velox* in the western Arkansas River from "intergrades" (Hubbs and Bailey 1940).

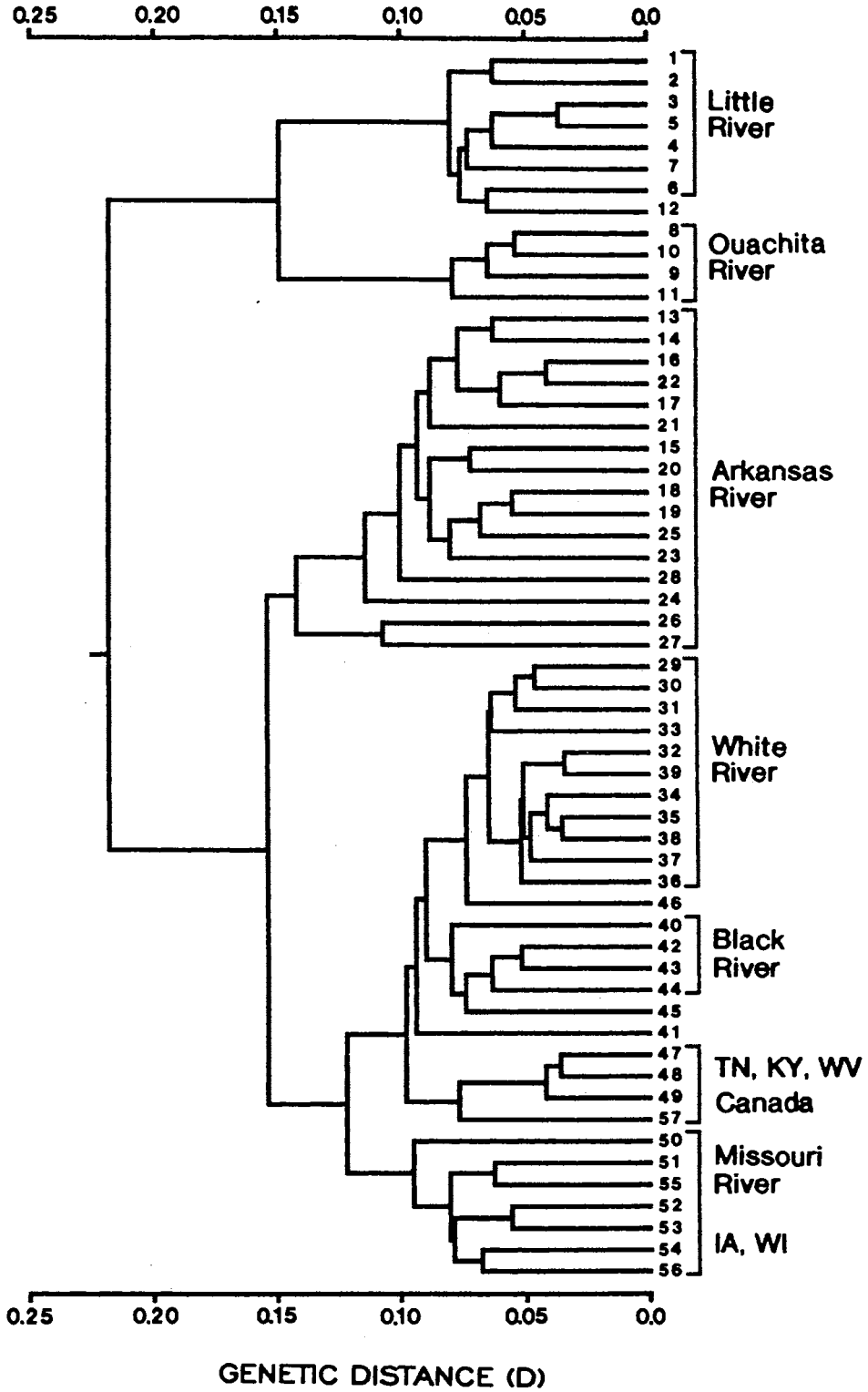


Figure 2. UPGMA dendrogram summarizing genetic distances among 57 smallmouth bass populations. Numbers correspond to those in Figure 1.

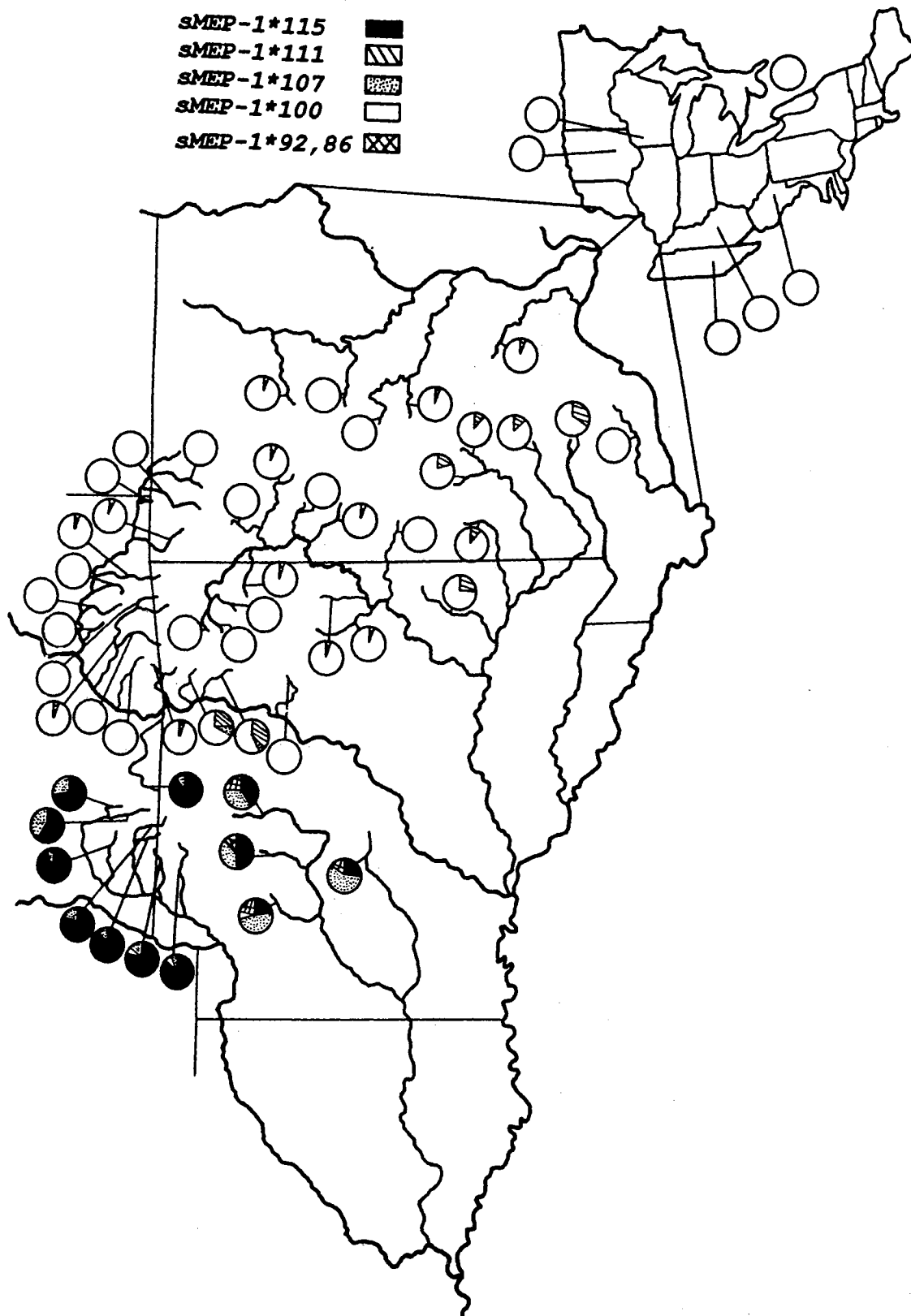


Figure 3. Allele frequency distributions at *sMEP-1\**.

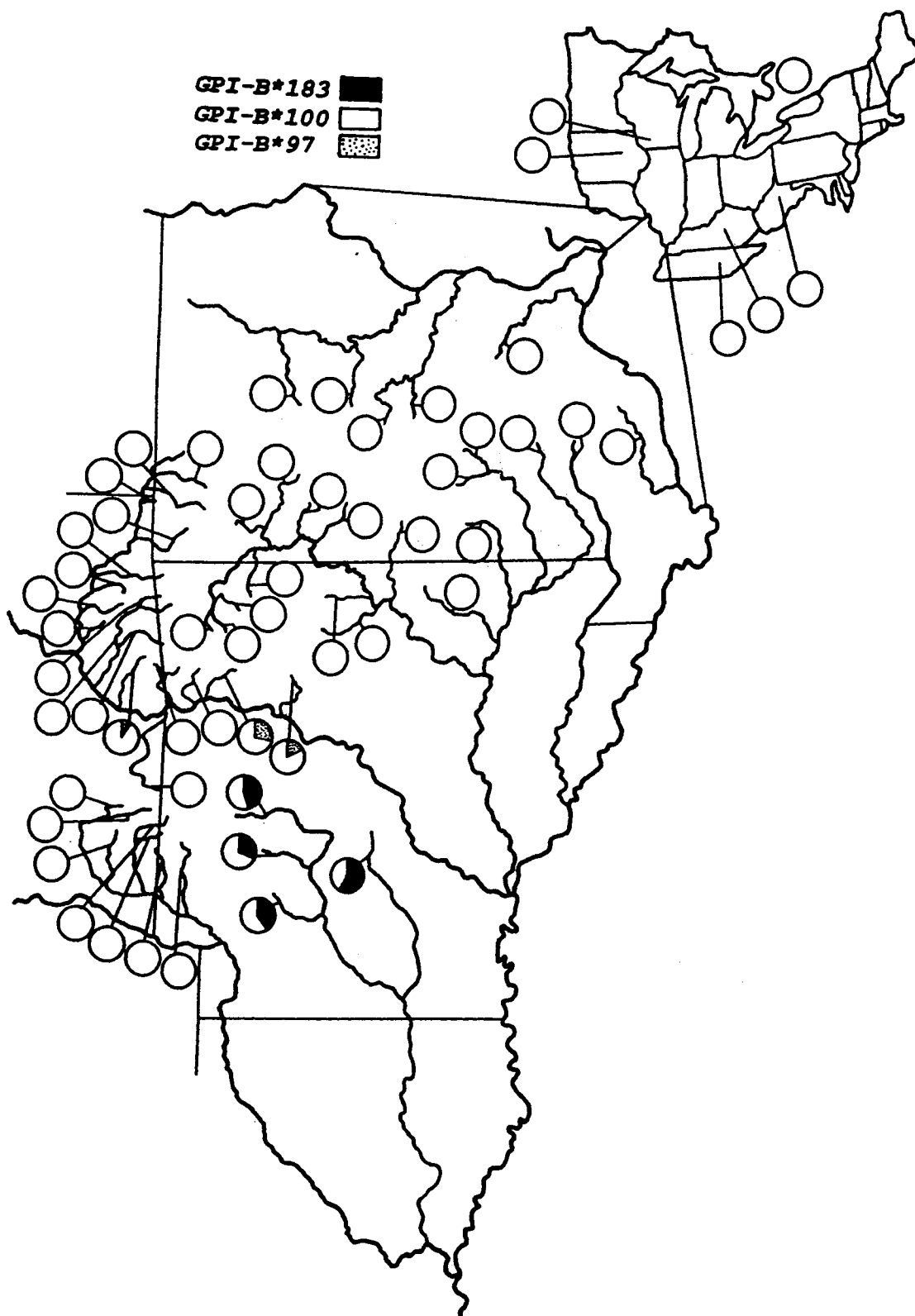


Figure 4. Allele frequency distributions at *GPI-B\**.



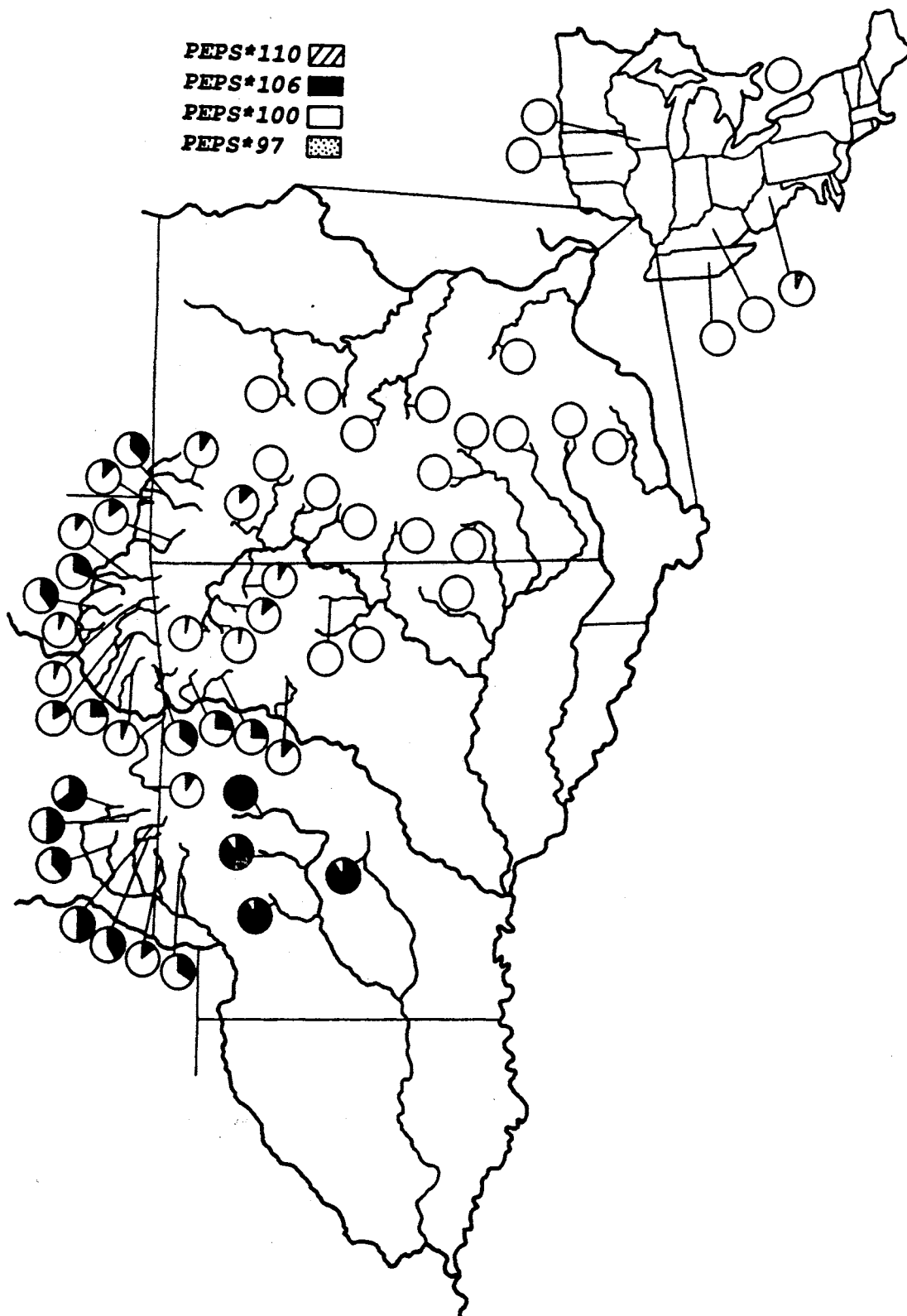


Figure 5. Allele frequency distributions at *PEPS\**.

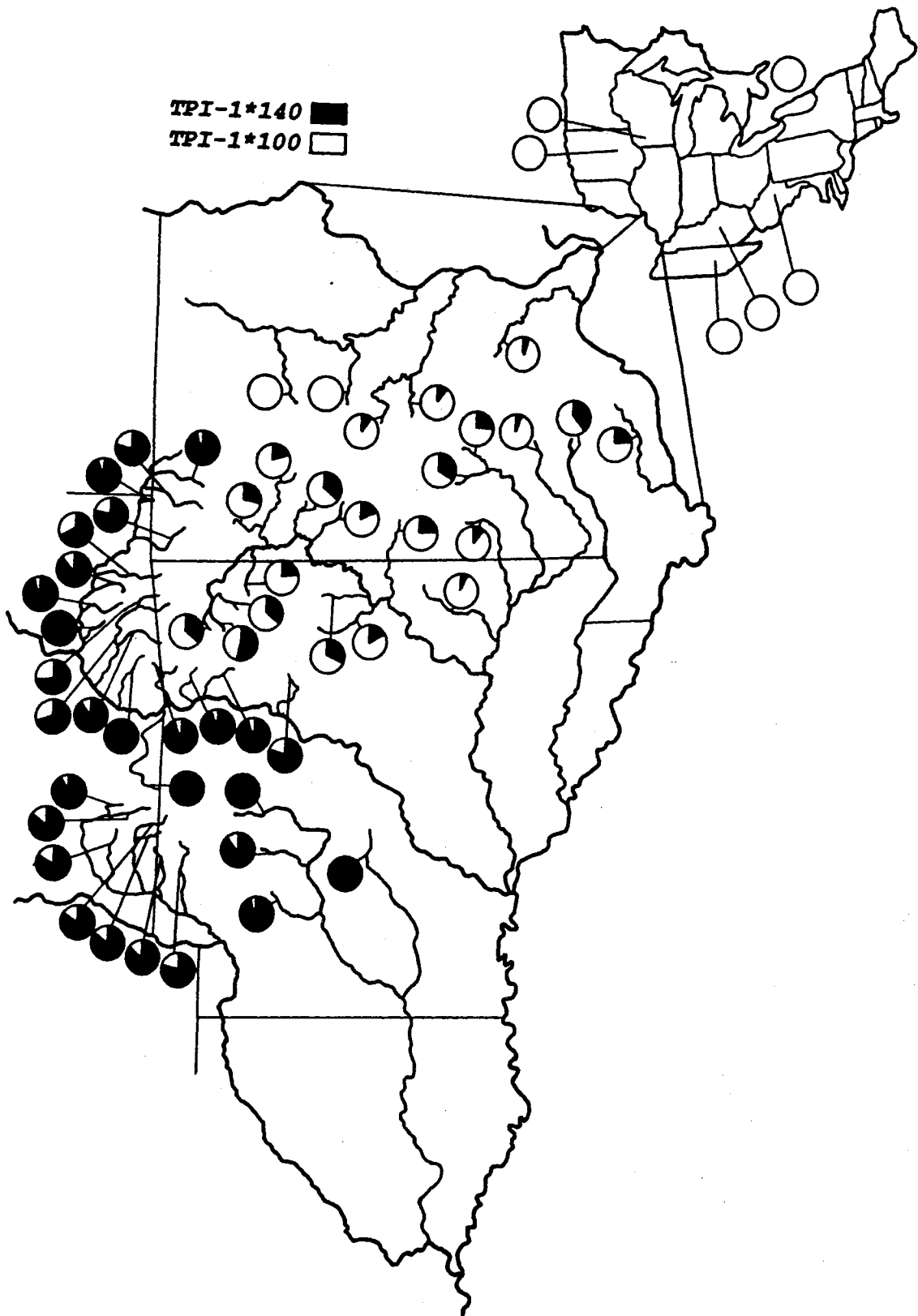


Figure 6. Allele frequency distributions at *TPI-1\**.

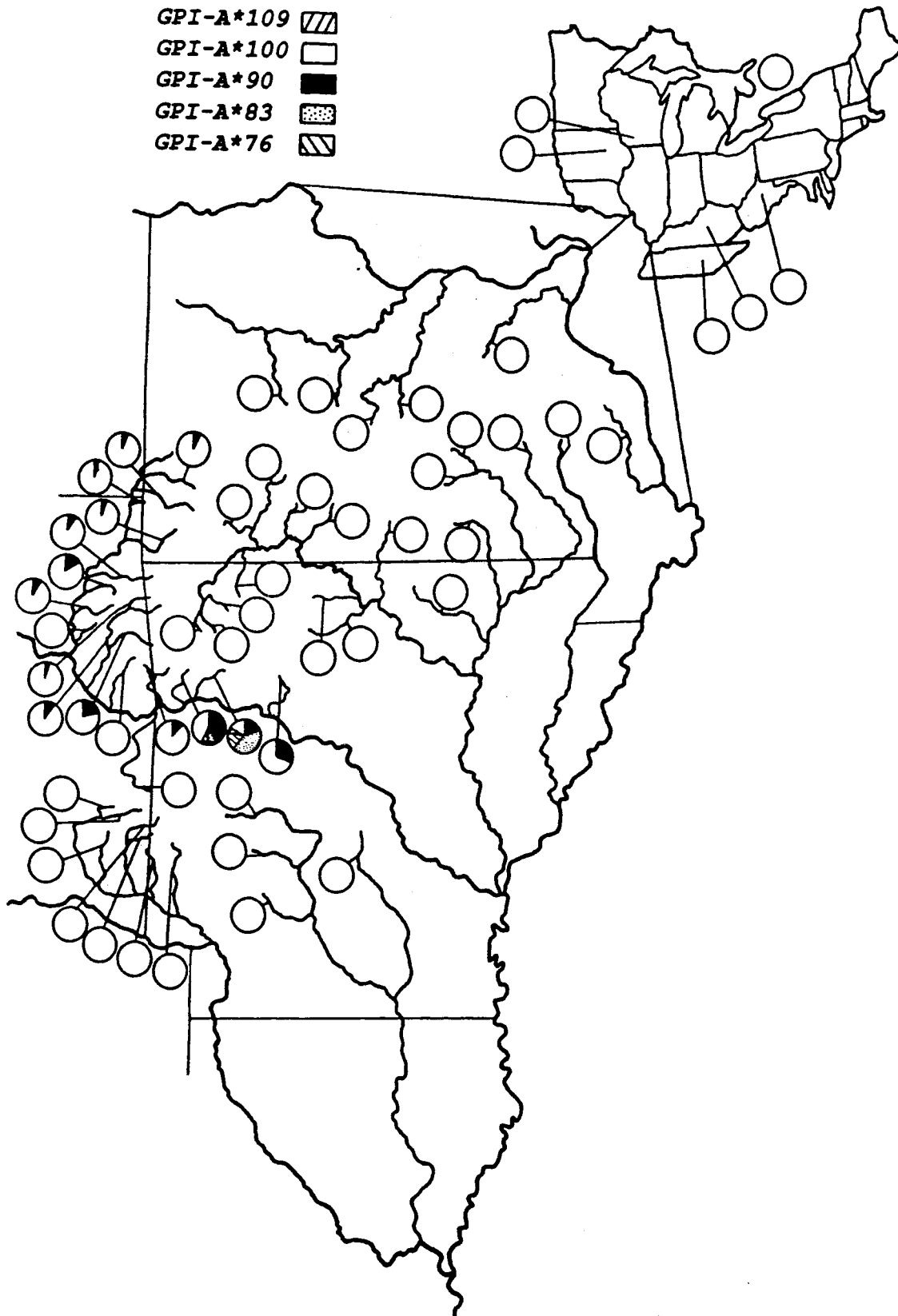


Figure 7. Allele frequency distributions at *GPB-A\**.

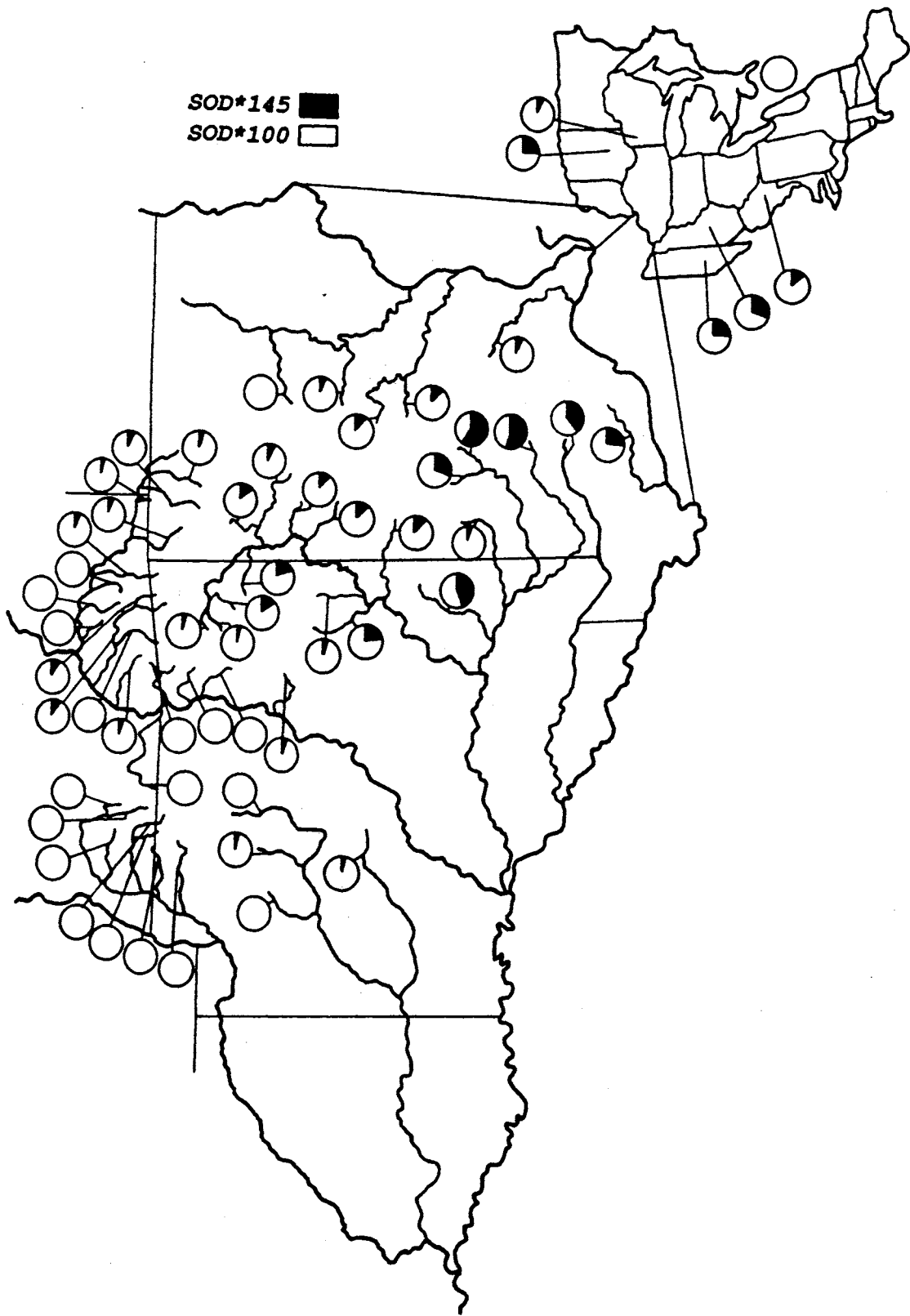


Figure 8. Allele frequency distributions at *SOD\**.

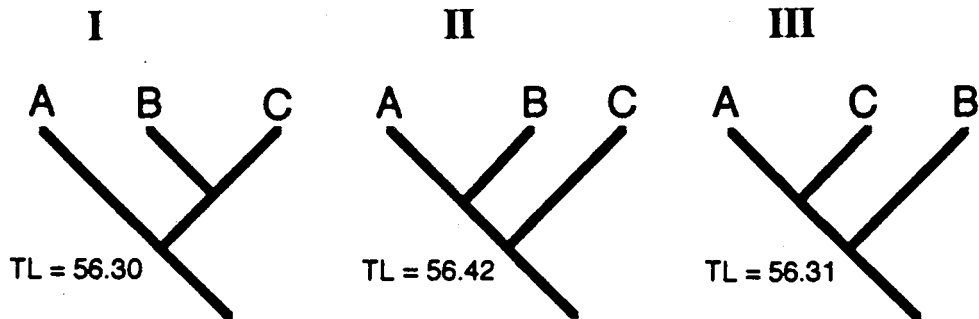
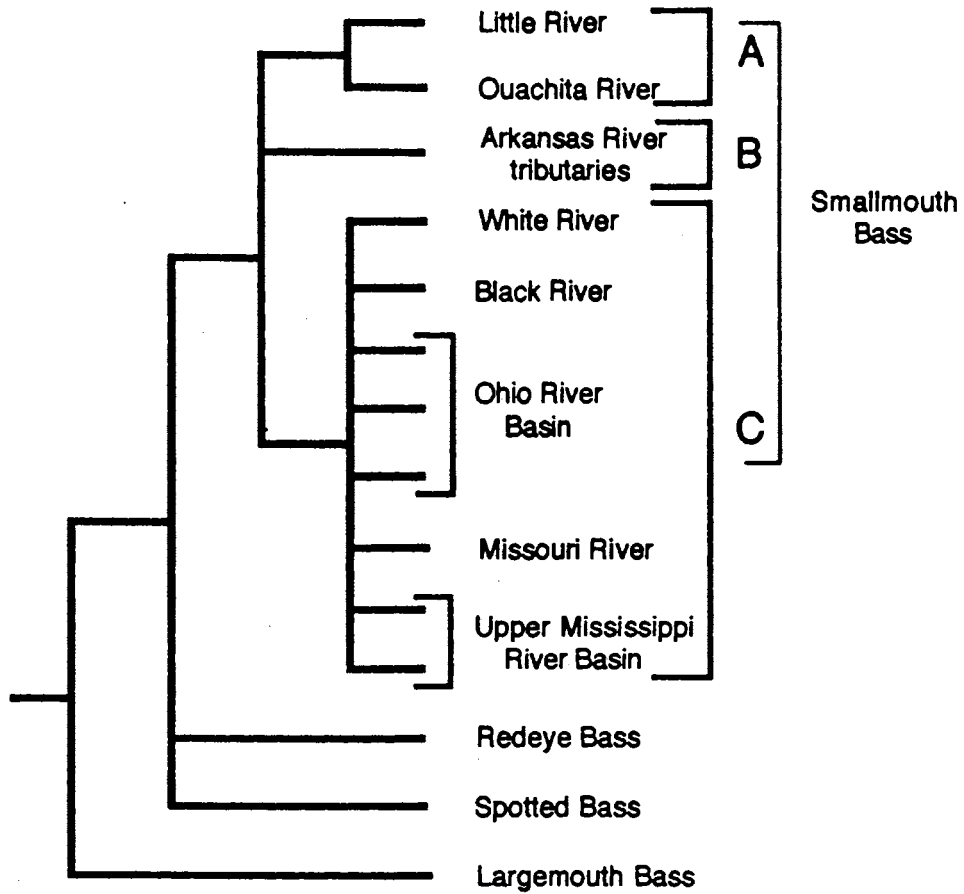


Figure 9. Consensus cladogram derived from 12 distance-Wagner trees and three hypotheses of relationship among the three major clades (A-C) of smallmouth bass (see text).

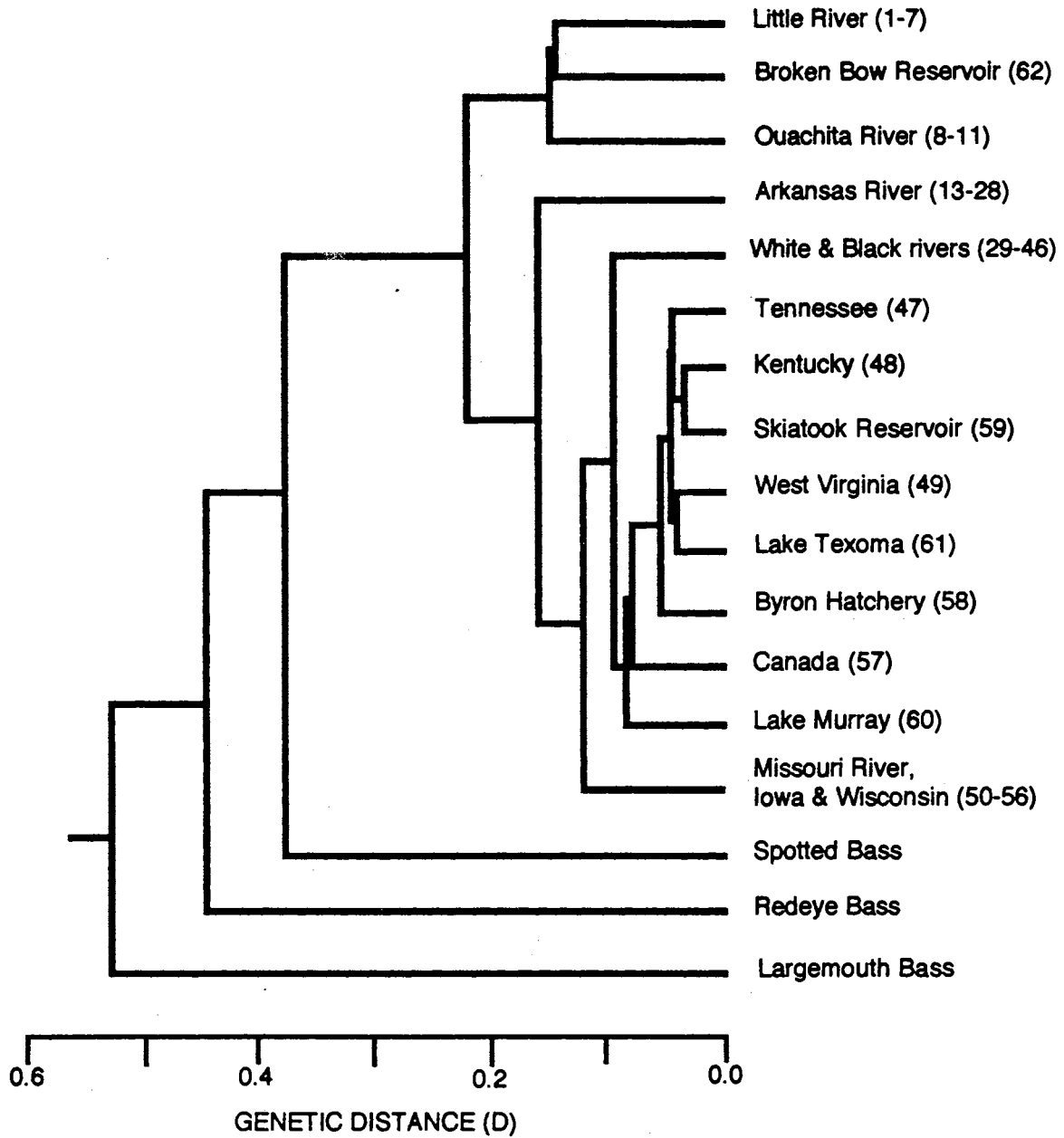


Figure 10. UPGMA dendrogram summarizing genetic distances among introduced reservoir stocks in Oklahoma (localities 58-62) and natural populations in the major drainage basins from Figure 1.

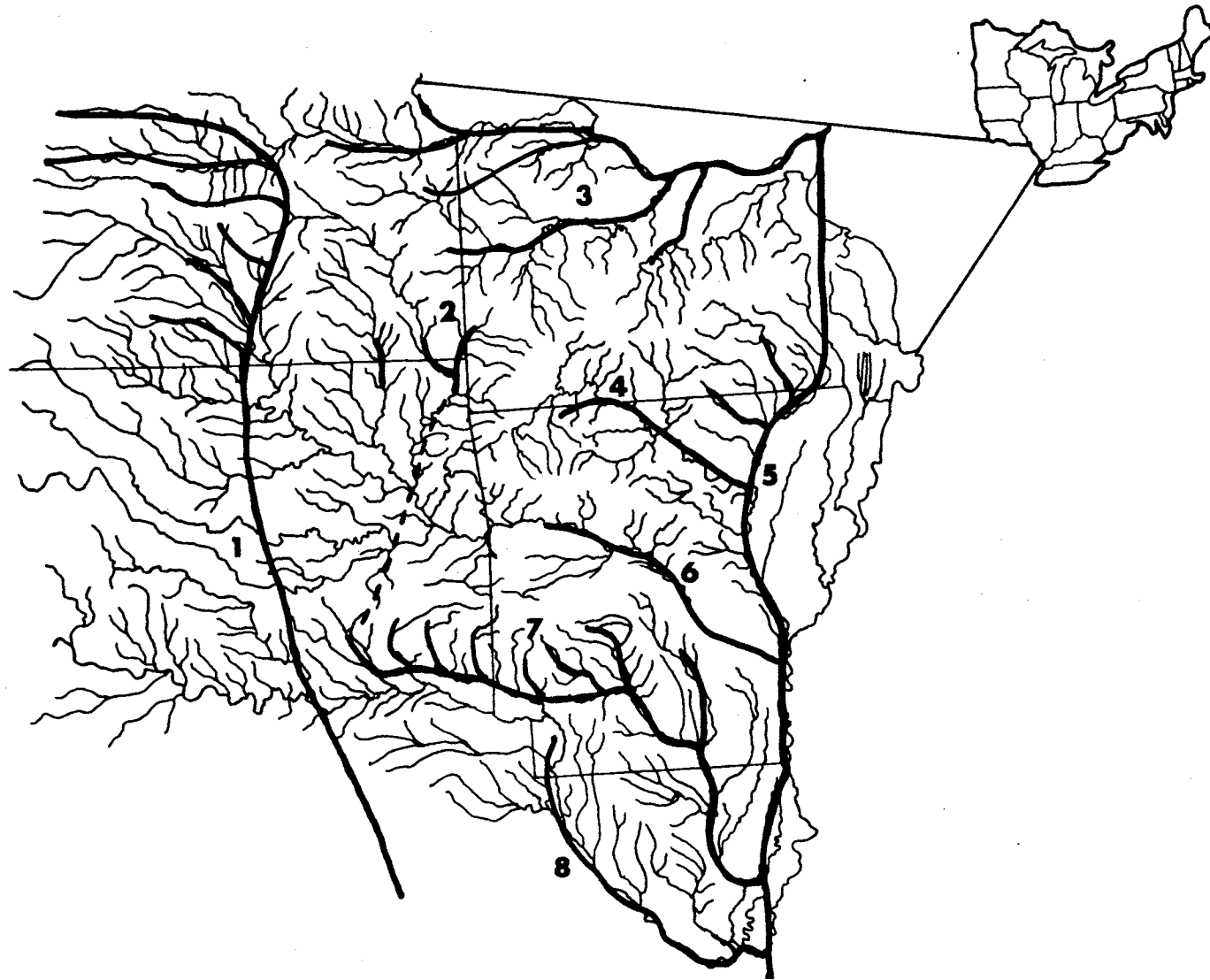


Figure 11. Pre-pleistocene drainage patterns (heavy lines) overlaid on contemporary drainage basins: 1) Ancestral Plains Stream, 2) Upper Neosho River, 3) Old Grand-Missouri River, 4) White River, 5) Old Mississippi River, 6) Old Arkansas River, 7) Old Ouachita River, and 8) Old Red River (after Cross et al. 1986; Mayden 1988a).

## APPENDIX I

Locality information for 65 samples of micropteryine bass and vernacular references where available. Numeric designations at the left correspond to Figure 1.

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### **Little River**

- 1 Little River: Black Fork; Pushmataha Co., OK. At the state highway 144 bridge. T1S, R19E, Section 1.
- 2 Little River: Pushmataha Co., OK. at the river bridge in Honobia.
- 5 Little River: Glover River; McCurtain Co., OK. 2 miles south and 3 miles west of Bethel. T2S, R23E, Section 34.
- 4 Little River: Mountain Fork River; McCurtain Co., OK. 1.75 miles south of Jet Tavern. T1S, R27E, Section 9.
- 5 Little River: Buffalo Creek; McCurtain Co., OK. 1 mile south and 0.5 miles east of Buffalo. T2S, R26E, section 17.
- 6 Little River: Rolling Fork River; Sevier Co., AR. 2.2 miles west of Grannis.
- 7 Little River: Cossatot River; Howard Co., AR. State Highway 4 bridge.

### **Ouachita River**

- 8 Ouachita River: Montgomery Co., AR. The Oden public access on State Highway 379.
- 9 Ouachita River: Caddo River; Montgomery Co., Norman, AR.
- 10 Ouachita River: Little Missouri River; Pike Co., AR. At State Highway 84 bridge. T5S, R27W, Section 16.
- 11 Ouachita River: North Fork Saline River; Benton Co., AR. 5 miles east of Paron.

### **Arkansas River**

- 12 Arkansas River: Black Fork; Leflore Co., Oklahoma.
- 13 Neosho River: White Oak Creek; Jasper Co., MO. 1.5 miles south and 1 mile east of Avilla. T28N, R29W, NW1/4 section 5.
- 14 Neosho River: Shoal Creek; Newton Co., MO. Two miles east of Wheaton. T24N, R29W, Section 36.
- 15 Neosho River: Fivemile Creek; Ottawa co., OK. 0.5 miles upstream from the swimming hole at Fivemile. T29N, R24E, NE1/4 Section 22.
- 16 Neosho River: Big Sugar Creek; McDonald Co., MO. 0.25 miles north and 0.25 miles west of Powell. T22N, R30W, Section 16.



Appendix I. Continued.

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- 17 Neosho River: Spavinaw Creek (Beaty Creek); Delaware Co., OK. 4.5 miles south and 1 mile east of Jay. T22N, R24E, SE1/4 Section 30.
- 18 Neosho River: Saline Creek; Mayes Co., OK. Blue Hole Park. 5.5 miles east and .5 miles north of Salina. T21N, R21E, NE1/4 Section 15.
- 19 Neosho River: Spring Creek; Cherokee Co., OK. 1.5 miles east of Peggs. T19N, R21E, NE1/4 Section 33.
- 20 Neosho River: Fourteenmile Creek; Cherokee Co., OK. Two miles east of Lost City; T17N, R21E, NE1/4 Section 6.
- 21 Arkansas River: Flint Creek; Delaware, Co, OK. 2 miles north and 2.25 miles east of Flint. T20N, R25E, NW1/4 Section 17.
- 22 Neosho River: Illinois River; Cherokee Co., OK. 1.25 miles north and 0.75 miles east of the intersection of state highway 10 and U.S. highway 62.
- 23 Arkansas River: Baron Fork; Cherokee Co., OK. 0.75 miles south and 0.25 miles east of Welling. T16N, R23E, NE1/4 Section 18.
- 24 Arkansas River: Sallisaw Creek; Adair Co., OK. 1.75 miles south and 4.25 miles east of Greasy. T14N, R24E, SE1/4 Section 32.
- 25 Arkansas River: Little Lee Creek; Adair Co., OK. T14N, R25E, NE1/4 Section 35.
- 26 Arkansas River: Frog Bayou; Washington Co., AR. 0.25 miles north and 1.5 miles east of Winfrey. T12N, R29W, SW1/4 Section 4.
- 27 Arkansas River: Little Mulberry River; Johnson Co., AR. 0.5 miles south of Friley.
- 28 Arkansas River: Big Piney Creek; Newton Co., AR. 2.5 miles and 0.5 miles east of Limestone Arkansas.

**White River**

- 29 White River: Madison Co., AR. State Highway 295 Bridge.
- 30 White River: West Fork; Washington Co., AR. T15N, R30W, NW1/4 Section 16.
- 31 White River: War Eagle River; Madison Co., AR. Near Aurora.
- 32 White River: Kings River; Carroll Co., AR. 4 miles south and 5 miles west of Berryville.
- 33 White River: Flat Creek; Barry Co., MO. T24N, R27W Section 13.
- 34 White River: James River; Webster Co., Mo. Highway KK bridge.
- 35 White River: Bull Creek; Taney Co., MO. 10 miles north and 2.5 miles east of Branson. T24N, R21W, S1/2 Section 11.

Appendix I. Continued.

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- 36 White River: Beaver Creek; Taney Co., Mo. 1.25 miles north and 0.25 miles east of Bradyville.
- 37 White River: North Fork White River; Douglas Co., Mo. 7.5 miles north and 3 miles west of Twin Bridges.
- 38 White River: Crooked Creek; Marion Co., AR. 0.25 miles south of Pyatt.
- 39 White River: Buffalo River; Newton Co., AR. State Highway 74 bridge.

**Black River**

- 40 Black River: Strawberry River; Izard Co., AR.
- 41 Black River: Eleven Point River; Oregon Co., MO. 1.5 miles south of Thomasville. T24N, R5W, NE1/4 Section 8.
- 42 Black River: Current River; Shannon Co., MO. 4 miles south and 2 miles east of Shannondale. T31N, R4W, SE1/4 Section 32.
- 43 Black River: Jacks Fork; Texas Co., MO. 2 miles south of Clear Springs.
- 44 Black River: West Fork Black River; Reynolds Co., MO. Sutton Bluff Campground. T32N, R1W, Section 12.
- 45 St Francis River; Madison Co., MO.
- 46 Whitewater River; Bollinger Co., MO. 0.5 miles east and 1 miles north of Yount.

**Ohio River**

- 47 Tennessee River: Clinch River; Eastern Tennessee.
- 48 Ohio River: Elkhorn Creek; Kentucky.
- 49 New River: 16 miles south of Hinton, West Virginia.

**Missouri River**

- 50 Missouri River: Pomme de Terre River; Polk Co., MO. T33N, R22W, SE1/4 Section 22.
- 51 Missouri River: Niangua River; Dallas Co., MO. T34N, R18W, W1/2 Section 2.
- 52 Missouri River: Gasconade River. 1.5 miles east of Hartville.
- 53 Missouri River: Big Piney River. Texas Co., MO. 6 miles north and 1 miles east of Houston.
- 54 Meramac River: Huzzah Creek; Crawford Co. MO. At State Highway 49 bridge. T35N, R3W, NE1/4 Section 24.

**Mississippi River**

- 55 Mississippi River: Maquoketa River; IA. Near Manchester--3 miles south of Delhi.
- 56 Mississippi River: Pecatonica River; Iowa Co., WI. State Highway 39 bridge. T5N, R2E, NW1/4 Section 36.
- 57 Fourteen Isle Lake: Ontario, CANADA.

**Reservoir Samples**

- 58 Byron Hatchery: Lake strain smallmouth bass provided by Steve Spade; Oklahoma Department of Wildlife Conservation.
- 59 Skiatook Reservoir: Osage Co., OK.
- 60 Lake Murray: Love Co., OK.
- 61 Lake Texoma: Bryan Co., OK.
- 62 Broken Bow Reservoir: McCurtain Co., OK.
  
- 63 Spotted bass: Cherokee Co., OK
- 64 Redeye bass: Walker Co., Georgia.
- 65 Largemouth bass: Payne Co., OK.

Appendix II. Allele frequencies at polymorphic loci in samples of 62 populations of smallmouth bass and one sample each of spotted, redeye, and largemouth bass. Locality numbers correspond to those in Appendix I.

Locus	Locality								
	1	2	3	4	5	6	7	8	9
<b>GPI-A*</b>									
(N)	19	19	18	19	20	15	19	20	18
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>									
(N)	19	20	18	19	20	15	19	20	18
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.450	0.306
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.550	0.694
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGM*</b>									
(N)	19	20	18	19	20	15	19	20	20
115	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.975	1.000	1.000	0.975	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000
<b>SMDH-A*</b>									
(N)	19	20	18	19	20	15	19	20	20
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.974	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
88	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
67	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-B*</b>									
(N)	19	20	18	19	20	15	19	20	20
109	0.000	0.000	0.000	0.026	0.050	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.921	0.950	1.000	1.000	1.000	1.000
87	0.000	0.000	0.000	0.053	0.000	0.000	0.000	0.000	0.000
<b>GP-F</b>									
(N)	19	20	18	19	20	15	19	20	20
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	19	20	18	19	20	15	19	20	20
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDHL*</b>									
(N)	19	20	18	19	20	15	19	20	19
127	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000
100	1.000	1.000	1.000	0.947	1.000	1.000	0.974	1.000	1.000
80	0.000	0.000	0.000	0.053	0.000	0.000	0.000	0.000	0.000
<b>SAAT-1*</b>									
(N)	19	20	18	17	20	15	19	20	10
100	1.000	1.000	0.972	0.882	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.028	0.118	0.000	0.000	0.000	0.000	0.000
<b>GDH*</b>									
(N)	19	20	18	19	20	15	19	20	19
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.842	1.000	1.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.158	0.000	0.000

## Appendix II. Continued.

Locus	Locality								
	1	2	3	4	5	6	7	8	9
<b>ADH*</b>									
(N)	19	20	18	19	20	15	19	20	19
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.974	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	19	20	18	19	20	15	19	20	19
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.053
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.947
<b>PEPC*</b>									
(N)	19	20	18	19	20	15	19	20	19
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.921	0.950	1.000	1.000	1.000	0.867	1.000	1.000	1.000
84	0.079	0.050	0.000	0.000	0.000	0.133	0.000	0.000	0.000
<b>PEPA*</b>									
(N)	19	20	18	19	20	15	19	20	18
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.632	0.825	0.722	0.895	0.725	0.700	0.737	0.950	0.972
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.368	0.125	0.278	0.105	0.275	0.300	0.263	0.050	0.028
<b>SMEP-1*</b>									
(N)	18	20	18	19	20	14	19	20	20
115	0.722	0.575	0.889	0.763	0.900	0.786	0.868	0.400	0.475
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
107	0.278	0.425	0.111	0.211	0.100	0.179	0.079	0.350	0.400
100	0.000	0.000	0.000	0.000	0.000	0.036	0.053	0.000	0.025
92	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.200	0.075
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.050	0.025
<b>TPI-1*</b>									
(N)	19	20	18	19	20	15	19	20	20
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.947	0.850	0.833	0.842	0.850	0.867	0.789	1.000	0.900
100	0.053	0.150	0.167	0.158	0.150	0.133	0.211	0.000	0.100
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SIDHP-1*</b>									
(N)	19	20	18	18	18	10	19	20	19
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.974	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.974
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.026
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PEPS*</b>									
(N)	18	20	18	17	19	10	19	20	19
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.639	0.500	0.389	0.500	0.421	0.150	0.342	1.000	0.895
100	0.361	0.500	0.611	0.500	0.579	0.850	0.658	0.000	0.105
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGDH*</b>									
(N)	19	20	18	19	20	10	19	20	19
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	1	2	3	4	5	6	7	8	9
<b>PEPB*</b>									
(N)	19	20	18	19	20	15	19	20	18
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>MPI-2*</b>									
(N)	7	7	7	7	7	7	7	8	7
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	1	7	1	1	1	1	6	8	7
121	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

## Appendix II. Continued.

Locus	Locality								
	10	11	12	13	14	15	16	17	18
<b>GPI-A*</b>									
(N)	20	19	12	22	20	20	33	41	19
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.932	0.950	0.975	0.970	0.902	0.842
90	0.000	0.000	0.000	0.068	0.050	0.025	0.030	0.098	0.158
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>									
(N)	20	19	12	22	20	20	33	41	19
183	0.400	0.553	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.600	0.447	1.000	1.000	1.000	1.000	1.000	1.000	1.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGM*</b>									
(N)	20	20	12	22	20	20	33	41	19
115	0.000	0.025	0.000	0.000	0.000	0.075	0.000	0.000	0.000
100	1.000	0.975	1.000	1.000	1.000	0.925	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-A*</b>									
(N)	20	20	12	22	20	20	33	41	19
109	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.818	0.850	0.925	0.924	0.951	0.868
80	0.000	0.000	0.000	0.159	0.150	0.075	0.076	0.049	0.132
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-B*</b>									
(N)	20	20	12	22	20	20	33	41	19
109	0.000	0.000	0.000	0.000	0.025	0.025	0.000	0.000	0.026
100	1.000	0.975	1.000	1.000	0.975	0.975	1.000	1.000	0.974
87	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>									
(N)	20	20	12	22	20	20	33	41	19
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	0.950	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	20	20	12	22	20	20	33	41	19
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDH1*</b>									
(N)	20	19	12	22	20	20	33	39	17
127	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.077	0.000
100	1.000	1.000	1.000	1.000	0.975	1.000	0.985	0.897	1.000
80	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.026	0.000
<b>SAAT-1*</b>									
(N)	20	14	12	22	20	20	33	35	19
100	1.000	1.000	1.000	1.000	1.000	1.000	0.985	0.957	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.043	0.000
<b>GDH*</b>									
(N)	20	19	12	22	20	20	33	40	19
105	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.053
100	1.000	1.000	1.000	1.000	1.000	0.975	1.000	1.000	0.947
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

## Appendix II. Continued.

Locus	Locality								
	10	11	12	13	14	15	16	17	18
<b>ADH*</b>									
(N)	20	19	12	22	20	20	33	40	19
104	0.000	0.000	0.000	0.091	0.125	0.000	0.045	0.025	0.000
100	1.000	1.000	1.000	0.909	0.875	1.000	0.955	0.975	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	20	19	12	22	20	20	33	40	19
145	0.000	0.026	0.000	0.045	0.075	0.025	0.076	0.063	0.000
100	1.000	0.974	1.000	0.955	0.925	0.975	0.924	0.938	1.000
<b>PEPC*</b>									
(N)	20	19	12	22	20	20	33	38	19
120	0.000	0.000	0.000	0.000	0.000	0.000	0.045	0.066	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.955	0.908	1.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000
<b>PEPA*</b>									
(N)	20	19	12	22	20	20	33	41	19
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.925	1.000	0.708	0.977	0.925	1.000	1.000	0.976	0.974
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.075	0.000	0.292	0.023	0.075	0.000	0.000	0.024	0.026
<b>SMEP-1*</b>									
(N)	20	20	12	22	20	20	33	40	19
115	0.225	0.275	0.917	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.038	0.000
107	0.475	0.550	0.083	0.000	0.000	0.000	0.000	0.000	0.000
100	0.075	0.000	0.000	1.000	1.000	1.000	0.985	0.962	1.000
92	0.175	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.050	0.150	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>TPI-1*</b>									
(N)	20	20	12	22	20	20	33	40	19
194	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000
140	0.975	1.000	1.000	0.955	0.800	0.975	0.773	0.663	0.895
100	0.025	0.000	0.000	0.045	0.175	0.025	0.227	0.338	0.105
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SIDHP-1*</b>									
(N)	20	19	12	22	20	20	33	39	19
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.970	0.936	0.974
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.030	0.064	0.026
<b>PEPS*</b>									
(N)	20	19	12	22	20	20	33	40	19
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.975	0.895	0.083	0.091	0.375	0.125	0.136	0.100	0.316
100	0.025	0.105	0.917	0.909	0.625	0.875	0.864	0.900	0.684
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGDH*</b>									
(N)	20	19	12	22	20	20	33	40	19
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.000
100	1.000	1.000	1.000	0.977	1.000	1.000	1.000	0.988	1.000
94	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000



Appendix II. Continued.

Locus	Locality								
	10	11	12	13	14	15	16	17	18
<b>PEPB*</b>									
(N)	20	19	12	22	20	20	33	41	19
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.950	1.000	1.000	0.818	0.800	1.000	0.924	0.902	0.921
80	0.050	0.000	0.000	0.182	0.200	0.000	0.076	0.098	0.079
<b>MPI-2*</b>									
(N)	7	8	12	7	7	7	14	14	8
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	7	8	12	7	7	7	14	14	8
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

## Appendix II. Continued.

Locus	Locality								
	19	20	21	22	23	24	25	26	27
<b>GPI-A*</b>									
(N)	19	20	11	37	21	20	22	21	18
109	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.028
100	0.921	1.000	0.955	0.905	0.786	1.000	0.886	0.452	0.222
90	0.079	0.000	0.045	0.095	0.143	0.000	0.114	0.429	0.194
83	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.095	0.389
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.024	0.167
<b>GPI-B*</b>									
(N)	19	20	11	37	21	20	22	21	18
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	0.925	1.000	1.000	0.722
97	0.000	0.000	0.000	0.000	0.000	0.075	0.000	0.000	0.278
<b>PGM*</b>									
(N)	19	20	11	37	21	20	22	21	19
115	0.000	0.025	0.000	0.014	0.000	0.000	0.000	0.000	0.000
100	1.000	0.975	1.000	0.986	1.000	1.000	0.977	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.000	0.000
<b>SMDH-A*</b>									
(N)	19	20	11	37	21	20	22	21	19
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.895	0.950	1.000	0.905	0.952	1.000	0.864	1.000	1.000
80	0.105	0.050	0.000	0.095	0.048	0.000	0.136	0.000	0.000
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-B*</b>									
(N)	18	20	11	37	21	20	22	21	19
109	0.000	0.000	0.045	0.000	0.024	0.000	0.000	0.000	0.000
100	1.000	1.000	0.955	1.000	0.976	1.000	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>									
(N)	19	20	11	37	21	20	22	21	20
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	19	20	11	37	21	20	22	21	20
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDHL*</b>									
(N)	19	20	11	37	21	20	22	21	20
127	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.048	0.000
100	1.000	0.975	1.000	1.000	0.976	0.975	1.000	0.929	1.000
80	0.000	0.025	0.000	0.000	0.024	0.025	0.000	0.024	0.000
<b>SAAT-1*</b>									
(N)	19	20	11	37	21	20	22	21	7
100	0.974	0.975	1.000	1.000	1.000	0.975	0.932	1.000	1.000
90	0.026	0.025	0.000	0.000	0.000	0.025	0.068	0.000	0.000
<b>GDH*</b>									
(N)	19	20	11	37	21	20	22	21	20
105	0.053	0.050	0.000	0.000	0.048	0.025	0.000	0.000	0.000
100	0.895	0.875	0.818	1.000	0.929	0.950	0.955	1.000	1.000
86	0.053	0.075	0.182	0.000	0.024	0.025	0.045	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	19	20	21	22	23	24	25	26	27
<b>ADH*</b>									
(N)	19	20	11	37	21	20	22	21	20
104	0.026	0.000	0.045	0.108	0.071	0.000	0.000	0.000	0.000
100	0.974	0.950	0.955	0.892	0.929	1.000	1.000	1.000	1.000
87	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	19	20	11	37	21	20	22	21	20
145	0.000	0.000	0.091	0.095	0.000	0.050	0.000	0.000	0.000
100	1.000	1.000	0.909	0.905	1.000	0.950	1.000	1.000	1.000
<b>PEPC*</b>									
(N)	19	20	11	37	21	20	22	21	20
120	0.000	0.000	0.045	0.027	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	0.909	0.973	1.000	1.000	0.932	1.000	0.875
84	0.000	0.000	0.045	0.000	0.000	0.000	0.068	0.000	0.125
<b>PEPA*</b>									
(N)	19	20	11	37	21	20	22	21	18
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.921	1.000	0.955	0.986	0.810	1.000	0.977	1.000	0.972
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.079	0.000	0.045	0.014	0.190	0.000	0.023	0.000	0.028
<b>sMEP-1*</b>									
(N)	19	20	11	37	21	20	22	21	19
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.027	0.000	0.000	0.045	0.238	0.368
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.026
100	1.000	1.000	1.000	0.973	1.000	1.000	0.955	0.690	0.605
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>TPI-1*</b>									
(N)	19	20	11	37	21	20	22	21	19
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.974	1.000	0.727	0.689	0.905	1.000	0.977	0.976	0.947
100	0.026	0.000	0.273	0.311	0.095	0.000	0.023	0.024	0.053
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sIDHP-1*</b>									
(N)	19	20	11	37	21	20	22	21	20
107	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.919	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.068	0.000	0.000	0.000	0.000	0.000
<b>PEPS*</b>									
(N)	19	20	11	37	21	19	20	21	20
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.395	0.050	0.045	0.162	0.238	0.053	0.350	0.262	0.250
100	0.605	0.950	0.955	0.838	0.762	0.947	0.650	0.738	0.750
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGDH*</b>									
(N)	19	20	11	37	21	20	22	21	20
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	19	20	21	22	23	24	25	26	27
<b>PEPB*</b>									
(N)	19	20	11	37	21	20	22	21	18
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.947	0.900	0.909	0.959	1.000	0.450	0.795	0.690	0.917
80	0.053	0.100	0.091	0.041	0.000	0.550	0.205	0.310	0.083
<b>MPI-2*</b>									
(N)	8	7	7	14	16	14	7	7	1
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	8	7	7	14	16	14	7	7	1
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

## Appendix II. Continued.

Locus	Locality								
	28	29	30	31	32	33	34	35	36
<b>GPI-A*</b>									
(N)	21	21	21	7	23	20	22	22	29
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.690	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.238	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.071	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>									
(N)	21	21	21	7	23	20	22	22	29
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.833	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
97	0.167	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGM*</b>									
(N)	20	21	21	7	22	20	22	22	29
115	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	0.952	1.000	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sMDH-A*</b>									
(N)	21	21	21	7	22	20	22	22	29
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sMDH-B*</b>									
(N)	21	21	21	7	22	20	22	22	29
109	0.000	0.048	0.048	0.000	0.000	0.025	0.000	0.000	0.000
100	1.000	0.952	0.952	1.000	1.000	0.975	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>									
(N)	21	21	21	7	23	20	22	22	29
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	21	21	21	7	23	20	22	22	29
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDH1*</b>									
(N)	21	21	21	7	23	20	22	22	28
127	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.036
100	1.000	0.976	1.000	1.000	1.000	1.000	1.000	0.977	0.929
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.036
<b>sAAT-1*</b>									
(N)	14	21	21	7	23	20	22	22	28
100	1.000	0.976	0.976	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.024	0.024	0.000	0.000	0.000	0.000	0.000	0.000
<b>GDH*</b>									
(N)	21	21	21	7	23	20	22	22	28
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

## Appendix II. Continued.

Locus	Locality								
	28	29	30	31	32	33	34	35	36
<b>ADH*</b>									
(N)	21	21	21	7	23	20	22	22	28
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	21	21	21	7	23	20	22	22	28
145	0.048	0.024	0.071	0.143	0.196	0.150	0.068	0.114	0.125
100	0.952	0.976	0.929	0.857	0.804	0.850	0.932	0.886	0.875
<b>PEPC*</b>									
(N)	21	21	21	7	23	20	22	22	28
120	0.000	0.000	0.000	0.000	0.087	0.000	0.023	0.023	0.000
100	1.000	1.000	1.000	1.000	0.913	1.000	0.977	0.977	1.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PEPA*</b>									
(N)	21	21	21	7	23	20	22	22	29
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.929	0.976	1.000	1.000	0.957	0.975	1.000	1.000	1.000
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.071	0.024	0.000	0.000	0.043	0.025	0.000	0.000	0.000
<b>SMEP-1*</b>									
(N)	18	21	21	7	22	20	22	22	29
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.023	0.000	0.023	0.000	0.017
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.977	1.000	0.977	1.000	0.983
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>TPI-1*</b>									
(N)	21	21	21	7	22	20	22	22	29
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.786	0.524	0.357	0.357	0.227	0.275	0.205	0.364	0.172
100	0.214	0.476	0.643	0.643	0.773	0.725	0.795	0.636	0.828
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SIDHP-1*</b>									
(N)	21	21	21	7	23	19	22	22	28
107	0.000	0.000	0.000	0.000	0.022	0.026	0.000	0.045	0.000
100	1.000	0.952	0.905	0.857	0.957	0.974	0.909	0.886	0.964
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.048	0.095	0.143	0.022	0.000	0.091	0.068	0.036
<b>PEPS*</b>									
(N)	21	21	19	7	22	20	22	22	28
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.119	0.024	0.026	0.143	0.000	0.125	0.000	0.000	0.000
100	0.881	0.976	0.974	0.857	0.977	0.875	1.000	1.000	1.000
97	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000
<b>PGDH*</b>									
(N)	21	21	21	7	23	20	22	22	28
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	28	29	30	31	32	33	34	35	36
<b>PEPB*</b>									
(N)	21	21	21	7	23	20	22	22	29
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.857	0.976	0.905	0.929	0.978	1.000	1.000	0.977	0.879
80	0.143	0.024	0.095	0.071	0.022	0.000	0.000	0.023	0.121
<b>MPI-2*</b>									
(N)	7	7	7	7	7	7	7	7	14
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	7	7	7	7	7	7	7	7	14
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

## Appendix II. Continued.

Locus	Locality								
	37	38	39	40	41	42	43	44	45
<b>GPI-A*</b>									
(N)	22	21	27	18	20	21	20	21	19
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>									
(N)	22	21	27	18	20	21	20	21	19
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGM*</b>									
(N)	21	20	29	18	21	21	17	21	19
115	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.972	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sMDH-A*</b>									
(N)	21	20	28	18	21	21	20	21	19
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.972	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.000	0.000
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sMDH-B*</b>									
(N)	21	20	28	18	21	21	20	21	19
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>									
(N)	22	21	29	18	21	22	20	21	19
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	22	21	29	18	21	22	20	21	19
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDH1*</b>									
(N)	22	21	28	18	21	21	20	21	19
127	0.023	0.000	0.018	0.028	0.024	0.000	0.000	0.000	0.000
100	0.932	1.000	0.982	0.972	0.976	0.976	1.000	0.976	0.974
80	0.045	0.000	0.000	0.000	0.000	0.024	0.000	0.024	0.026
<b>sAAT-1*</b>									
(N)	22	13	27	18	21	21	20	11	19
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GDH*</b>									
(N)	22	21	28	18	21	21	20	21	19
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000



Appendix II. Continued.

Locus	Locality								
	37	38	39	40	41	42	43	44	45
<b>ADH*</b>									
(N)	22	21	28	18	21	21	20	21	19
104	0.000	0.000	0.000	0.056	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.944	1.000	1.000	1.000	1.000	0.947
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.053
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	22	21	28	18	21	21	20	21	19
145	0.114	0.048	0.232	0.444	0.048	0.310	0.575	0.524	0.395
100	0.886	0.952	0.768	0.556	0.952	0.690	0.425	0.476	0.605
<b>PEPC*</b>									
(N)	22	21	28	18	21	21	20	21	19
120	0.068	0.000	0.018	0.000	0.000	0.000	0.000	0.071	0.079
100	0.932	1.000	0.982	0.972	1.000	1.000	1.000	0.905	0.921
84	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.024	0.000
<b>PEPA*</b>									
(N)	22	21	27	18	20	21	20	21	19
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	0.981	1.000	1.000	1.000	1.000	1.000	0.947
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.000	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.053
<b>sMEP-1*</b>									
(N)	21	20	28	18	21	21	20	21	19
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.025	0.018	0.250	0.095	0.214	0.075	0.143	0.395
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	0.975	0.982	0.750	0.905	0.786	0.925	0.857	0.605
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>TPI-1*</b>									
(N)	21	20	28	18	21	21	20	21	19
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.238	0.325	0.161	0.056	0.095	0.333	0.250	0.071	0.395
100	0.762	0.675	0.839	0.944	0.905	0.667	0.750	0.929	0.605
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sIDHP-1*</b>									
(N)	22	21	28	18	21	21	20	21	19
107	0.000	0.024	0.036	0.000	0.000	0.024	0.000	0.000	0.000
100	0.932	0.881	0.929	0.778	0.976	0.857	0.875	0.976	0.974
90	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.068	0.095	0.036	0.222	0.024	0.119	0.100	0.024	0.026
<b>PEPS*</b>									
(N)	22	21	28	18	21	21	20	21	19
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.977	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
97	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	37	38	39	40	41	42	43	44	45
<b>PGDH*</b>									
(N)	22	21	28	18	21	21	20	21	19
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PEPB*</b>									
(N)	22	21	27	18	20	21	20	21	19
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	0.952	0.944	0.972	0.500	0.810	0.875	0.905	0.921
80	0.000	0.048	0.056	0.028	0.500	0.190	0.125	0.095	0.079
<b>MPI-2*</b>									
(N)	7	7	14	7	7	7	7	7	7
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	7	7	14	7	7	7	7	7	7
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Appendix II. Continued.

Locus	Locality								
	46	47	48	49	50	51	52	53	54
<b>GPI-A*</b>									
(N)	19	22	25	24	21	21	22	21	21
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>									
(N)	19	22	25	24	21	21	22	21	21
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PGM*</b>									
(N)	20	23	25	24	21	21	22	20	20
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-A*</b>									
(N)	20	23	25	23	21	21	22	20	20
109	0.000	0.065	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.975	0.935	1.000	1.000	0.976	1.000	1.000	1.000	1.000
80	0.025	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SMDH-B*</b>									
(N)	20	23	25	23	21	21	22	20	20
109	0.000	0.000	0.000	0.000	0.119	0.024	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.881	0.976	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>									
(N)	20	23	25	24	21	21	22	21	21
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-2*</b>									
(N)	20	23	25	24	21	21	22	21	21
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>XDH1*</b>									
(N)	19	23	25	24	21	21	22	20	20
127	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.977	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.000	0.000
<b>SAAT-1*</b>									
(N)	19	7	16	24	20	13	12	12	11
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GDH*</b>									
(N)	19	23	25	24	21	21	22	20	20
105	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.952	1.000	1.000	1.000	1.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	46	47	48	49	50	51	52	53	54
<b>ADH*</b>									
(N)	19	23	25	24	21	21	22	20	20
104	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000
100	0.947	1.000	0.980	1.000	1.000	1.000	1.000	1.000	1.000
87	0.053	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>SOD*</b>									
(N)	19	23	25	24	21	21	22	20	20
145	0.263	0.261	0.300	0.146	0.000	0.071	0.114	0.125	0.075
100	0.737	0.739	0.700	0.854	1.000	0.929	0.886	0.875	0.925
<b>PEPC*</b>									
(N)	19	23	25	24	21	21	22	20	20
120	0.000	0.000	0.000	0.000	0.000	0.024	0.114	0.075	0.000
100	1.000	1.000	1.000	1.000	1.000	0.976	0.818	0.900	1.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.068	0.025	0.000
<b>PEPA*</b>									
(N)	20	23	25	24	21	21	22	21	21
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.119	0.000	0.119	0.000
100	1.000	1.000	0.980	1.000	0.690	0.500	0.500	0.548	0.262
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
90	0.000	0.000	0.020	0.000	0.310	0.381	0.500	0.333	0.738
<b>sMEP-1*</b>									
(N)	20	23	25	24	21	21	22	20	20
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.025	0.050
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.976	1.000	1.000	0.975	0.950
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>TPI-1*</b>									
(N)	20	23	25	24	21	21	22	20	20
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.225	0.000	0.000	0.000	0.000	0.000	0.091	0.100	0.025
100	0.775	1.000	1.000	1.000	1.000	1.000	0.909	0.900	0.975
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>sIDHP-1*</b>									
(N)	20	23	25	24	21	21	22	20	20
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.975	1.000	1.000	1.000	0.857	0.976	0.977	0.875	0.975
90	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.143	0.024	0.023	0.125	0.025
<b>PEPS*</b>									
(N)	20	23	25	24	21	21	22	20	20
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	0.938	1.000	1.000	1.000	1.000	1.000
97	0.000	0.000	0.000	0.063	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality								
	46	47	48	49	50	51	52	53	54
<b>PGDH*</b>									
(N)	20	23	25	23	21	21	22	20	20
105	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.950	1.000	1.000	1.000	0.976	0.952	0.886	0.925	0.875
94	0.025	0.000	0.000	0.000	0.024	0.048	0.114	0.075	0.125
<b>PEPB*</b>									
(N)	19	22	25	23	21	21	22	21	21
105	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	0.977	0.952	0.881
80	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.048	0.119
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>MPI-2*</b>									
(N)	6	7	7	6	7	8	1	8	7
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
<b>MPI-1*</b>									
(N)	4	6	6	1	7	8	1	8	7
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

## Appendix II. Continued.

Locus	Locality										
	55	56	57	58	59	60	61	62	SPB	RED	LMB
<b>GPI-A*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
83	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
76	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>GPI-B*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.988	1.000	0.875
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000
<b>PGM-A</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
115	0.000	0.000	0.000	0.095	0.000	1.000	0.000	0.000	1.000	0.000	1.000
100	1.000	1.000	1.000	0.905	1.000	0.000	1.000	1.000	0.000	0.000	0.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
<b>SMDH-A*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	0.850	1.000	1.000	0.000	0.100	0.000
80	0.000	0.000	0.000	0.000	0.000	0.150	0.000	0.000	1.000	0.900	0.500
68	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.500
<b>SMDH-B*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
109	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
87	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PROT-1*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000	0.000
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
<b>PROT-2*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000	0.000	0.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
<b>XDH1*</b>											
(N)	36	22	3	21	19	20	20	16	41	20	20
127	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
80	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>AAT</b>											
(N)	20	22	3	21	19	20	20	16	41	20	20
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
<b>GDH*</b>											
(N)	36	22	3	21	19	20	20	16	41	20	20
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

## Appendix II. Continued.

Locus	Locality										
	55	56	57	58	59	60	61	62	SPB	RED	LMB
<b>ADH</b>											
(N)	36	22	3	21	19	20	20	16	41	20	20
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	0.921	1.000	1.000	0.750	1.000	0.650	1.000
87	0.000	0.000	0.000	0.000	0.079	0.000	0.000	0.250	0.000	0.000	0.000
53	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.350	0.000
<b>SOD*</b>											
(N)	36	22	3	21	19	20	20	16	41	20	20
145	0.250	0.068	0.000	0.262	0.342	0.250	0.150	0.219	0.000	0.000	0.000
100	0.750	0.932	1.000	1.738	0.658	0.750	0.850	0.781	1.000	1.000	1.000
<b>PEPC*</b>											
(N)	36	18	3	21	19	20	20	16	41	20	20
120	0.000	0.056	0.000	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000
100	1.000	0.889	1.000	1.000	1.000	1.000	1.000	0.969	1.000	1.000	1.000
84	0.000	0.056	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<b>PEPA*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
106	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.444	0.227	0.800	1.000	1.000	0.825	1.000	0.812	0.671	0.000	0.000
96	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
90	0.556	0.773	0.100	0.000	0.000	0.175	0.000	0.188	0.329	0.000	0.000
<b>sMEP-1*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.313	0.000	0.000	0.000
111	0.000	0.000	0.000	0.048	0.053	0.025	0.025	0.063	0.000	0.000	0.000
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.250	0.000	0.000	0.000
100	1.000	1.000	1.000	0.952	0.947	0.975	0.975	0.313	1.000	1.000	1.000
92	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000
<b>TPI-1*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025
140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.469	1.000	0.000	0.975
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.531	0.000	0.000	0.000
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000
<b>IDH-L</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	1.000	1.000	1.000	1.000	1.000	0.900	1.000	1.000	0.000	1.000	0.000
90	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000
84	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000
76	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000
<b>PEPS*</b>											
(N)	36	22	5	21	19	20	20	16	41	20	20
114	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.000	0.000	0.000	0.000
106	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.679	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000
100	1.000	1.000	1.000	1.000	1.000	0.975	1.000	0.321	0.000	0.000	1.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix II. Continued.

Locus	Locality											
	55	56	57	58	59	60	61	62	SPB	RED	LMB	
<b>PGDH*</b>												
(N)	36	22	5	21	19	20	20	16	41	20	20	
105	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
<b>PEPB*</b>												
(N)	36	22	5	21	19	20	20	16	41	20	20	
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.063	0.000	0.000	1.000	
100	1.000	0.750	1.000	1.000	1.000	0.975	1.000	0.875	0.976	1.000	0.000	
80	0.000	0.250	0.000	0.000	0.000	0.025	0.000	0.063	0.024	0.000	0.000	
<b>MPI-2*</b>												
(N)	7	7	5	21	19	20	20	16	11	20	20	
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000	
<b>MPI-1*</b>												
(N)	7	7	5	21	19	20	20	16	11	20	20	
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	
100	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000	0.000	



VITA 

William J. Stark

Candidate for the Degree of

Doctor of Philosophy

**Dissertation:** GENETIC STRUCTURE AND SYSTEMATICS OF SMALLMOUTH BASS: ZOOGEOGRAPHY AND IMPLICATIONS FOR CONSERVATION

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