

WISCONSIN DEPARTMENT OF NATURAL RESOURCES
**Guidelines For The Genetic Management Of
Inland Fisheries In Wisconsin**

**Timothy Simonson, Brian Brecka, Paul Cunningham, Joanna Griffin, Joseph
Hennessy, Steve Hewett, Greg Matzke, Matthew Mitro and Todd Kalish**

Wisconsin Department of Natural Resources
Bureau of Fisheries Management
101 South Webster Street
PO BOX 7921
Madison, WI 53707-7921

and

Dr. Wes Larson

U.S. Geological Survey, Wisconsin Cooperative Fishery Research Unit,
University of Wisconsin-Stevens Point
Stevens Point, WI

Administrative Report #97

January 2022

Introduction

The management of Wisconsin fishes has a long history dating back more than one hundred and fifty years. Over this time, fisheries management has constantly been evolving. This evolution has been especially evident within Wisconsin's fish hatchery system with its continual advancements in science and technology. More advanced propagation techniques and renovations to the hatchery system have led to fish being produced more efficiently. In addition, a greater understanding of ecosystem needs and genetic conservation has dramatically increased the quality of the hatchery product and its return to the angler. All these advancements have led to revisions of management strategies for many of Wisconsin's popular fisheries. As such, management goals and associated stocking guidelines are periodically reviewed for many of the major fisheries in the state.

A legislative audit of the department's propagation program in 1997 prompted a consolidated review and description of our stocking practices, which included genetic management (WDNR 1999). This allowed a comparison of statewide needs with existing facility capacity, as described in an earlier report to the legislature (WDNR 1998). A 2009-10 review of our propagation system by consulting engineers prompted a revision and update of the 1999 report on stocking practices (Simonson et al. 2010). The "Aquaculture Bill" (2017 Wisconsin Act 21) prompted a review of the role and extent that genetics is involved in the department's fish stocking strategies and required subsequent promulgation of administrative rules that define the role of genetics in the management of Wisconsin's fisheries. While the 1999 and 2010 reports addressed the role of genetics in the department's fish stocking strategies, several scientific and technological advancements have occurred, and an updated review is warranted.

Species-specific stocking guidelines, which are developed and reviewed periodically by species teams within the Bureau of Fisheries Management, (1) provide information on the demand for cultured fish; (2) ensure the most efficient use of hatchery products when needed for management purposes; and (3) ensure the most prudent management of Wisconsin's exploited stocks and associated communities and ecosystems. Clearly, stocking cannot be considered in a vacuum.

Central to this and previous efforts was a consideration of the overall *management goals* for the various fisheries of the state. The ultimate success of any stocking activity should be judged based on its contribution to achieving those management goals. Species-specific stocking strategies outline where, how many, what size and types (e.g., genetic strain) of fish are needed to meet overall program goals. Considerable research has been done on the differentiation, fitness and performance of individual populations within a species (Philipp et al. 1983; Gharrett et al. 1988; Beachum et al. 1989; Krueger et al. 1989; Philipp 1991). The "stock concept" (i.e., managing individual breeding populations) has been bolstered with improved technology (ability to discern distinct genetic stocks; see Ryman and Utter 1987) and documentation of the superior performance of "locally adapted" populations (e.g., Philipp and Claussen 1995). The goal of this effort was to evaluate and update, where needed, genetic guidelines for stocking fish in Wisconsin waters. This report outlines which strains of fish should be raised and stocked to meet the overall management goals of the program.

GENETICS MANAGEMENT

Preserving the genetic integrity of native fish populations is a central goal of fisheries management in Wisconsin (i.e., do no harm). The three guiding principles of this management strategy are to (1) protect populations that are self-sustained through natural reproduction, (2) ensure that natural genetic boundaries are maintained, and (3) protect existing genetic diversity by developing management strategies that do not overexploit genetically distinct populations. Native and naturalized populations that are self-sustained through natural reproduction provide high-quality fishing opportunities in the state and are the most cost-effective to manage, and, if impacted or lost, cannot be replaced. Stocking should, first and foremost, be considered an important restoration tool used to reestablish naturally-reproducing populations and should never be conducted to the potential detriment of natural reproduction.

On the surface, all fish of a particular species may appear similar. However, each fish population is the product of thousands of years of natural selection that has led to a phenotype that is well suited (i.e., locally adapted) to its environment. The suite of fish populations found across a landscape can be considered a portfolio of population diversity. In other words, maintaining a diverse portfolio of locally adapted populations can buffer against environmental variability and is akin to the benefits of maintaining a diverse investment portfolio (Schindler et al., 2010). These benefits were empirically proven in Sockeye Salmon from Bristol Bay, where Schindler et al. (2010) and Hilborn et al. (2003) showed that the existence of thousands of locally adapted populations had created a sustainable fishery that is highly buffered from environmental variability.

Indiscriminate transfer and mixing of disparate populations negatively affect the genetic resources of a species by homogenizing genetic structure among populations (e.g., Hargrove et al. 2019). Genetic mixing of populations also decreases the genetic fitness of locally adapted populations through outbreeding depression (i.e., when genetically differentiated populations interbreed to produce inferior offspring, e.g., Goldberg et al. 2005; Philipp and Whitt 1991; Philipp et al. 2002). Griffiths et al. (2014) illustrated this point with a meta-analysis of salmon populations along the West Coast of the United States. Their study indicated that populations with larger hatchery influences and smaller portfolios of genetically distinct populations were more prone to large fluctuations in run sizes and fishery collapses. Individual fitness of different locally adapted strains has also been shown to be highly variable. For example, researchers from Illinois stocked bass from Florida, Illinois, Wisconsin and Texas together in four lakes. In each location the survival, growth and reproduction of the local fish were best (summarized by Philipp et al. 2002). In other words, nature had already produced the best-adapted fish for the local conditions. However, the few surviving transplants interbred with the locals and eventually, all the bass in the lakes were hybrids with inferior performance relative to the local stock, resulting in outbreeding depression. A similar experiment was conducted at a smaller scale by transplanting bass from two different watersheds in Illinois (Philipp and Claussen 1995). In this study, similar results were found: local stocks had better performance (growth and survival) and fitness (reproduction). These studies suggest that indiscriminate stocking of bass in waters with naturally-reproducing populations will likely result in more harm than good (see Philipp et al. 2002 for an overview).

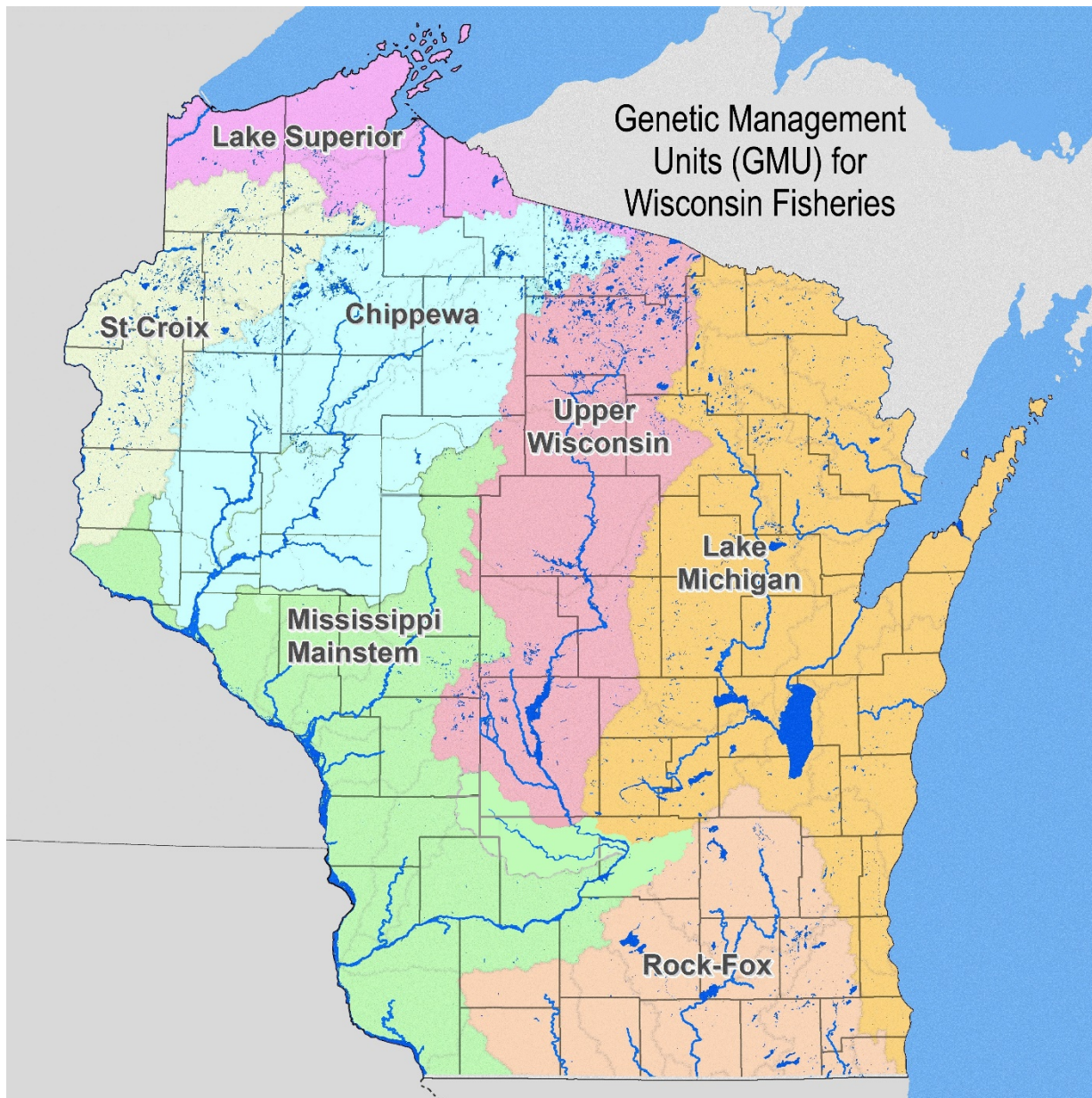
Creating species-specific genetic management plans requires three major phases: (1) conducting genetic analysis on wild populations to understand stock structure across the landscape, (2) identifying Genetic Management Units (GMUs), and (3) if stocking is required, designing a propagation strategy that preserves genetic diversity and integrity within GMUs. Genetic analysis of wild populations involves collecting samples from as many wild populations as feasible and using polymorphic genetic markers (e.g., microsatellites or single-nucleotide polymorphisms) to investigate levels of genetic differentiation and diversity across the landscape (Utter and Ryman, 1993). These studies have traditionally investigated neutral markers (i.e., markers that are not under selection) because they provide information on population size and connectivity and are thought to be a suitable proxy for adaptive differences. However, recent advances in genetic sequencing technology have facilitated the collection of genomic data from thousands of genetic markers that include both neutral markers and markers under selection (Allendorf et al. 2010). Data from markers under selection make it possible to directly assess adaptive differences and integrate them into management, an important development in conservation genetics that will likely become more common in the future (Funk et al. 2012).

Once data on genetic population structure are available, they are used to create GMUs that encompass genetically similar populations (reviewed in Funk et al., 2012). Finally, information on genetic population structure, reproductive biology and genetic diversity are integrated to construct a propagation plan that is logistically feasible and will do the best job possible of maintaining the genetic integrity and diversity of the species within each GMU (e.g., Jennings et al. 2010). These propagation plans outline broodstock collection protocols that include the minimum number of fish required to preserve genetic diversity, the specific locations from which brood fish can be taken and locations where the fish can be stocked. Genetic management plans constructed using this three-step approach have been or are being created for the following species in Wisconsin: Muskellunge, Walleye, Brook Trout and sturgeon. However, logistical and financial constraints have prevented the development of these protocols for species such as Largemouth Bass and Bluegill. For these species, the best approach is to leverage genetic data on other similar species and create management plans based on known barriers to gene flow, such as drainage boundaries.

GENETIC MANAGEMENT UNITS

We identified seven GMUs in Wisconsin based on available genetic data on differences in stock-structure from multiple species across the state. The units are Rock/Fox Rivers, Mississippi River Mainstem, Lake Michigan, Upper Wisconsin River (upstream of Kilbourn Dam), Chippewa River, St. Croix River and Lake Superior. Genetic data from Walleye, Muskellunge and sturgeon have demonstrated strong genetic differentiation between the Mississippi and Great Lakes drainages, suggesting that fish populations from these two major drainages have been isolated for thousands of years. Additionally, significant differences in genetic structure were observed between Muskellunge and sturgeon from Lake Michigan and Lake Superior, prompting us to create separate management units for each of these lakes. Significant differences in genetic structure among major tributaries draining into Mississippi River have been observed in Walleye, Muskellunge, Rock Bass and Johnny Darter, prompting us to create separate management units for the Rock/Fox Rivers, Upper Wisconsin River, Chippewa River and St. Croix River. However, data from Smallmouth Bass and sturgeon suggest that migration among the lower reaches of tributaries connected to the Mississippi River is relatively common. These data prompted us

to create a Mississippi River Mainstem genetic unit that encompasses the lower reaches of multiple Mississippi River tributaries. Additional genetic structure in multiple species certainly exists in many of these management units. However, these units represent a compromise that will help to maintain the genetic integrity of fish species across Wisconsin. These units do not represent a “one size fits all” approach. They can be modified, if necessary, for each species of interest (e.g., stocking Lake Sturgeon above the Kilbourn Dam because it is the only source of fish available for restoration efforts upstream from this historically natural barrier).



The primary threat to genetic integrity is the stocking/transfer of fish across GMU boundaries, resulting in outbreeding depression and the breakdown of locally adapted gene complexes that optimize stock performance (Philipp et al. 2002). In populations with limited natural reproduction (or potential for natural reproduction), stocking practices should help to conserve rather than reduce genetic structure among populations, as well as the diversity

that exists within populations; stocking should not occur in self-sustaining populations. Based on all available scientific information, we recommend a conservative approach to all species stocking (based on Fields et al. 1997), assuming the variety of studies conducted on the importance of genetics to fish propagation and stocking are generally applicable to all freshwater fish species. These recommendations for sources of fish, based on whether the species is native to the waterbody or GMU (based on Greene 1935) and the reproductive status of the population in the receiving water, are summarized in the table below.

Table of Stocking Decisions for Conservation of Native Stocks (from Simonson et al. 2010; modified from Fields et al. 1997). "NR" means natural reproduction; "GMU stock" means the broodstock originate from within the Genetic Management Unit of the receiving water.

STOCK ORIGIN	REPRODUCTIVE STATUS	RECOMMENDED SOURCE OF BROODSTOCK
Native To Waterbody	Self-Sustained Through NR	Fish Should Not Be Stocked
	Some NR; Not Self-Sustained	GMU Stock
	Extirpated (Rehabilitation)	GMU Stock
	Dependent On Stocking	GMU Stock
Introduced To Waterbody; Native To GMU	Self-Sustained Through NR	Fish Should Not Be Stocked
	Some NR; Not Self-Sustained	GMU Stock
	Dependent On Stocking; Or New Introduction	GMU Stock
Introduced To Waterbody; Not Native To GMU	Self-Sustained Through NR	Fish Should Not Be Stocked
	Some NR; Not Self-Sustained	Nearest GMU Stock
	Dependent On Stocking; Or New Introduction	Nearest GMU Stock

Stocking guidelines for fish species stocked in Wisconsin (by the Wisconsin Department of Natural Resources (DNR) and private sources) are presented in Section 620 of the Fish Management Handbook. Existing *Species Management Teams*, which include both internal and external partners, reviewed, revised and updated management goals and developed stocking strategies to ensure that the management goals are met. This report presents the "desired state" for our stocking program from the perspective of genetics management. It should be viewed as a working document that will undergo ongoing improvements and updates, which will typically be reflected in the department's stocking guidelines.

REFERENCES

- Allendorf, F. W., P.A. Hohenlohe and G. Luikart. 2010. Genomics and the future of conservation genetics. *Nature Reviews Genetics* 11:697-709.
- Beacham, T., C.B. Murray, and R.E. Withler. 1989. Age, morphology, and biochemical genetic variation of Yukon River chinook salmon. *Transactions of the American Fisheries Society* 118:46-63.
- Fields, R.D., M.D.G. Desjardins, J.M. Hudson, T.W. Kassler, J.B. Ludden, J. V. Tranquilli, C.A. Toline, and D.P. Philipp. 1997. Genetic analyses of fish species in the upper Midwest. Aquatic Ecology Technical Report 97/5. Illinois Natural History Survey. Champaign.
- Funk, W. C., J.K. McKay, P.A. Hohenlohe and F.W. Allendorf. 2012. Harnessing genomics for delineating conservation units. *Trends in Ecology & Evolution* 27:489-496.
- Gharrett, A.J., C. Smoot, and A.J. McGregor. 1988. Genetic relationships of even-year northwest Alaska pink salmon. *Transactions of the American Fisheries Society* 117:536-545.
- Greene, C.W. 1935. The distribution of Wisconsin fishes. Wisconsin Conservation Commission. 235 pp.
- Griffiths, J. R., D.E. Schindler, J.B. Armstrong, M.D. Scheuerell, D.C. Whited, R. A. Clark, R. Hilborn, C.A. Holt, S.T. Lindley, J.A. Stanford and E.C. Volk. 2014. Performance of salmon fishery portfolios across western North America. *Journal of Applied Ecology* 51:1554-1563.
- Goldberg, T.L., E.C. Grant, K.R. Inendino, T.W. Kassler, J.E. Claussen and D.P. Philipp. 2005. Increased infectious disease susceptibility resulting from outbreeding depression. *Conservation Biology* 19:455-462.
- Hargrove, J.S., M.W. Rogers, P.T. Kacmar, and P. Black. 2019. A statewide evaluation of Florida bass introgression in Tennessee. *North American Journal of Fisheries Management*.
- Hilborn, R., T.P. Quinn, D.E. Schindler and D.E. Rogers. 2003. Biocomplexity and fisheries sustainability. *Proceedings of the National Academy of Sciences* 100:6564-6568.
- Jennings, M. J., B.L., Sloss, G.R. Hatzenbeler, J.M. Kampa, T.D. Simonson, S.P. Avelallemant, G.A. Lindenberger and B.D. Underwood. 2010. Implementation of Genetic Conservation Practices in a Muskellunge Propagation and Stocking Program. *Fisheries*, 35(8), 388-395.
- Krueger, C.C., E.J. Marsden, H.L. Kincaid, B. May. 1989. Genetic differentiation among lake trout strains stocked into Lake Ontario. *Transactions of the American Fisheries Society* 118:317-330.
- Philipp, D.P. 1991. Genetic implications of introducing Florida largemouth bass *Micropterus salmoides floridanus*. *Canadian Journal of Fisheries and Aquatic Science* 48:58-65.

Philipp, D.P. and G.S. Whitt. 1991. Survival and growth of northern, Florida, and reciprocal F1 hybrid largemouth bass in central Illinois. *Transactions of the American Fisheries Society* 120:58-64.

Philipp, D.P. and J.E. Claussen. 1995. Fitness and performance differences between two stocks of largemouth bass from different river drainages within Illinois. *American Fisheries Society Symposium* 15:236-243.

Philipp D.P., J.E. Claussen, T.W. Kassler, and J.M. Epifanio. 2002. Mixing stocks of largemouth bass reduces fitness through outbreeding depression. *American Fisheries Society Symposium* 31:349–363.

Philipp, D.P., W.F. Childers and G.S. Whitt. 1983. Management implications for different genetic stocks of largemouth bass (*Micropterus salmoides*) in the United States. *Canadian Journal of Fisheries and Aquatic Science* 38:1715-1723.

Ryman, N. and F. Utter. 1987. *Population genetics and fishery management*. University of Washington Press, Seattle.

Schindler, D. E., R. Hilborn, B. Chasco, C.P. Boatright, T. P. Quinn, L.A. Rogers and M.S. Webster. 2010. Population diversity and the portfolio effect in an exploited species. *Nature* 465:609-612.

Simonson, T.D., L. Claggett, P. Cunningham, A. Fayram, J. Hennessey, W. Horns and K. Scheidegger. 2010. *A Review of Stocking Strategies in Wisconsin, With an Analysis of Projected Stocking Needs: 2010-2019*. Administrative Report 71, WDNR, Bureau of Fisheries Management, Madison.

Utter, F. and N. Ryman. 1993. Genetic markers and mixed stock fisheries. *Fisheries* 18(8): 11-21.

WDNR (Wisconsin Department of Natural Resources). 1998. *Production capacities of the Wisconsin Department of Natural Resources' Fish Propagation Facilities*. WDNR, Bureau of Fisheries Management and Habitat Protection, Madison.

WDNR (Wisconsin Department of Natural Resources). 1999. *Evaluation of Stocking Strategies in Wisconsin, With an Analysis of Projected Stocking Needs*. WDNR, Bureau of Fisheries Management and Habitat Protection, Madison.