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ILLINOIS NATURAL HISTORY SURVEY

THE ESTABLISHMENT OF A STATE FISHERIES GENETICS PROGRAM IN ILLINOIS

Aquatic Biology Section Technical Report

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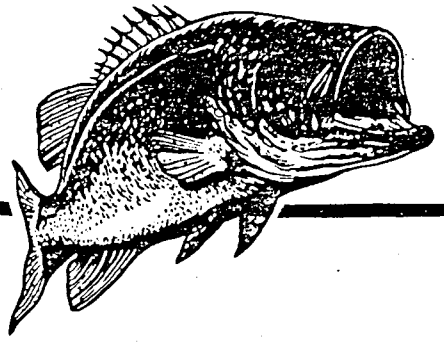

Project Number F-45-R
Final Federal Aid Report

AQUATIC BIOLOGY TECHNICAL REPORT 1986(7)

Aquatic Biology Technical Report 1986(7)
Illinois Natural History Survey

Final Federal Aid Report

The Establishment of a State Fisheries Genetics Program in Illinois

Project Number F-45-R

October 1, 1983 through June 30, 1986

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INTRODUCTION

It has become increasingly clear that within a single species of fish there often exists a variety of different genetic stocks (Utter and Allendorf, 1977; Ryman et al., 1979; Altukov and Salmenkova 1981, Brown et al., 1981; Colby et al., 1981; Ihssen et al., 1981; Philipp et al., 1983). These stocks have been generated over time as a result of natural and in some cases artificial selection. That is, each stock has arisen through a fixation of alleles through random drift or inbreeding or as a consequence of different selection pressures present in different environments. As a result, stocks found in different geographic locales often have somewhat different genetic and physiological characteristics. However, identification and characterization of discrete stocks have been attempted for only a few species of sportfish. For truly effective management of sportfish species within Illinois, it is imperative that for these species, the different genetic stocks currently existing in our waters or being propagated for future introduction to these waters, be identified and characterized (Philipp et al., 1981).

The culture and introduction of stocks into environments for which they are not well suited is an undesirable practice. At best, this practice is an inefficient use of our limited resources. At worst, it is detrimental to existing native populations, lowering the overall performance of a population through the introduction of maladaptive genes or the disruption of specific advantageous gene combinations. The culture of fish and their use for introduction into native environments without adequate information concerning the genetic structure of the populations involved could easily lead to the irrevocable deterioration of a species. Management decisions need to incorporate this information in designing the most effective programs. Once

such programs are initiated, the biochemical genetic analyses of the resultant population structure will provide unambiguous data about the relative success of such introductions.

To most effectively accomplish these desired goals, a statewide program has been established, coordinating the efforts of Department of Conservation field biologists and propagation personnel with the efforts of the Natural History Survey fisheries genetics laboratory. An integrated approach of this nature, combining the skills of personnel from both agencies, generates the genetic data needed for management decisions and produces an applied research program capable of detecting and solving a variety of specific fisheries problems.

OBJECTIVES

The objectives of this research project were to establish a program that would be a coordinated effort of DOC field biologists, DOC propagation biologists and NHS fisheries geneticists:

1. to assess the strengths and limitations of specific stocks of largemouth bass in Illinois for propagation and stocking programs in different regions of the State;
2. to assess the genetic impact of striped bass and F_1 hybrid striped x white bass hybrids on native white bass populations;
3. to define the genetic composition of all of the species of sportfishes produced at or procured by the DOC hatchery facilities for comparison with the existing populations in the state.

APPROACH

Personnel of the Illinois Natural History Survey supervised the research. The INHS research group consisted of the principal investigator, Dr. David P. Philipp, one co-investigator, Dr. Gregory S. Whitt, three research associates, Mr. Jeffrey B. Koppelman, Ms. Julie E. Claussen, and Mr. John M. Epifanio, plus a number of field and laboratory assistants. Field collection and sampling efforts were coordinated with various Department of Conservation management personnel. Propagation collection and sampling efforts were coordinated with Department of Conservation fish culture personnel.

RESEARCH RESULTS

Study 1: Production and Evaluation of Stocks of Largemouth Bass for Introduction into Northern and Southern Illinois Waters

Problem:

Our previous study (F-35-R) demonstrated significant differences in the thermal requirements of different genetic stocks of largemouth bass (Philipp and Whitt, 1982). The significantly different survival and growth characteristics in Illinois of these different genetic stocks are evidence that some stocks are better suited for some environments than others. For maximum success of culture/introduction programs, different stocks of largemouth bass inhabiting Illinois waters must be identified and their performance characteristics assessed. This increased genetic information will allow culture programs to maximize their effectiveness by producing individuals with genotypes which are optimal for the habitats into which they will be introduced. This will result in populations with high survival and reproductive fitness attributes.

Job 1. Collection of Northern and Southern Illinois Brood Stocks of Largemouth Bass

Objective: To collect northern Illinois largemouth bass brood stock and southern Illinois largemouth bass brood stock from lakes identified from our electrophoretic analysis.

Results: Based upon our previously completed electrophoretic study of 48 largemouth bass populations in Illinois (DJ Project F-35-R, The Production and Evaluation of Different Genetic Stocks of Largemouth Bass, Micropterus salmoides, for Different Thermal Environments), the following largemouth bass populations were selected as sources for brood stocks to produce a northern Illinois stock (NILMB) and a southern Illinois stock (SILMB):

	Allele Frequency			
	Mdh-B^1 -B^2	Aat-B^1 -B^2	Ck-C^1 -C^2	Gpi-B^2 -B^3
NILMB (Average heating degree days = 6381)				
Lake Marie	0.850	0.550	0.075	0.025
	0.150	0.450	0.925	0.975
Lake Catherine	0.800	0.600	0.100	-
	0.200	0.400	0.900	1.000
Grass Lake	0.825	0.650	0.125	-
	0.175	0.350	0.875	1.000
SILMB (Average heating degree days = 4065)				
Crab Orchard Lake	0.750	0.875	0.025	0.050
	0.250	0.125	0.975	0.950
Devil's Kitchen Lake	0.550	0.850	0.025	-
	0.450	0.150	0.975	1.000
Washington County Lake	0.625	0.625	0.325	-
	0.375	0.375	0.675	1.000

Although it was originally planned to collect from these selected populations, 70 NILMB and 70 SILMB, to transport them to the Little Grassy Hatchery facility, and spawn them in on-site hatchery ponds, this was not accomplished. Combined electrofishing efforts of DOC and INHS biologists were reasonably successful in collecting SILMB brood stock from the three southern sources. Although most of these fish were transported in early spring to the Little Grassy Hatchery, 8 male and 8 female SILMB were also transported to INHS laboratory facilities in Champaign. However, problems arose in collecting NILMB from the Fox Chain O' Lakes. The extreme northerly location of these lakes within the state, combined with the very late arrival of spring in 1984, caused the water temperatures to remain very cold well into April and May. Since adult largemouth bass were not moving into the cold shallows to spawn, collection of these fish by DOC biologists was fairly unsuccessful, even though a great amount of electrofishing effort was expended. As a result, use of NILMB as production brood stock for the Little Grassy Hatchery was abandoned.

As an alternative means of producing the NILMB and SILMB stocks of fingerlings needed for Study 1, the few NILMB collected during spring, 1984 (20 individuals) were transported to INHS facilities in Champaign. Further collection of NILMB and SILMB brood stocks was terminated.

Job 2. Production of Northern and Southern Illinois Stocks of Fingerling Largemouth Bass

Objective: To set up production ponds at a single hatchery facility to produce fingerling bass using the northern Illinois brood stock and fingerling bass using the southern Illinois brood stock so that fingerlings of both stocks would be of similar size and age.

Results: Four 0.08 hectare ponds at the INHS Aquatic Research Field Laboratory (ARFL) were allocated for production of the NILMB and SILMB stocks of fingerlings. Two ponds each were stocked with 4 male and 4 female SILMB on April 30, 1984 and two each with 4 male and 4 female NILMB on May 15, 1984. Schools of fry were observed in all four ponds on June 11, 1985, confirming that successful spawning had occurred. Visual monitoring of size and numbers of fingerlings was conducted throughout July and August by snorkelling through the ponds. These inspections revealed that a substantial number of NILMB and SILMB fingerlings had been produced and that these fish were approximately 50 mm total length in all ponds by the first week in August. This size was judged to be sufficient for harvesting and stocking of the fingerlings into the test ponds. Unfortunately, due to an unforeseen mix-up among DOC hatchery personnel, the private ponds designated for this study were prematurely stocked with other largemouth bass fingerlings in July. As a result, stocking had to be postponed until new study ponds could be identified, and actual introductions did not occur until after October 1, 1984. The SILMB-No. 1 pond was drained on October 2, 1984 and the NILMB-No. 1 pond was drained on October 3, 1984. The SILMB-No. 2 pond was drained on October 15, 1984 and the NILMB-No. 2 pond was drained on October 16, 1984. All fingerlings to be stocked received a fin-clip for external identification. A random sample of fingerlings was removed, and these fingerlings were measured and genetically analyzed using starch gel electrophoresis and histochemical staining procedures. The following is a summary of the pond production data:

Pond	TL (mm)	Allele Frequency Mdh-B^1 -B^2	Aat-B^1 -B^2	CK-C^1 -C^2	Gpi-B^2 -B^3
NILMB-1	51.8 + 1.9	0.850	0.700	----	1.000
		0.150	0.300	1.000	----
NILMB-2	54.5 + 2.5	1.000	1.000	----	1.000
		----	----	1.000	----
SILMB-1	55.9 + 2.4	0.600	0.975	----	0.650
		0.400	0.025	1.000	0.350
SILMB-2	52.8 + 2.1	0.600	0.975	----	0.650
		0.400	0.025	1.000	0.350

These allele frequencies do not, however, reflect the diagnostic differences between the two stocks. Seventy percent of the SILMB fingerlings were heterozygous, Gpi-B^1B^2, compared to 0% of the NILMB fingerlings. Also, 80% of the SILMB fingerlings were heterozygous, MDH-B^1B^2, as opposed to only 15% of the NILMB fingerlings. Therefore, if the external marking system had failed due to regeneration of the pelvic fin clips, we still would have been able to identify the two stocks in the test ponds more than 90-95% of the time. This genetic difference between the two stocks also permits assessment of the reproductive contribution of the two stocks to future generations.

Job 3. Evaluation of Survival and Growth of the Northern and Southern Illinois Stocks of Largemouth Bass in Different Regions of the State

Objective: To introduce equal numbers of marked fingerlings of both stocks of largemouth bass into 2-3 ponds devoid of bass located in three regions of the state (north, central and south) and to monitor survival and growth of each stock.

Results: A search of stocking request records by the DOC during winter, 1984 identified a list of twelve ponds (4 each in the northern, central, and southern regions of the state) to serve as study ponds for this job. Unfortunately, through some confusion among DOC hatchery staff, all but two of

these ponds were stocked in July, 1984 with largemouth bass fingerlings produced at the Little Grassy Hatchery, not the NILMB and SILMB stocks produced at INHS facilities Champaign. This search for new ponds required that a new set of ponds be identified for the stock evaluation experiment, causing a significant delay in stocking the test ponds. This was accomplished by September 30, 1984. The following is a listing of the study ponds stocked during October, 1984:

Region	Pond	Date	Temperature	Acres	Fish
North	Stritzel's (Crystal Lake, IL)	10/5	16°C	1.8	90 ea. NILMB-1 SILMB-1
North	Plum Grove (Rolling Meadows, IL)	10/5	16°C	0.6	30 ea. NILMB-1 SILMB-1
North	Timber (Mt. Carol, IL)	10/17	17°C	10	500 ea. NILMB-2 SILMB-2
Central	Elder (Shelbyville, IL)	10/4	18°C	1.6	80 ea. NILMB-1 SILMB-1
Central	Madden (Decatur, IL)	10/17	18°C	0.6	30 ea. NILMB-2 SILMB-2
Central	Deer (Decatur, IL)	10/17	17°C	16	800 ea. NILMB-2 SILMB-2
Central	Lieson's (Clayton, IL)	10/5	18°C	2.0	100 ea. NILMB-1 SILMB-1
South	Mt. Vernon (Mt. Vernon, IL)	10/4	20°C	1.5	75 ea. NILMB-1 SILMB-1
South	Simpson's (Barnhill, IL)	10/4	20°C	0.4	20 ea. NILMB-1 SILMB-1
South	Carol (Jonesboro, IL)	10/4	22°C	1.5	75 ea. NILMB-1 SILMB-1

The study ponds were sampled using a boat-mounted electrofishing unit in Spring 1985, Fall 1985, Fall 1986. Fish were weighed, measured, and identified to stock by fin-clip. The relative survival of each stock in each pond is shown below as percentage composition of the various samples:

Pond	Percentage NILMB		
	Spring 1985	Fall 1985	Fall 1986
North:			
1. Timber	58.8	72.2	70.3
2. Stritzel's	50.0	50.0	NA
3. Plum Grove	NA	61.1	64.3
Total % NILMB = 66.7 (N = 174)			
Central:			
1. Elder	60.0	58.8	45.0
2. Madden	33.3	53.8	50.0
3. Deer	60.0	41.7	57.1
4. Lieson's	52.4	42.4	50.0
Total % NILMB = 47.9 (N = 169)			
South:			
1. Simpson's	33.3	33.3	30.0
2. Carol	40.0	27.3	33.3
3. Mt. Vernon	NA	NA	NA
Total % NILMB = 33.3 (N = 99)			

From these results it is apparent that in the northern areas of Illinois, the NILMB stock has greater survival than the SILMB stock. The reverse is true in the sourthern areas of Illinois. However, the survival of these two stocks in central Illinois, is approximately equal. Unfortunately, the population of largemouth bass established in the Mt. Vernon pond was eliminated as a result of heavy predation from stocked rainbow trout in 1984-85, and that established in Stritzel's pond apparently experienced a total winter-kill during the 1985-86 winter.

The relative sizes (total length in mm) of each stock sampled in each pond during each period is shown below:

Pond		Total Length (mm)		
		NILMB	SILMB	NILMB/SILMB Ratio
North:				
1. Timber	Spring 1985	103	85	1.21
	Fall 1985	259	246	1.05
	Fall 1986	283	266	1.06
2. Stritzel's	Spring 1985	69	67	1.03
	Fall 1985	197	172	1.15
	Fall 1985	NA	NA	NA
3. Plum Grove	Spring 1985	NA	NA	NA
	Fall 1985	184	176	1.05
	Fall 1986	188	178	1.06
Central:				
1. Elder	Spring 1985	81	79	1.02
	Fall 1985	267	254	1.05
	Fall 1986	338	350	0.97
2. Madden	Spring 1985	64	69	0.93
	Fall 1985	112	158	0.71
	Fall 1986	330	328	1.01
3. Deer	Spring 1985	61	61	1.00
	Fall 1985	206	228	0.90
	Fall 1986	310	327	0.95
4. Lieson's	Spring 1985	100	99	1.01
	Fall 1985	222	255	0.87
	Fall 1986	288	284	1.01
South:				
1. Simpson's	Spring 1985	67	70	0.96
	Fall 1985	233	236	0.98
	Fall 1986	300	310	0.97
2. Carol	Spring 1985	82	84	0.97
	Fall 1985	227	242	0.94
	Fall 1986	267	287	0.93

	Average of Final NILMB/SILMB Ratio	
North	1.09	(N = 3)
Central	0.99	(N = 4)
South	0.95	(N = 2)

Similarly, the relative sizes (weight in g) of each stock sampled in each pond during each period is also shown below:

Pond		Weight		
		NILMB	SILMB	NILMB/SILMB Ratio
North:				
1. Timber	Spring 1985	13	7.4	1.76
	Fall 1985	305	236	1.29
	Fall 1986	291	228	1.28
2. Stritzel's	Spring 1985	4.5	3.9	1.15
	Fall 1985	107	67	1.59
	Fall 1986	NA	NA	NA
3. Plum Grove	Spring 1985	NA	NA	NA
	Fall 1985	85	75	1.13
	Fall 1986	91	68	1.34
Central:				
1. Elder	Spring 1985	6.9	6.8	1.01
	Fall 1985	265	239	1.11
	Fall 1986	672	715	0.94
2. Madden	Spring 1985	4.1	4.1	1.00
	Fall 1985	14	56	0.25
	Fall 1986	596	586	1.02
3. Deer	Spring 1985	2.1	2.6	0.81
	Fall 1985	139	194	0.72
	Fall 1986	497	568	0.88
4. Lieson's	Spring 1985	13	12	1.08
	Fall 1985	199	221	0.90
	Fall 1986	338	277	1.22
South:				
1. Simpson's	Spring 1985	3.8	4.7	0.81
	Fall 1985	153	165	0.93
	Fall 1986	360	400	0.90
2. Carol	Spring 1985	6.9	7.5	0.92
	Fall 1985	134	168	0.80
	Fall 1986	225	260	0.80

	Average of Final NILMB/SILMB Ratio	
North	1.40	(N = 3)
Central	1.02	(N = 4)
South	0.88	(N = 2)

From the results comparing relative sizes (total length and weight) of the two stocks, it is apparent that the NILMB are growing faster than the SILMB in northern Illinois, but that the reverse is true in southern Illinois. The two stocks are growing approximately equally in central Illinois.

Job 4. Evaluation of the Reproductive Success of the Northern and Southern Illinois Stocks of Largemouth Bass in Different Regions of the State

Objective: To sample young-of-the-year largemouth bass produced in each study pond and determine the relative parental input from each stock through electrophoretic analysis.

Results: Spawning of largemouth bass occurred in both southern study ponds and in three of the four central study ponds in 1986, but no evidence for successful spawning was observed in any of the northern ponds. These individual YOY were analyzed electrophoretically to determine their genotype at the two diagnostic loci, Mdh-B and Gpi-B. From these genotypes, allele frequencies for the 1986 year class produced in each was calculated and compared to expected values based on: (1) original stocking data - assuming equal survival and equal reproduction of all introduced fish, and (2) final Fall 1986 survival data of introduced fish - still assuming equal reproduction of all fish in the study pond. These results are shown below:

Pond		Expected Values from Original Stocking: Allele Freq	Expected Values from Original Stocking: % NILMB	Expected Values from Fall 1986 Data: Allele Freq	Expected Values from Fall 1986 Data: % NILMB	Observed Values Fall 1986 Data: Allele Freq	Observed Values Fall 1986 Data: % NILMB	Average %
North								
1. Timber:	Mdh-B^1	.800	50.0	.881	70.3			
	B^2	.200		.119				
							No Spawning	
	Gpi-B^2	.825	50.0	.896	70.3			
	B^3	.175		.104				
2. Plum Grove:	Mdh-B^1	.725	50.0	.761	64.3			
	B^2	.275		.239				
							No Spawning	
	Gpi-B^2	.825	50.0	.875	64.3			
	B^3	.175		.125				
Central								
1. Elder:	Mdh-B^1	.725	50.0	.713	45.0	.735	54.0	46.5
	B^2	.275		.287		.265		
	Gpi-B^2	.825	50.0	.808	45.0	.786	38.9	
	B^3	.175		.192		.214		
2. Madden:	Mdh-B^1	.800	50.0	.800	50.0			
	B^2	.200		.200		No Spawning		
	Gpi-B^2	.825	50.0	.825	50.0			
	B^3	.175		.175				
3. Deer:	Mdh-B^1	.800	50.0	.828	57.1	.872	68.0	
	B^2	.200		.172		.128		78.2
	Gpi-B^2	.825	50.0	.850	57.1	.959	88.3	
	B^3	.175		.150		.041		
4. Lieson's:	Mdh-B^1	.725	50.0	.725	50.0	.963	100	
	B^2	.275		.275		.037		94.7
	Gpi-B^2	.825	50.0	.825	50.0	.963	89.4	
	B^3	.175		.175		.037		
South								
1. Simpson's:	Mdh-B^1	.725	50.0	.675	30.0	.700	40.0	
	B^2	.275		.325		.300		41.5
	Gpi-B^2	.825	50.0	.755	30.0	.800	42.9	
	B^3	.175		.245		.200		

Pond		Expected Values from Original Stocking		Expected Values from Fall 1986 Data		Observed Values Fall 1986 Data		Average
		Allele Freq	% NILMB	Allele Freq	% NILMB	Allele Freq	% NILMB	%
2. Carol:	Mdh-B[1]	.725	50.0	.683	33.3	.417	0.0	
	B[2]	.275		.317		.593		
								14.3
	Gpi-B[2]	.825	50.0	.767	33.3	.750	28.6	
	B[3]	.175		.233		.250		

Study Conclusions:

1. Survival of NILMB is superior to that of SILMB in areas of northern Illinois, whereas the reverse is true for areas of southern Illinois.
2. Growth of NILMB is superior to that of SILMB in areas of northern Illinois, whereas the reverse is true for areas of southern Illinois.
3. Studies assessing the reproductive success of the two stocks were inconclusive since 1986 was the first year of spawning and not all ponds experienced reproduction.

Recommendations:

1. This study should be continued for several more years to
   a. confirm continuation of survival and growth differential between stocks in the different regions,
   b. determine the reproductive success of the two stocks over several years in each region to determine long-term impact.
2. Based upon the results obtained from a continuation/completion of this study, we will make recommendations concerning the need for the IDOC hatchery system to propagate two distinct genetic stocks of largemouth bass (i.e., NILMB and SILMB) for introduction into waters in various ponds of Illinois.

Study 2: A Genetic Evaluation of the Striped Bass and F_1 Hybrid Striped x White Bass Stocking Programs in Illinois

Problem: Striped bass and F_1 hybrid x white bass have been and are continuing to be cultured and released into Illinois waters. The effects of this program on the native stocks of white bass has not been adequately assessed. The extent of self reproduction or of cross reproduction with native white bass is unknown, although recent evidence suggests that at least in some

mixed populations, hybridization may occur to a significant degree (Crawford, et al., personal communication).

A significant amount of gene flow between striped bass and white bass or between F_1 hybrid bass and white bass would create problems at two levels. First, this artificially created bridge between the two species of Morone may seriously compromise the genetic integrity of the white bass throughout Illinois. Second, significant mixing would create immediate problems in the identification of these species, and for the regulation of their harvest. In addition, depending upon the effectiveness of the F_1 hybrid bass to back cross to either parental species or to produce F_2 generations, attempts to keep separate records for white bass and F_1 hybrid bass would be meaningless, unless there was an unambiguous way of determining the types and proportions of genomes present.

Job 1. Evaluation of the Reproductive Patterns of Striped Bass and White Bass in a Mixed Population

Objective: To sample young-of-the-year Morone produced in mixed populations of striped bass anad white bass in Illinois lakes, and to identify their parentage using vertical starch gel electrophoresis and histochemical staining procedures in an assessment of the degree of interspecific hybridization.

Results: Striped bass (Morone saxatilis) and white bass (M. chrysops) populations were analyzed for electrophoretic variation among proteins encoded at 45 loci. These two species were found to be fixed for the same single allele at 40 of these loci. There was observed genetic variation between these two species at the Gpdh-A, Sod-A, F-dp-A, Gpi-B, and Cbp-A loci. Tables 1 and 2 present the results of these analyses, illustrating the diagnostic loci which

can be used to distinguish the genomes of these two species. The year given after each sample represents the year that sample was collected and/or genetically analyzed. Additional information is in parentheses below each sample. All of the hatchery produced populations of striped bass examined to date show no indication of influence by the white bass genome, confirming their specific purity. There is no evidence to suggest that any backcrossed individuals were produced by mistake, as has been the case for other states. In addition, all of the populations of white bass examined appear to be uncontaminated examples of that species.

Table 1. Genetic variation among populations of striped bass, Morone saxatilis.

Locus/ Allele	Sand Ridge* '84 (Eagle Bend, TN)	Collins Lake '84 (Adults)	Dresden Lake '84 (Adults)	Jake Wolfe '85 (Eagle Bend, TN)
N	20	20	2	20
Gpdh-A				
1	1.000	1.000	1.000	1.000
2	0.000	1.000	0.000	0.000
Sod-A				
1	1.000	1.000	1.000	1.000
2	0.000	0.000	0.000	0.000
F-dp-A				
1	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000
Gpi-B				
1	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000
Cbp-A				
1	1.000	0.900	0.750	1.000
2	0.000	0.100	0.250	0.000

*The Sand Ridge Hatchery was renamed Jake Wolfe Hatchery between the 1984 and 1985 collections.

Table 2. Genetic variation among populations of white bass, Morone chrysops.

Locus/ Allele	Collins Lake '83 (Adults)	Collins Lake '84 (Adults)	Sangchris Lake '85 (Adults)	Baldwin Lake '85 (Adults)
N	20	6	2	3
Gpdh-A				
1	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000
Sod-A				
1	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000
F-dp-A				
1	1.000	1.000	1.000	1.000
2	0.000	0.000	0.000	0.000
Gpi-B				
1	1.000	1.000	1.000	1.000
2	0.000	0.000	0.000	0.000
Cbp-A				
1	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000

To date, however, no strong, naturally reproducing populations of striped bass have been established in an Illinois lake containing a native population of white bass. Thus, assessment of natural production of F_1 interspecific hybrids was not possible. Natural hybridization between these two species has been observed in Arkansas, and perhaps Texas, Tennessee, and South Carolina.

Job 2. Evaluation of the Reproductive Patterns of F_1 Hybrid Bass and White Bass in a Mixed Population

Objective: To sample young-of-the-year Morone produced in mixed populations of F_1 hybrid bass and white bass in Illinois lakes, and to identify their parentage using vertical starch gel electrophoresis and histochemical staining procedures in an assessment of the degree of natural F_1 hybrid reproduction, (i.e., production of F_2 offspring, and the back-crossing of F_1 hybrid bass and white bass).

Results: A number of hybrid striped bass collections were genetically analyzed for comparison with natural white bass and striped bass samples. The loci surveyed were those showing fixed specific differences between white and striped bass. The results for these analyses are shown in Table 3. Both 1984 Sand Ridge hatchery specimens were part of a 1983 stocking of Spring Lake and were obtained from Dr. Larry Jahn at Western Illinois University. The crosses were performed using Lake Texoma, TX, striped bass x Powerton Lake white bass. Another hybrid obtained from Sand Ridge via Dr. Jahn was a 1983 fish from Marion, AL that was caught in Spring Lake in 1984. The 1984 Collins Lake hybrid adults were from a variety of SIU stockings, including a Sand Ridge hatchery cross. Both hybrids and pure stripers, from North Carolina and South Carolina, respectively, were stocked into Dresden Lake by SIU in 1984. All samples of young (40) taken from Dresden the same year proved to be hybrids.

DOC personnel collected the Rend Lake sample from young produced at Monks Corners Fish Hatchery, SC, prior to being stocked into Rend Lake in 1984. The Baldwin Lake hybrids are of unknown origin and were obtained from Illinois Power Company and DOC personnel.

Three hybrid striped bass population samples were genetically analyzed in 1985. These samples represented hatchery production efforts. In addition one specimen was collected from Otter Lake. One population was sampled in 1986, and that represented an acquired batch of F_1 hybrids from Bowens State Fish Hatchery in Georgia. The results of all these additional analyses are also given in Table 3. To date, four populations have exhibited allele frequencies somewhat uncharacteristic for F_1 interspecific hybrids, Collins '84, Dresden '84, Rend Lake '84, and Spring Lake '84. However, all of these possible discrepancies were observed at a single locus Cbp-A, and represented very minimal differences. This may indicate that some native populations of pure white bass may contain low frequencies of the Cbp-A^1 allele, characteristic of striped bass. However, it may also indicate some distant contamination during hatchery procedures. No other diagnostic locus confirms this event. In summary, no real positive evidence exists for mistaken production of non-F_1 hybrids. The Cbp-A^1A^1 genotype of the one Spring Lake fish sampled does suggest a questionable nature for the parental genotypes in this population.

Table 3. Genetic variation among populations of F^1 hybrids, striped bass x white bass.

Locus/ Allele	Spring Lake '84 ('83 Sand Ridge) ('83 Marion, AL)	Collins Lake '84 (Adults)	Dresden '84 (South Carolina '84)	Rend Lake '84 (Monks Corners, SC)	Baldwin Lake '84 (Adults)
N	3	20	40	18	4
Gpdh-A					
1	.500	.500	.500	.500	.500
2	.500	.500	.500	.500	.500
Sod-A					
1	0.500	0.500	0.500	0.500	0.500
2	0.500	0.500	0.500	0.500	0.500
F-dp-A					
1	.500	0.500	.500	0.500	.500
2	.500	0.500	.500	0.500	.500
Gpi-B					
1	0.500	0.500	0.500	0.500	0.500
2	0.500	0.500	0.500	0.500	0.500
Cbp-A					
1	0.500	0.525	0.525	0.525	0.500
2	0.500	0.475	0.475	0.475	0.500

Table 3. Continued.

Locus/ Allele	Jake Wolfe '85 (Eagle Bend, TN)	Little Grassy '85 (East Fork Htch., IN)	Carlyle Lake '85 (East Fork Htch., IN)	Otter Lake '85 (Adult)	Jake Wolfe '86 (Bowens, GA)
N	20	20	20	1	20
Gpdh-A					
1	0.500	0.500	0.500	0.500	.500
2	0.500	0.500	0.500	0.500	.500
Sod-A					
1	0.500	0.500	0.500	0.500	.500
2	0.500	0.500	0.500	0.500	.500
F-dp-A					
1	0.500	0.500	0.500	0.500	.500
2	0.500	0.500	0.500	0.500	.500
Gpi-B					
1	0.500	0.500	0.500	0.500	.500
2	0.500	0.500	0.500	0.500	.500
Cbp-A					
1	0.500	0.500	0.500	0.500	.500
2	0.500	0.500	0.500	0.500	.500

To assess the degree of natural reproduction of introduced, F_1 hybrid bass populations YOY were sampled at Lake Baldwin and at Clinton Lake, both below the dam in the tail race and in the lake proper. Only a few YOY were obtainable in 1985 and 1986, so sample size was small (N = 14). However, all fish obtained were identified as pure white bass based upon electrophoretic analysis.

Study Conclusions:

1. All striped bass produced or obtained by the IDOC for introduction were, in fact, pure striped bass, and were not contaminated with any white bass or other Morone alleles.

2. All F_1 hybrid bass produced or obtained by the IDOC for introduction were, in fact good F_1 generation fish, and did not represent backcrossed or F_2 individuals.

3. There was no evidence for any natural reproduction or hybridization with native white bass of introduced striped bass of F_1 hybrid bass.

Recommendations:

1. Genetic monitoring of the purity of production efforts for both striped bass and F_1 hybrid bass continue in Illinois.

2. An assessment of potential natural introgression of the two Morone species be repeated if and when good self-sustaining populations of striped bass or F_1 hybrids are established sympatrically with native Illinois white bass populations.

Study 3: A Genetic Evaluation of Fishes Produced, Collected or Obtained for Introduction in Illinois

Problem:

Culture of fish species for introduction into waters of Illinois is becoming an increasingly important technique for fisheries management. This is particularly so in light of the construction and initial operation of the Jake Wolfe Hatchery facility. It is becoming increasingly evident that for any given species of sportfish, it is possible to select brood stock from a multitude of different genetic stocks. Unfortunately, the data do not exist to enable managers to identify these different stocks, their degree of genetic diversity, how these stocks differ, nor which stocks would serve as the best brood stock for a given region. It is imperative that these data be collected, particularly during the start-up period of a hatchery such as Jake Wolfe.

The initiation of culture practices at Jake Wolfe, as well as continuation of practices at the newly renovated Little Grassy facility provide an excellent opportunity to start a genetic catalog of all fish species cultured in Illinois. These data will serve as baseline data to evaluate the effectiveness of certain programs, the appropriateness of brood stock selection and the long-term effects upon the genetic composition of the native populations affected.

Job 1. Evaluation of Stocks of Fish of All Species Produced in the Illinois State Hatchery System

Objective: To define the genetic composition of batches of fish of all species which are produced in Illinois hatcheries operated by the Department of Conservation.

Job 2. Evaluation of Stocks of Fish of All Species Obtained for Introduction into Illinois Waters

Objective: To define the genetic composition of all batches of fish obtained by the Department of Conservation for introduction into Illinois waters.

Results: For ease of presentation, the results for these two similar jobs will be presented together. For these jobs, samples of each batch of fish to be analyzed were taken by DOC staff, wrapped live and immediately frozen awaiting shipment to the INHS Fisheries Genetics Research Laboratory in Champaign. For the analyses, muscle, eye or liver tissue were excised and homogenates prepared as described in Philipp et al., 1979. The electrophoretic conditions and histochemical staining procedures used were as described in Philipp et al., 1979 and Koppelman et al., 1986. Allele frequencies presented in the various data tables are only for those loci showing polymorphism. All loci analyzed which proved to be monomorphic are not listed in these tables, but are given in the text for each species. The results obtained for each species will be given separately.

Brown Trout

Five collections of brown trout (Salmo trutta) produced or reared at the Jake Wolfe Hatchery were analyzed. Three were the year classes of Plymouth Rock YOY brown trout produced at the hatchery in 1983, 1984, and 1985, and two were samples of the parental fish held as broodstock and used to produce these year classes. Loci examined and found to be monomorphic were Adh-A Gpdh-A^b, Sdh-A, Ldh-A^a, A^b, B^a, B^b and C, Mdh-A^a and B, Me-A^a, A^b and B, Idh-A and B, 6-Pgdh-A, Gapdh-A^a and A^b, Xdh-A, Sod-A, Aat-A, B, M^a and M^b, Ck-A^a, A^d, B, C^a, and C^b, Pgm-A, Ald-A, C^a and C^b, Acon-A and B, Gpi-B^a, Cbp-A, and Prot-A, B, C, D, and E. The results of these analyses are given in Table 4. Although there are minor shifts in allele frequencies and changes in heterozygosity levels among the three-year classes of YOY produced at the hatchery, no major differences indicating any inbreeding or contamination problems were evidenced.

Table 4. Genetic variation among populations of brown trout, Salmo trutta.

Locus/ Allele		Sand Ridge '83 YOY	Sand Ridge '84 (All Fish Are From Plymouth Rock, MA Stock) YOY	Jake Wolfe '85 YOY	Jake Wolfe '85 (Adults)	Jake Wolfe '86 (Adults)
N		20	20	20	20	20
Gpdh-A[a]	1	0.075	0.175	0.075	0.125	0.100
	2	0.925	0.825	0.925	0.875	0.900
Mdh-A[b]	1	0.625	0.575	0.500	0.500	0.550
	2	0.375	0.425	0.500	0.500	0.450
Me-C	1	0.000	0.050	0.050	0.000	0.025
	2	1.000	0.950	0.950	1.000	0.975
Ck-A[a]	1	0.900	0.950	1.000	1.000	0.975
	2	0.100	0.050	0.000	0.000	0.025
Ck-A[b]	1	0.200	0.300	0.350	0.275	0.275
	2	0.800	0.700	0.650	0.725	0.725
Gpi-A	1	0.900	0.850	0.750	0.625	0.700
	2	0.100	0.150	0.250	0.375	0.300
Gpi-B[b]	1	1.000	0.975	0.900	0.925	0.925
	2	0.000	0.025	0.100	0.075	0.975
Est-A	1	0.025	0.000	0.000	0.075	0.025
	2	0.975	1.000	1.000	0.925	0.975
Est-B	1	0.075	0.000	0.000	0.000	0.000
	2	0.925	1.000	1.000	1.000	1.000

Rainbow Trout

Eight collections of rainbow trout (Salmo gairdneri) have been analyzed. These samples were from production batches of the Wytheville and Arlee strains produced at Jake Wolfe, the Madison strain produced at the Lanesboro State Hatchery in Minnesota, and the Skamania strain of steelhead produced or obtained by Indiana. Allele frequencies at fourteen polymorphic loci are shown in Table 5. Loci examined but not found to be polymorphic include Adh-A, Gpdh-A^a, Sdh-A^a and A^b, Ldh-A^a, A^b, and B^b, Mdh-A and M, Me-A and B, Idh-A, 6-Pgdh-A, Gapdh-A^a and A^b, Xdh-A, Aat-A, B^a, B^b, M and M^b, Ck-A^b, A^c, A^d, B, C^a, and C^b, Ald-A^a and A^b, Acon-A and C, Gpi-A, B^a, and B^b, Est-C, Cpb-A, anad Prot-A, B, and D.

From evidence obtained at the Gpdh-A^b, Ldh-B^a, Ldh-C, Mdh-B^a, Mdh-B^b, Acon-A, Prot-A, and Prot-B loci, it appears possible that genetic variability among the year classes of Arlee strain produced in Illinois may be decreasing. It may be advisable to supplement the existing Arlee broodstock with other Arlee strain fish from other hatchery sources. Interestingly, comparing the four strains so far analyzed, Wytheville, Arlee, Madison, and Skamania, Arlee has the highest degree of genetic variability. The others, in decreasing order are Madison, Skamania, Wytheville. The decreased level of performance observed for the Wytheville strain by Illinois hatchery/management personnel may be related to this relatively low level of variability.

Table 5. Genetic variation among populations of rainbow trout, Salmo gairdneri.

Locus/ Allele		Sand Ridge '84 (Wytheville, VA)	Sand Ridge '83 (Arlee, MT)	Sand Ridge '84 (Arlee, MT)	Jake Wolfe '85 (Arlee, MT)	Jake Wolfe '85 (Madison)	Jake Wolfe '85 (Skamania Steelhead)	Indiana '86 (Winter-Run)	Indiana '86 (Skamania)
N		20	20	20	20	20	20	25	25
Gpdh-A[b]	1	0.900	0.950	1.000	1.000	1.000	0.925	0.980	0.800
	2	0.100	0.050	0.000	0.000	0.000	0.075	0.020	0.200
Ldh-B[a]	1	0.000	0.025	0.025	0.000	0.000	0.000	0.000	0.120
	2	0.850	0.950	0.975	1.000	1.000	1.000	1.000	0.880
	3	0.150	0.025	0.000	0.000	0.000	0.000	0.000	0.000
Ldh-C	1	0.000	0.100	0.100	0.000	0.000	0.000	0.000	0.000
	2	1.000	0.900	0.900	1.000	1.000	1.000	1.000	1.000
Mdh-B[a]	1	0.000	0.000	0.325	0.000	0.000	0.200	0.040	0.120
	2	0.000	0.350	0.100	0.200	0.000	0.000	0.060	0.000
	3	1.000	0.650	0.575	0.800	0.950	0.800	0.820	0.860
	4	0.000	0.000	0.000	0.000	0.050	0.000	0.080	0.020
Mdh-B[b]	1	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000
	2	1.000	1.000	0.975	1.000	1.000	1.000	1.000	1.000
Idh-B	1	0.050	0.050	0.050	0.050	0.075	0.000	0.200	0.020
	2	0.450	0.875	0.900	0.825	0.550	0.975	0.760	0.880
	3	0.500	0.050	0.050	0.200	0.000	0.000	0.000	0.000
	4	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000
	5	0.000	0.025	0.000	0.075	0.125	0.025	0.040	0.100
Sod-A	1	0.800	0.850	0.850	0.825	0.325	0.800	0.840	0.760
	2	0.200	0.150	0.150	0.175	0.675	0.200	0.160	0.240
Pgm-A	1	0.150	0.050	0.050	0.025	0.050	0.000	0.000	0.000
	2	0.850	0.950	0.950	0.975	0.950	1.000	1.000	
Acon-A	1	0.000	0.225	0.050	0.250	0.450	0.450	0.000	0.000
	2	1.000	0.775	0.900	0.750	0.550	0.550	1.000	1.000
	3	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000

Table 5. Continued.

Locus/ Allele		Sand Ridge '84 (Wytheville,VA)	Sand Ridge '83 (Arlee, MT)	Sand Ridge '84 (Arlee, MT)	Jake Wolfe '85 (Arlee, MT)	Jake Wolfe '85 (Madison)	Jake Wolfe '85 (Skamania Steelhead)	Indiana '86 (Winter-Run)	Indiana '86 (Skamania)
Est-A	1	0.000	0.100	0.250	0.150	0.025	0.175	0.250	0.140
	2	1.000	0.900	0.650	0.850	0.800	0.825	0.750	0.860
	3	0.000	0.000	0.100	0.000	0.175	0.000	0.000	0.000
Est-B	1	0.000	0.000	0.000	0.050	0.050	0.000	0.000	0.000
	2	0.000	0.100	0.150	0.100	0.100	0.100	0.100	0.100
	3	1.000	0.900	0.850	0.750	0.750	0.900	0.900	0.900
	4	0.000	0.000	0.000	0.100	0.100	0.000	0.000	0.000
Prot-A	1	0.000	0.000	0.075	0.000	0.075	0.000	0.000	0.000
	2	1.000	1.000	0.925	1.000	0.925	1.000	1.000	1.000
Prot-B	1	0.000	0.000	0.100	0.000	0.100	0.000	0.000	0.000
	2	1.000	1.000	0.900	1.000	0.900	1.000	1.000	1.000
Prot-C	1	0.275	0.475	0.450	0.733	0.725	0.500	0.360	0.440
	2	0.725	0.525	0.550	0.267	0.275	0.500	0.640	0.560

Lake Trout

Lake trout (Salvelinus namaycush) fingerlings or parr were collected from the Jake Wolfe Hatchery in 1984 and 1985 and genetically analyzed to reveal the amount of variation present at 48 loci. These fish were originally produced at the Iron River National Hatchery in Wisconsin. Unfortunately, Lake trout exhibit one of the least amounts of electrophoretic variation among the members of the Salmonid family. Only three of the 48 loci studied were polymorphic, and their allele frequencies are presented in Table 6. The following loci were monomorphic: Adh-A, Gpdh-A^a, A^b, B^a, and B^b, Sdh-A, Ldh-A^a, A^b, B^a, B^b, C^a, and Mdh-A, B, and M, Me-A and B, Idh-A^a, A^b, and B, 6-Pgdh-A, Gapdh-A, Xdh-A, Sod-A, Aat-A^b, B, M^a, and M^b, Ck-A^a, A^b, A^c, A^d, B, and C, Ald-A, C^a, and C^b, Gpi-A, B^a, and B^b, Est-B, Cbp-Aa, and Prot-A, C^a, and C^b. The results for the two years were quite similar, as would be expected. How these results might differ from those obtainable for other natural or hatchery stocks is currently unknown. A 1986 collection has not yet been obtained from the hatchery, however, a collection of lake trout adults was made from Lake Michigan in November and awaits analysis.

Table 6. Genetic variation among populations of Lake trout, *Salvelinus namaycush*.

Locus/ Allele	Sand Ridge '84 (Iron River National Hatchery, WI)	Jake Wolfe '85 (Iron River National Hatchery, WI)
N	20	20
Aat-A^a		
1	0.525	0.500
2	0.475	0.500
Pgm-A^a		
1	0.975	1.000
2	0.025	0.000
Prot-B		
1	0.425	0.500
2	0.575	0.500

Chinook Salmon

Three samples of Chinook Salmon, Oncorhynchus tshawytscha, have been collected from the Jake Wolfe Hatchery and electrophoretically analyzed. These fish were produced in 1984, 1985, and 1986 and originated from the Little Manistee River, Michigan. The allele frequencies at six polymorphic loci are presented for all samples in Table 7. Those loci examined and containing no variation included Adh-A, Gpdh-A^a, A^b, and B, Ldh-A^a, A^b, B^a, B^b, and C, Mdh-A, Me-A, Idh-A, 6-Pgdh-A, Gapdh-C^a and C^b, Sod-A, Aat-A, B^a, B^b, M^a, M^b, Ck-A^a, A^b, A^c, A^d, B, C^a, and C^b, Ald-A^a, A^b, C^a, and C^b, Fum-A, Gpi-A and B, Est-A, C^a and C^b, Cbp-A, and Prot-$^-$A, $^-$B, A, and B. No significant differences were observed between the three-year classes. However, rare alleles at the Mdh-B and Me-B loci present in the 1984 year class were not observed in the 1985 and 1986 year classes.

Table 7. Genetic variation among populations of Chinook salmon, Onchorhynchus tshawytscha.

Locus/ Allele	Sand Ridge '84 (Little Manistee R., MI)	Jake Wolfe '85 (Little Manistee R., MI)	Jake Wolfe '86 (Little Manistee,R., MI)
N	20	20	20
Mdh-B			
1	0.050	0.000	0.000
2	0.950	1.000	1.000
Me-B			
1	0.075	0.000	0.000
2	0.925	1.000	1.000
Idh-B			
1	0.850	0.925	0.925
2	0.150	0.075	0.075
Xdh-A			
1	0.850	0.625	0.750
2	0.150	0.375	0.250
Acon-A			
1	0.175	0.100	0.075
2	0.750	0.800	0.850
3	0.075	0.100	0.075
Est-B			
1	0.075	0.025	0.050
2	0.875	0.850	0.850
3	0.050	0.125	0.100

Coho Salmon

Four collections of Coho salmon (Oncorhynchus kisutch) parr and smolts were collected from the Jake Wolfe Hatchery and genetically analyzed at 63 loci. The stocks produced originated from the Platte River Hatchery in Michigan for all years. Only three of the 63 loci contained any variation. These results are presented in Table 8. This high number of monomorphic loci included Adh-A, Gpdh-A^a, A^b, Sdh-A^a and A^b, Ldh-A^a, A^b, B^a, B^b, and C, Mdh-A and B, Me-A and B, Idh-A^a, A^b, and B, 6-Pgdh-A, Gapdh-A, B, C^a, and C^b, Sod-A, Aat-A, B, M^a, M^b, and M^c, Ck-A^a, A^b, A^c, A^d, and B, Pgm-A^a and A^b, Ald-A, B, C^a and C^b, Acon-A^a and A^b, Gpi-A^a, A^b and B, Est-A, C^a, C^b, D, and E, Cpb-A^a and A^b, and Prot-A, B, C, D, E, F, G, and H. The allele frequencies differed significantly among each of the four samples, however. This may indicate that these samples each originated from small numbers of brood stock, or may reflect yearly differences in the populations of breeding coho taken for gametes.

Table 8. Genetic variation among populations of Coho salmon, Oncorhynchus kisutch.

Locus/ Allele	Sand Ridge '84 (Platte River Htch, MI;Parr)	Sand Ridge '84 (Platte River Htch, MI;Smolt)	Jake Wolfe '85 (Platte River Htch, MI;Parr)	Jake Wolfe '86 (Platte River Htch, MI;Parr)
N	20	20	20	20
Xdh-A				
1	1.000	0.800	1.000	0.950
2	0.000	0.200	0.000	0.050
Est-B				
1	0.150	0.000	0.075	0.000
2	0.850	1.000	0.925	1.000
Est-G				
1	0.000	0.575	0.075	0.250
2	1.000	0.425	0.925	0.750

Walleye

During 1984, 1985, 1986 the walleye (Stizostedion vitreum) fry produced in Illinois originated from brood stock obtained from Collins, Fox Chain, Clinton, and Shelbyville Lakes. Samples of all of these production efforts were genetically analyzed after being reared to advanced fry at the INHS. Walleye fry were also obtained from sources outside Illinois including Senecaville, Ohio; St. Paul, Minnesota; Gavins Pt., South Dakota; Genoa and Woodruff, Wisconsin; and Oneida, New York. Fry from all of these stocks were also reared to advanced stages at the INHS and evaluated genetically. A sample of advanced Senecaville walleye fingerlings raised at the Jake Wolfe Hatchery was also obtained and analyzed electrophoretically for comparison with the fry results. Only previously identified polymorphic loci were examined due to the minimal amount of sample obtainable for individual fry and the lack of adequate activity for those enzymes encoded in loci not expressed until later in embryonic development. Results for these populations are illustrated in Table 9. Comparing Illinois populations, a fair degree of interpopulational and intrapopulational genetic variation exists. Certainly, ample variation exists among local stocks to successfully construct genetically tagged stocks of this species to use for fishery evaluation experiments. In fact, if certain stocks have been introduced in combination within the same lakes, it may be possible in the near future to evaluate each stock's performance (growth and survival) in these lakes.

Table 9. Genetic variation among populations of Walleye, Stizostedion vitreum.

Locus/N	Cedar Lake 10	Lake Shelbyville 10	Lakes Clinton/ Shelbyville 20	Collins Lake 40	Kankakee River 4	Fox Chain O' Lakes 20	Mississippi R., Wisconsin 20	Oneida, New York 20	Gavins Pt. Hatchery, South Dakota 20
Adh-A									
1	0.200	0.250	-----	0.000	0.000	-----	-----	-----	-----
2	0.800	0.750	-----	1.000	1.000	-----	-----	-----	-----
Mdh-A									
1	1.000	0.850	1.000	1.000	1.000	1.000	1.000	1.000	1.000
2	0.000	0.150	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Mdh-B									
1	0.800	0.700	0.775	0.788	1.000	0.900	0.725	0.950	0.625
2	0.200	0.300	0.225	0.213	0.000	0.100	0.275	0.050	0.375
Idh-B									
1	0.500	0.550	0.450	0.653	0.625	0.525	0.400	0.600	0.575
2	0.500	0.450	0.550	0.347	0.375	0.475	0.600	0.400	0.425
6-Pgdh-A									
1	0.350	0.450	0.000	0.000	0.125	0.000	0.000	0.000	0.000
2	0.650	0.550	1.000	1.000	0.875	1.000	1.000	1.000	1.000
Cbp-A									
1	0.750	0.500	-----	0.400	0.625	-----	-----	-----	-----
2	0.250	0.500	-----	0.600	0.375	-----	-----	-----	-----

Saugeye

In addition to the samples of walleyes analyzed, a sample of sauger x walleye F_1 hybrids (saugeyes) produced at the SIU-LaSalle Hatchery facility, was also collected and genetically analyzed. The cross was made using one sauger female from the Illinois River and two walleye males from Collins Lake. The results of this analysis are shown in Table 10. Only those enzymes polymorphic among the F_1 hybrids are shown. The remaining loci studied within the walleye were monomorphic for these hybrids. The table contains allele frequencies of walleye for comparison with those obtained from the SIU saugeyes. Results were as expected for F_1 hybrids, with Adh-A, and Pgm-A serving as the best diagnostic loci.

Table 10. Genetic variation among walleye and the walleye x sauger F_1 hybrid (saugeye).

Locus/ Allele	Walleye:SIU Htch. '85 (Collins)	F_1 Hybrid:SIU Htch. '85 (IL.R. S x Collins W)
N	20	20
Adh-A		
1	0.000	0.500
2	1.000	0.500
Mdh-A		
1	1.000	1.000
2	0.000	0.000
Mdh-B		
1	0.775	0.275
2	0.225	0.725
Idh-B		
1	0.500	0.175
2	0.500	0.825
6-Pgdh-A		
1	0.000	0.000
2	1.000	1.000
Pgm-A		
1	0.000	0.500
2	1.000	0.500
Cbp-A		
1	0.425	0.250
2	0.575	0.750

Muskellunge

A number of samples of muskellunge, have been obtained from Iowa, Wisconsin, and Minnesota, and reared at the Spring Grove Hatchery. A shipment obtained from Kentucky by the Little Grassy Hatchery unfortunately was not sampled because all of the fish in the batch were directly stocked. Two muskellunge from the 1984 introduction were caught in gillnets in Collins Lake by SIU personnel and were genetically evaluated. Three fish, part of the 1985 production efforts by the SIU hatchery introduced into Collins Lake, were also saved and genetically evaluated. Only those loci identified as polymorphic during a previous large-scale analysis of muskellunge variation were examined. The following loci were previously shown to be monomorphic: Adh-A, Gpdh-A and B, Sdh-A, Ldh-A and B, Mdh-A, B^a, and B^b, Me-A^a and A^b, Idh-B, Gpdh-A and C, Sod-A, Aat-A, B^a, B^b, and M^a, F-dp-A, Pk-A and B, Pgk-A, Ck-A, B, and C, Pgm-A, Ada-A, Ald-A and C, Fum-A and B, Acon-A and B, Tpi-A, Mpi-A, Gpi-A, Est-C and D, Cbp-A, and Prot-A, B, C, D, E, F, G, and H. The two populations obtained from Iowa and from Minnesota showed significant genetic variation (Table 10) from the Carlton Lake population and perhaps from the Collins Lake population being produced at the SIU hatchery facility. Construction of a variety of genetically tagged stocks is quite feasible for this species.

Table 11. Genetic variation among populations of muskellunge, Esox masquinongy.

Locus/ Allele	Carlton Lake, IL '84 (Adults)	Spring Grove '84 (WI & IA Htch)	Otter Lake, IL '84 (Adults)	Spring Grove '85 (Spirit Lake, IA Htch)	Spring Grove '85 (St. Paul, MN Htch)	Collins Lake, IL '85 ('84 Prod.)	SIU Ponds '85 ('85 Prod.)
N	10	10	2	20	20	2	3
Ldh-C							
1	0.000	0.200	0.000	0.250	0.200	0.500	0.500
2	1.000	0.800	1.000	0.750	0.800	0.500	0.500
Idh-A							
1	0.600	0.800	0.750	1.000	1.000	1.000	1.000
2	0.400	0.200	0.250	0.000	0.000	0.000	0.000
6-Pgdh-A							
1	0.750	0.900	0.750	0.575	0.550	0.500	1.000
2	0.250	0.100	0.250	0.425	0.450	0.500	0.000
Xdh-A							
1	1.000	1.000	1.000	1.000	1.000	1.000	1.000
2	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Aat-M^b							
1	0.000	0.400	0.750	0.325	0.500	0.500	0.500
2	1.000	0.600	0.250	0.675	0.500	0.500	0.500
AK-A							
1	0.000	0.000	0.000	0.250	0.100	0.000	0.000
2	1.000	1.000	1.000	0.750	0.900	1.000	1.000
Gpi-B							
1	0.000	0.000	0.000	0.100	0.000	0.250	0.000
2	1.000	1.000	1.000	0.900	1.000	0.750	1.000
Est-A							
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Est-B							
1	0.400	0.150	1.000	0.775	0.975	0.500	0.000
2	0.600	0.850	0.000	0.225	0.025	0.500	1.000

Tiger Muskellunge

Tiger muskellunge analyzed included samples of the production effort of Wolf Lake Hatchery (Michigan) reared at the Sand Ridge (1984), the Little Grassy (1985), and the Spring Grove (1986) hatcheries. Another sample of Wolf Lake Hatchery tiger muskellunge was obtained from the SIU-LaSalle Hatchery. A single, large adult fish taken from Clinton Lake by Illinois Power biologists was also evaluated. The results of the electrophoretic analysis is shown in Table 12. Loci examined included those polymorphic for muskellunge and those displaying diagnostic allelic differences between muskellunge and northern pike. Analyzing northern pike stocks reared by DOC biologists has unfortunately not been accomplished in 1984 or 1985 because samples have not been obtained for analysis. Samples of these fish would help greatly in understanding the interspecific relationships between these Esox species and what impact this genetic variation may have upon the various tiger muskellunge stocks produced.

Table 12. Genetic variation among populations of tiger muskellunge (muskellunge x northern pike) F_1 hybrids.

Locus/ Allele		Sand Ridge '84 (Wolf Lake,MI Htch)	Little Grassy '85 (Wolf Lake,MI Htch)	SIU-LaSalle '85 (Wolf Lake,MI Htch)	IP-Clinton Lake '85 (Adult)	Spring Grove '86 (Wolf Lake,MI Htch)
N		20	20	6	1	15
Adh-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Gpdh-A	1	1.000	1.000	1.000	0.500	1.000
	2	0.000	0.000	0.000	0.500	0.000
Ldh-C	1	0.000	0.000	0.250	0.000	0.000
	2	1.000	1.000	0.750	1.000	1.000
Me-B	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Idh-A	1	1.000	1.000	1.000	1.000	1.000
	2	0.000	0.000	0.000	0.000	0.000
Idh-B	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
6-Pgdh-A	1	0.500	0.500	0.583	0.500	0.500
	2	0.500	0.500	0.417	0.500	0.500
Xdh-A	1	1.000	1.000	1.000	1.000	1.000
	2	0.000	0.000	0.000	0.000	0.000
Sod-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Aat-M^b	1	0.500	0.400	0.333	0.500	0.500
	2	0.500	0.600	0.667	0.500	0.500
Ck-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Ak-A	1	0.050	0.050	0.167	0.000	0.000
	2	0.950	0.950	0.833	1.000	1.000

Table 12. Continued.

Locus/ Allele		Sand Ridge '84 (Wolf Lake,MI Htch)	Little Grassy '85 (Wolf Lake,MI Htch)	SIU-LaSalle '85 (Wolf Lake,MI Htch)	IP-Clinton Lake '85 (Adult)	Spring Grove '86 (Wolf Lake, MI Htch)
Fum-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
^{a}Gpi-A	1	0.000	0.000	0.000	0.000	0.000
	2	1.000	1.000	1.000	1.000	1.000
Gpi-B	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Est-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500
Est-B	1	0.000	0.000	0.000	0.000	0.000
	2	1.000	1.000	1.000	1.000	1.000
Cbp-A	1	0.500	0.500	0.500	0.500	0.500
	2	0.500	0.500	0.500	0.500	0.500

Largemouth Bass

A number of collections of largemouth bass, Micropterus salmoides, were sampled from a variety of sources in Illinois including some from the Genoa National Fish Hatchery, Wisconsin. Gary Lutterbie, DOC Biologist, reared one of the Genoa batches for stocking into Clinton Lake, one batch was reared at the Jake Wolfe Hatchery, and one at the Little Grassy Hatchery. The Jake Wolfe Hatchery produced young using broodstock collected from Powerton Lake. The Little Grassy Hatchery produced young using broodstock from both LaSalle Lake and Crab Orchard Lake. Adults from Pierce Lake (collected by Mike Sule, DOC Biologist) and young-of-the-year from Baldwin Lake (collected by Illinois Power biologists) were also genetically evaluated. The results of these analyses are presented in Table 13. All fish were analyzed to determine genetic variability at the six loci which have been determined previously to be significantly polymorphic throughout the species' range.

Two allelic variants previously undescribed have been observed in largemouth bass handled recently by the Illinois hatchery system; (1) Idh-B$^{\cdot 5}$, and (2) Gpi-B^{1}. In a 1984 Spring Grove collection of fish produced by Little Grassy personnel using a Lake Sara and/or Crab Orchard broodstock, a fourth Idh-B allele was detected. This allele has not been found in fish produced exclusively from Crab Orchard broodstock, indicating that this allele most likely originated from the Lake Sara population. Two out of three batches of 1985 Genoa Hatchery fish possessed a third Gpi-B isozyme at frequencies of 0.075 and 0.100. Curiously, the batch of Genoa Hatchery fish sampled from the Little Grassy Hatchery did not possess this allele at any

frequency. Since the Genoa Hatchery fish stocked into Clinton Lake do possess this allele and largemouth bass already in the lake do not, this represents an excellent genetic marker which can be used to evaluate the long-term impact of this introduced stock of largemouth bass.

Table 13. Genetic variation among populations of largemouth bass, Micropterus salmoides.

Collection	N	Locus/Allele																
		Mdh-B		Idh-B			Sod-A		Aat-B				CK-C		Gpi-B			
		1	2	0.5	1	3	1	2	1	2	3	4	1	2	1	2	3	
Sand Ridge '84 (Powerton Lake)	20	0.925	0.075	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	
Spring Grove '84 (Little Grassy Htch.: Lake Sara and Crab Orchard Lake)	24	0.770	0.230	0.313	0.687	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	
Little Grassy '84 (Crab Orchard Lake)	30	0.767	0.233	0.000	1.000	0.000	0.000	1.000	0.800	0.200	0.000	0.000	0.000	1.000	0.000	1.000	0.000	
Jake Wolfe '85 (Powerton Lake)	20	0.975	0.025	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.150	0.850	0.000	1.000	0.000	
Jake Wolfe '85 (Genoa Nat'l. Htch., WI)	20	0.925	0.075	0.000	1.000	0.000	0.000	1.000	0.750	0.250	0.000	0.000	0.075	0.925	0.075	0.925	0.000	
Clinton '85 (Genoa Nat'l. Htch., WI)	20	0.900	0.100	0.000	1.000	0.000	0.000	1.000	0.775	0.225	0.000	0.000	0.100	0.900	0.100	0.900	0.000	
Little Grassy '85 (Genoa Nat'l. Htch., WI)	20	0.800	0.200	0.000	1.000	0.000	0.000	1.000	0.900	0.100	0.000	0.000	0.025	0.975	0.000	1.000	0.000	
Little Grassy '85 (LaSalle Lake)	20	0.875	0.125	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.125	0.875	0.000	1.000	0.000	
Little Grassy '85 (LaSalle x Crab Orchard)	20	0.900	0.100	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.200	0.800	0.000	1.000	0.000	
Pierce Lake '85 (Adults)	17	0.805	0.195	0.000	1.000	0.000	0.000	1.000	0.917	0.083	0.000	0.000	0.000	1.000	0.000	1.000	0.000	
IP-Baldwin Lake '85 (YOY)	10	0.950	0.050	0.000	1.000	0.000	0.000	1.000	1.000	0.000	0.000	0.000	0.050	0.950	0.000	1.000	0.000	
Little Grassy '86 (YOY Prod.)	20	0.875	0.125	0.000	1.000	0.000	0.000	1.000	0.950	0.050	0.000	0.000	0.000	1.000	0.000	1.000	0.000	

Smallmouth Bass

One 1984 collection of smallmouth bass, Micropterus dolomieui, produced in a Baldwin Lake nursery pond and raised at Sand Ridge was analyzed in 1985. Another collection of fish produced at Cikana Hatchery, Indiana and raised at the Jake Wolfe Hatchery was also analyzed in 1985. Unfortunately, a collection of fish from the Neosho National Hatchery, Missouri which were stocked into Lake Michigan during 1985 was not obtained for genetic analysis. In addition, 5 populations of smallmouth bass were obtained from Georgia. Twelve loci were previously determined to be variable, and the resulting allele frequencies at these loci are listed in Table 13. Other loci examined but not variable included Adh-A, Gpdh-B, Ldh-A and B, Adh-M, A and B, Me-A and B, Idh-A, 6-Pgdh-A, Gapdh-A, Xdh-A, Aat-M, A, and B, F-dp-A, Pk-A and B, Ck-A and B, Ak-A, Ada-A, Ald-A and B, Fum-A and B, Tpi-A, Gpi-A and B, Est-B, D, and E, Cbp-A, and Prot-A, B, and C. These samples may represent potentially different genetic stocks since fairly large genetic differences were observed among them.

Table 14. Genetic variation among populations of smallmouth bass, Micropterus dolomieui.

Locus/ Allele		Sand Ridge '84 (Baldwin Lake Nursery Pond)	Jake Wolfe '85 (Cikana, IN Hatchery)	Georgia Populations (Reservoirs) Fontanta	Santeetlah	Hiwassee	Blue Ridge	Chatuge
N		20	20	20	9	20	20	20
Gpdh-A	1	0.475	0.000	0.000	0.000	0.000	0.000	0.000
	2	0.525	1.000	1.000	1.000	1.000	1.000	1.000
Sdh-A	1	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	2	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Ldh-C	1	0.500	0.675	0.500	0.611	0.625	0.925	0.850
	3	0.500	0.325	0.500	0.389	0.375	0.075	0.150
Idh-B	3	0.725	1.000	1.000	1.000	1.000	1.000	1.000
	4	0.275	0.000	0.000	0.000	0.000	0.000	0.000
Sod-A	2	0.850	0.550	0.625	0.778	0.575	0.775	0.525
	3	0.150	0.450	0.375	0.222	0.425	0.225	0.475
Ck-C	1	0.000	0.000	0.125	---	0.075	0.075	---
	2	1.000	1.000	0.875	1.000	0.925	0.925	1.000
Pgm-A	2	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	3	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Acon-A	1	0.375	0.175	1.000	1.000	1.000	1.000	1.000
	2	0.625	0.825	0.000	0.000	0.000	0.000	0.000
Mpi-A	1	0.950	1.000	1.000	1.000	1.000	1.000	1.000
	2	0.050	0.000	0.000	0.000	0.000	0.000	0.000
Est-A	1	0.775	0.925	0.700	0.944	0.750	0.900	0.825
	2	0.225	0.075	0.300	0.056	0.250	0.100	0.175
Est-C	1	0.775	1.000	1.000	1.000	1.000	1.000	1.000
	2	0.225	0.000	0.000	0.000	0.000	0.000	0.000

Crappie

The Little Grassy Hatchery produced black crappie (*Pomoxis nigromaculatus*) in 1985 from Baldwin Lake and Rend Lake brood fish. Interspecific F_1 hybrid crappie produced and reared by Dr. Homer Buck, Illinois Natural History Survey, were also obtained for analysis. Both black and white crappie were produced at Little Grassy Hatchery in 1986. These hatchery stocks were genetically examined at six gene loci known to be fixed for different alleles for black and white crappie. The results of these analyses are illustrated in Table 15. Our results indicate that the black crappie produced at the Little Grassy Hatchery were indeed pure black crappie, that the white crappie were indeed white crappie, and that the INHS hybrid crappies were indeed F_1's.

Table 15. Genetic variation among populations of black crappie, Pomoxis nigromaculatus, white crappie, Pomoxis annularis and their F_1 interspecific hybrid.

Locus/ Allele	Black: Little Grassy '85 (Baldwin and Rend Lakes)	Black: Little Grassy '86 (Production)	Hybrid: Little Grassy '85 (H. Buck, INHS)	White: Little Grassy '86 (Production)
N	20	40	20	20
Mdh-A				
1	1.000	1.000	0.500	0.000
2	0.000	0.000	0.500	1.000
Pgm-A				
1	0.000	0.000	0.500	1.000
2	1.000	1.000	0.500	0.000
Gpi-A				
1	1.000	1.000	0.500	0.000
2	0.000	0.000	0.500	1.000
Gpi-B				
1	1.000	1.000	0.500	0.000
2	0.000	0.000	0.500	1.000
Est-A				
1	1.000	1.000	0.500	0.000
2	0.000	0.000	0.500	1.000
ProT-A				
1	1.000	1.000	0.500	0.000
2	0.000	0.000	0.500	1.000

Bluegill

Bluegill sunfish, Lepomis macrochirus, have been produced at the Little Grassy and Jake Wolfe Hatcheries. For comparative purposes, a "wild" population (Homer Lake) was also examined in 1984. A total of 30 loci were examined and the resulting allele frequencies for variable loci are presented in Table 16. Additional loci examined but containing no variation include Adh-A, Gpdh-A, Ldh-A, B, and C, Mdh-A and B, Idh-A, Gapdh-A and C, Sod-A, Aat-A, B, and M, Ck-A, B, and C, Ak-A and B, Pgm-A, Ald-A and C, Gpi-A and B, and Cpb-A. These results indicate that there is little difference between these two stocks and that neither is contaminated by one of the southern subspecies.

Table 16. Genetic variation among populations of bluegill, Lepomis macrochirus.

Locus/ Allele	Little Grassy '84 (Traditional)	Little Grassy '85 (Traditional)	Little Grassy '86 (Traditional)	Homer Lake (Adults)
N	20	20	20	20
Sdh-A				
1	0.800	0.925	0.825	0.925
2	0.200	0.075	0.175	0.075
Idh-B				
1	0.550	0.500	0.575	0.725
2	0.450	0.500	0.425	0.275
6-Pgdh-A				
1	0.000	0.000	0.000	0.025
2	1.000	1.000	1.000	0.950
3	0.000	0.000	0.000	0.025
Xdh-A				
1	0.000	0.000	0.000	0.100
2	1.000	1.000	1.000	0.850
3	0.000	0.000	0.000	0.050
Est-A				
1	0.150	0.225	0.200	0.150
2	0.850	0.775	0.800	0.850

Redear Sunfish

Redear sunfish, Lepomis microlophus, have been produced at the Little Grassy and Jake Wolfe Hatcheries. Results of the analysis for the 1984, 1985, and 1986 collections for the nine loci expressing variation are given in Table 17. Those loci evaluated but found to contain no variation included Adh-A, Gpdh-A, Sdh-A, Ldh-A, B, and C, Mdh-Aa and B, Idh-A, 6-Pgdh-A, Xdh-A, Aat-M and A, F-dp-B, Pk-A and B, Ck-A, B, and C, Ak-A, Ald-A and B, Fum-A and B, Acon-A, Tpi-A, Mpi-A, Gpi-A, Est-A and B, Cdp-A, and Prot-B. Based upon previous experience with hybrids between this and other Lepomis species, we expected to observe a high level of variation within these populations, and did. Differentiation among batches, however, was small.

Table 17. Genetic variation among populations of redear sunfish, *Lepomis microlophus*.

Locus/ Allele		Little Grassy 1984	Little Grassy 1985	Little Grassy 1986	Jake Wolfe 1985
N		20	20	20	20
Gpdh-B	1	0.575	0.700	0.525	0.725
	2	0.425	0.300	0.475	0.275
Me-A	1	0.725	0.725	0.650	0.725
	2	0.275	0.275	0.350	0.275
Gapdh-A	1	0.875	1.000	0.975	1.000
	2	0.125	0.000	0.025	0.000
Sod-A	1	0.700	0.800	0.675	0.825
	2	0.300	0.200	0.525	0.175
F-dp-A	1	0.450	0.475	0.500	0.500
	2	0.550	0.525	0.500	0.500
Pgm-A	1	0.425	0.400	0.400	0.300
	2	0.575	0.600	0.600	0.700
Gpi-B	1	0.425	0.500	0.450	0.500
	2	0.425	0.500	0.500	0.500
	3	0.150	0.000	0.050	0.000
Prot-A	1	0.950	1.000	1.000	1.000
	2	0.050	0.000	0.000	0.000
Prot-C	1	0.950	0.950	1.000	0.925
	2	0.050	0.050	0.000	0.075

Channel Catfish

Channel catfish, Ictalurus punctatus, collected in 1984, 1985, and 1986, have been analyzed and the information for the observed nine variable loci is presented in Table 18. One stock of the 1984 fish sampled the non-vulnerable fish produced at the Little Grassy Hatchery in 1983. Samples of channel catfish have been collected from the Little Grassy Hatchery in 1985 and 1986, as well. Loci electrophoretically analyzed, containing no variation included Adh-A, Sdh-A, Ldh-B, Mdh-B, Me-A and B, Idh-A and B, Gapdh-A, Xdh-A, Sod-A, Aat-M and B, Pk-B, Pgk-A and B, Ck-A, B, and C, Ak-A and B, Ald-A, Fum-A and B, Acon-B, Tpi-A, Est-A, B, and C, Cdp-A, and Prot-A, A, and B.

Table 18. Genetic variation among populations of channel catfish, *Ictalurus punctatus*.

Locus/ Allele	Sand Ridge '84 (Little Grassy '83;non-vuln.)	Sand Ridge '84 (Powerton Lake)	Little Grassy 1985	Little Grassy 1985
N	20	20	20	20
Gpdh-A				
1	0.975	1.000	1.000	1.000
2	0.025	0.000	0.000	0.000
Ldh-A				
1	0.000	0.025	0.000	0.000
2	1.000	0.975	1.000	1.000
Mdh-A				
1	0.975	0.900	1.000	0.950
2	0.025	0.075	0.000	0.050
3	0.000	0.025	0.000	0.000
6-Pgdh-A				
1	1.000	0.975	1.000	1.000
2	0.000	0.025	0.000	0.000
Pk-A				
1	1.000	0.950	1.000	1.000
2	0.000	0.050	0.000	0.000
Pgm-A				
1	0.875	0.725	0.800	0.850
2	0.000	0.150	0.000	0.000
3	0.125	0.125	0.200	0.150
Acon-A				
1	0.400	0.500	0.525	0.500
2	0.600	0.500	0.475	0.500
Gpi-A				
1	0.975	0.975	0.950	0.925
2	0.025	0.025	0.050	0.975
Gpi-B				
1	0.675	0.675	0.600	0.575
2	0.250	0.300	0.250	0.400
3	0.075	0.025	0.150	0.025

Job 3. Establishment of a Genetic Analysis Service to Identify Unknown Fish or Fish of Questionable Classification

Objective: To provide for the State of Illinois a service by which individual fish of unknown, or hybrid composition or questionable classification could be identified.

Results: A variety of fishes have been obtained from IDOC and other sources for taxonomic identification. Four Morone individuals were obtained which had been questionably identified as pure white bass. Three of these fish would have qualified as new state records (2 in Illinois, 1 in Arkansas), and one would have qualified as a new world record. Following electrophoretic analysis, all of these fish were shown to be striped x white bass F_1 hybrids. Two Morone individuals taken from Collins Lake were confirmed to be F_1 hybrids and qualified as state records.

Three Lepomis from southern Illinois ponds have been genetically analyzed to determine suitability as new state record hybrid sunfish. Two were delivered to the NHS through Dr. Roy Heidinger of SIU and one through Don Garver, IDOC biologist. Electrophoretic analysis, however, showed that all of these fish were pure redear sunfish, not hybrids, and thus, not records. A potential state record redear sunfish (2 lbs. 10.5 ozs.) was obtained from Ray Fisher (DOC Biologist) and identified as indeed a pure redear sunfish. However, that record was subsequently broken. Unfortunately, the new record fish was not received by this laboratory for certification. This is particularly unfortunate because the great majority of fish obtained for verification prove not to be of record status.

Two Stizostedion from North Dakota were obtained for analyses and were thought to be either potential sauger world records or state line-class records. North Dakota holds the world record at 8 lbs. 12 ozs. The largest

fish (13-14 lbs.) was a saugeye and was too small for the saugeye record (state or world). The second fish (7-8 lbs.) was a sauger and proved to be a line-class record.

Study Conclusions:

1. Electrophoretic methods of stocks analysis are proving quite useful in compiling background genetic composition data.

2. For each species studied, polymorphic loci have been identified which can be used to construct genetically tagged stocks.

Recommendations:

1. These analyses be continued at the current level of coverage.

2. Analyses of certain species, particularly lake trout, which show little observable genetic variation in protein molecules, be expanded to include analysis of restriction endonuclease digestion fragment analysis of mitochondrial DNA.

LITERATURE CITED

Altukov, Yu, P. and E. A. Salmenkova. 1981. Applications of the stock concept to fish populations of the USSR. Can. J. Fish. Aquat. Sci. 38:1591-1600.

Brown, E. H., G. W. Eck, N. R. Foster, R. M. Horrall and C. E. Coberly. 1981. Historical evidence for discrete stocks of lake trout (Salvelinus namaycush) in Lake Michigan. Can. J. Fish. Aquat. Sci. 38:1747-1758.

Colby, P. J. and S. J. Nepszy. 1981. Variation among stocks of walleye (Stizostedion vitreum vitreum): Management implications. Can. J. Fish. Aquat. Sci. 38:1814-1831.

Hynes, J. D., E. H. Brown, J. H. Helle, N. Ryman and D. A. Webster. 1981. Guidelines for the culture of fish stocks for resource management. Can. J. Fish. Aquat. Sci. 38:1867-1876.

Ihssen, P. E., D. O. Evans, W. J. Christie, J. A. Reckahn and R. H. DesJardine. 1981. Life history, morphology and electrophoretic characteristics of five allopatric stocks of lake whitefish (Coregonus clupeaformis) in the Great Lakes Region. Can. J. Fish. Aquat. Sci. 38:1790-1807.

Krueger, C. C., A. J. Gharrett, J. R. Dehring and F. W. Allendorf. 1981. Genetic aspects of fisheries rehabilitation programs. Can. J. Fish. Aquat. Sci. 38:1877-1881.

MacLean, J. A. and D. O. Evans. 1981. The stock concept, discreteness of fish stocks, and fisheries management. Can. J. Fish. Aquat. Sci. 38:1889-1898.

Philipp, D. P. and G. S. Whitt. 1984. The production and evaluation of specific genetic stocks of largemouth bass (Micropterus salmoides) for different thermal environments. Final report, Federal Aid Project F-35-R. U.S. Fish and Wildlife Service, 265 pp.

Philipp, D. P., W. F. Childers and G. S. Whitt. 1981. Management implications for different genetic stocks of largemouth bass (Micropterus salmoides) in the United States. Can. J. Fish. Aquat. Sci. 38:1715-1723.

Philipp, D. F., W. F. Childers and G. S. Whitt. 1983. A biochemical genetic evaluation of the northern and Florida subspecies of largemouth bass. Trans. Am. Fish. Soc. 112:1-20.

Ryman, N., F. W. Allendorf and G. Stahl. 1979. Reproductive isolation with little genetic divergence in sympatric populations of brown trout (Salmo trutta). Genetics 92:247-262.

Schweigert, J. f., F. J. Ward and J. W. Clayton. 1977. Effects of fry and fingerling introductions on walleye (Stizostedion vitreum vitreum) production in West Blue Lake, Manitoba. J. Fish. Res. Bd. Can. 34:2142-2150.

Spangler, G. R., A. H. Berts and J. F. Koonce. 1981. Perspectives and policy recommendations on the relevance of the stock concept to fishery management. Can. J. Fish. Aquat. Sci. 38:1908-1914.

Utter, F. M. and F. W. Allendorf. 1977. Determination of the breeding structure of steelhead populations through gene frequency analysis. Pages 44-54 In T. J. Hassler and R. R. Vankirk, editors. Genetic implications of steelhead management. Calif. Fish. Res. Unit Spec. Rep. 77-1.