WISCONSIN COOPERATIVE FISHERY RESEARCH UNIT

Annual Report
October 1, 2006 – September 30, 2007

COOPERATING AGENCIES

U.S. Geological Survey
Wisconsin Department of Natural Resources
University of Wisconsin – Stevens Point

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University of Wisconsin – Stevens Point

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MISSION STATEMENT
of the
Wisconsin Cooperative Fishery Research Unit

The Wisconsin Cooperative Fishery Research Unit has been an integral part of fisheries and aquatic science research and education in the College of Natural Resources at the University of Wisconsin – Stevens Point since 1971. The cooperators of this partnership include the U.S. Geological Survey, the Wisconsin Department of Natural Resources, and the University of Wisconsin - Stevens Point. The Unit objectives are to conduct world-class fisheries and aquatic science research of interest to cooperators, educate and train students at the Master's degree level in fisheries and aquatic sciences, and provide extension services in fisheries and aquatic resource management. Areas of study that have been emphasized by the Unit during the past 30 years include: fish biology; fisheries management; conservation genetics; fish habitat analysis, design, and modeling; stock identification and assessment; Great Lakes fisheries; limnology; integrated land-water linkages; aquatic toxicology; and aquatic entomology. The Unit has a special interest in understanding how ecosystem processes are altered by anthropogenic activities having conducted several multidisciplinary projects assessing linkages between aquatic and terrestrial environments, and how to conserve genetic resources across landscapes. Wisconsin Cooperative Fishery Research Unit studies have met and continue to meet the needs of the U.S. Geological Survey, the Wisconsin Department of Natural Resources, the University of Wisconsin - Stevens Point, the U.S. Fish and Wildlife Service, the U.S. Forest Service, the Great Lakes Fishery Commission, other agencies, and the public.

TABLE OF CONTENTS

PERSONNEL AND COOPERATORS.....1

Unit Coordinating Committee.....1
Cooperative Unit Staff
Permanent 1
Graduate Degree Candidates 2
Research Associates.....2
University of Wisconsin-Stevens Point Faculty Cooperators.....2
Wisconsin Department of Natural Resources Cooperators 2
International Cooperators 3
Federal Agency Cooperators 3
Private Organizations.....3
Other University Cooperators.....4
Other Cooperators.....4

PROJECTS

Continuing Projects

An evaluation of walleye (*Sander vitreus*) spawning potential in a north temperate lake 6

An ichthyofaunal study of Paleocene and Eocene fishes in the Sentinel Butte and Green River Formation.....7

Cooper's hawk genetic structure and parentage assessment.....8

Delineation of muskellunge genetic structure in northern Wisconsin 9

Development of a habitat quality index for littoral zones of north temperate lakes in Wisconsin.....10

Effects of managing riparian vegetation to increase the length of suitable trout water 11

Estimating strain contribution for lake trout naturally produced at Lake Michigan's mid-lake reef complex.....12

Fish community dynamics in Escanaba Lake, Wisconsin 13

Forecasting future riparian forest stand characteristics and sustainable contributions of riparian trees to littoral zone woody habitats in developing watersheds 14

Genetic concerns and paddlefish propagation.....15

Genetic analysis of North American yellow perch strains 16
Genetic assessment of the Humboldt River Lahontan cutthroat trout distinct

population segment....17

Genetic stock structure and genetic diversity of Wisconsin walleye....18

Lake sturgeon rehabilitation using stream-side rearing facilities....19

Spawning habitat selection of sympatric smallmouth bass and rock bass in two north temperate lakes: Habitat separation in space and time....20

Spawning strategies and impacts on the maintenance of genetic diversity in lake sturgeon propagation....21

The genetic impact of broodstock selection strategies in Wisconsin's wild trout stocking program....22

Tournament-associated mortality and the effects of culling in Wisconsin black bass tournaments....23

Completed Projects

Determining the response of macrophytes to human perturbation in the watersheds and along the lakeshores of small Wisconsin lakes....25

Genetic and demographic analyses of remnant Menominee River lake sturgeon: implications for rehabilitation and reintroduction....26

Stock structure identification of Lake Michigan lake whitefish using microsatellites and mitochondrial DNA....27

The impact of stocking on the genetic integrity of the walleye population in Escanaba Lake, Wisconsin....28

PEER-REVIEWED PUBLICATIONS **29**

TECHNICAL REPORTS **29**

SCIENTIFIC MEETING PRESENTATIONS **30**

COMPLETED GRADUATE THESES **32**

COURSES/LECTURES **33**

PROFESSIONAL AND FACULTY SERVICE BY COOPERATIVE **33**

SCHOLARSHIPS AND AWARDS **34**

PERSONNEL AND COOPERATORS

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Permanent

Michael Bozek	Unit Leader
Brian Sloss	Assistant Unit Leader
Andrea Musch	Unit Program Assistant

Project Staff Support

Ryan Franckowiak	Conservation Genetics Lab Manager

Federal (USGS)

Nancy Orlowske	Administrative Operations Assistant

Graduate Degree Candidates M.S. (* Indicates field analysis complete-thesis currently in progress) (Year indicates graduation)

Benjamin Cross
Jeremy Hammen
Michael Hughes*
Todd Kittel*
Benjamin Mann
Edward Murphy*
Andrea Musch*
Meaghan Proctor
Luke Roffler
Sara Schmidt
Brandon Spude
Jonathon Stoffregen
Craig Williamson*
Lauren Williamson*
Laura Canny (2007)
Joshua Raabe (2007)
Justin VanDeHey (2007)

Research Associates
Jesse Coleman
Preston Debele
Andy Janicki
Rachel Koehler
Jake Lindloff
Luke Schultz
Alex Smith

UNIVERSITY OF WISCONSIN – STEVENS POINT
FACULTY COOPERATORS

Eric Anderson	Associate Professor – Ecology
James Cook	Professor – Forestry Ecology
Ronald Crunkilton	Associate Professor –Aquatic Toxicology
Shelli Dubay	Assistant Professor – Wildlife
Christopher Hartleb	Assistant Professor – Fishery Science
Paul McGinley	Associate Professor – Water Resources
Robert Rosenfield	Professor – Raptor Ecology
Stanley Szczytko	Professor – Limnology
Eric Wild	Associate Professor – Biology
Bob Freckman	Professor – Biology

WISCONSIN DEPARTMENT OF NATURAL RESOURCES COOPERATORS

Heath Benike	Fisheries Biologist – Northern Region
Ron Benjamin	Basin Team Supervisor – LaCrosse Station
Ron Bruch	Basin Team Supervisor – Upper Fox River Team

Brad Eggold	Basin Supervisor – South Lake Michigan Fisheries Team
Edward Emmons	Section Chief – Aquatic Ecological Systems, Bureau of Integrated Science Services
Steve Fajfer	Operations Supervisor – Wild Rose Hatchery
David Giehtbrock	Assistant Coordinator – Statewide Propagation Program
Joanna Griffin	Assistant Fisheries Data Coordinator
Jen Hauxwell	Research Scientist – Bureau of Integrated Science Services
Steven Hewett	Section Chief – Fisheries Operations, Bureau of Fisheries and Habitat Protection
Steve Hogler	Fisheries Biologist – Lake Shore Team
Martin Jennings	Research Scientist – Bureau of Integrated Science Services
Al Kaas	Coordinator – Statewide Fish Propagation Program
Gary Kubenik	Research Technician – Bureau of Integrated Science Services
Tom Meronek	Fisheries Biologist – Wausau Station
Matt Mitro	Research Scientist – Bureau of Integrated Science Services
Dave Neuswanger	Fisheries Management and Habitat Protection-Upper Chippewa Team
Steve Newman	Research Scientist – Bureau of Integrated Science Services
Randy Piette	Research Technician – Bureau of Integrated Science Services
Paul Peeters	Fisheries Team Supervisor – Sturgeon Bay Fisheries Team
Dennis Pratt	Fisheries Biologist – Superior Station
David Sample	Research Scientist – Bureau of Integrated Science Services
Pat Schmalz	Staff Specialist – Fisheries Policy and Operations Section
Tim Simonson	Fisheries Lake Sampling Coordinator
Michael Staggs	Director – Bureau of Fisheries and Habitat Protection

INTERNATIONAL COOPERATORS

Andrew C. Stewart	British Columbia Environment, Lands, and Parks
Chris Wilson	Trent University; Ontario Ministry of Natural Resources

FEDERAL AGENCY COOPERATORS

Deahn DonnerWright	US Forest Service, Rhinelander, Wisconsin
Rob Elliott	US Fish and Wildlife Service, Green Bay, Wisconsin
Rob Klumb	US Fish and Wildlife Service, Pierre, South Dakota
Greg Moyer	US Fish and Wildlife Service, Warm Springs, Georgia
Robert K. Murphy	US Fish and Wildlife Service
Dave Potter	US Fish and Wildlife Service, Reno, Nevada
John Probst	US Forest Service, Rhinelander, Wisconsin
Chris Ribic	WI Cooperative Wildlife Research Unit, USGS
Wendylee Stott	US Geological Survey, Great Lakes Science Center

PRIVATE ORGANIZATIONS

Beaver Dam Lake Association
Wisconsin Electric Power Company

OTHER UNIVERSITY COOPERATORS

Neil Billington	Troy State University
Ed Heist	Southern Illinois University
John Janssen	University of Wisconsin – Milwaukee
Susan Knight	University of Wisconsin – Madison
Loren Miller	University of Minnesota
Michael A. Romano	Western Illinois University
Trent Sutton	University of Alaska-Fairbanks

OTHER COOPERATORS

Ed Baker	Michigan Department of Natural Resources
Dwayne Etter	Michigan Department of Natural Resources
J. Marty Holtgren	Little River Band of Ottawa Indians
Phil Schneeberger	Michigan Department of Natural Resources
Marc White	Riveredge Nature Center, Inc.
Phil Schneeberger	Michigan Department of Natural Resources

CONTINUING PROJECTS

An evaluation of walleye (*Sander vitreus*) spawning potential in a north temperate lake

Research Assistant: Lauren Williamson**,** M.S. Candidate

Principal Investigators: Michael Bozek

Funding Source: Beaver Dam Lake Association
Wisconsin Department of Natural Resources

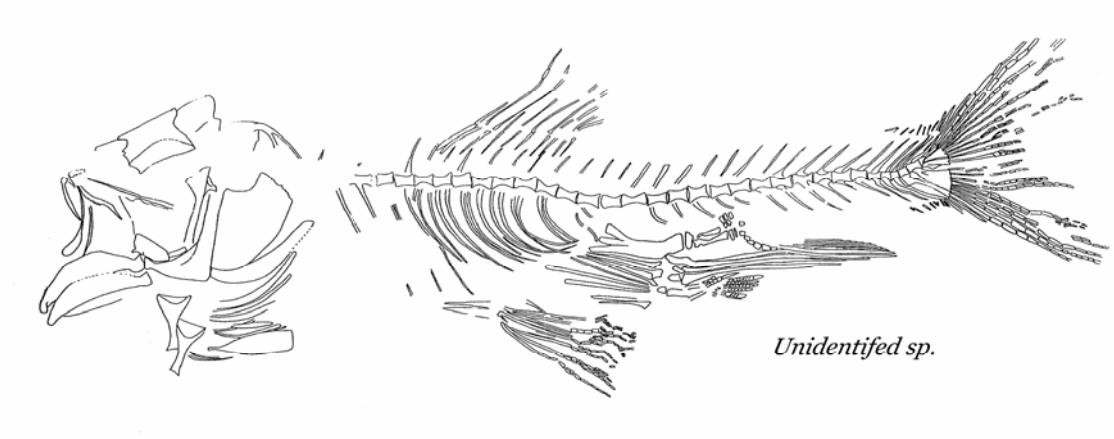
Poor spawning habitat can limit walleye reproduction in north temperate lakes and artificial spawning reefs constructed in an attempt to augment recruitment, have had limited success. Understanding the physical components of high quality natural spawning reefs could provide insight into why artificial reefs have failed and provide information crucial to protecting natural spawning sites and augmenting spawning in lakes with low recruitment. The objectives of this study are to: 1) quantify physical characteristics of high quality walleye spawning reefs in lakes with high natural recruitment, 2) develop a model that predicts spawning habitat potential in lakes, and 3) evaluate spawning habitat and predict the potential success of adding an additional artificial spawning reef in a lake with low recruitment. Two lakes in northern Wisconsin, Red Cedar and Big Crooked Lakes which have high natural recruitment, will be used to develop walleye spawning habitat models. Spawning habitat in a third lake, Beaver Dam Lake will be evaluated using those models to assess if spawning habitat is limited. To develop these models, data on walleye spawning and overall lake littoral zone habitat will be collected and analyzed in each lake. Spotlighting and SCUBA surveys will be conducted after ice-out to quantify distribution of spawning and extent of egg deposition by walleye in littoral zones. Survey quadrats will be placed along transects within egg deposition zones to characterize habitat on spawning reefs while transects will be placed randomly in sample lakes to quantify available habitat. Logistic regression will be used to create the spawning habitat models based on habitat data from used and available quadrats from Red Cedar and Big Crooked Lakes. Relative probability-of-use for each littoral zone quadrat will be assigned in Beaver Dam Lake using those models; histograms of the proportion of littoral zone sites having various spawning probabilities from 0-1.0 will be evaluated for the overall shoreline and the current artificial spawning reef. These models will also be available for use in evaluating the relative spawning potential of walleye in lakes across Wisconsin and to create a standardized methodology for evaluating walleye spawning habitat. By quantifying characteristics of high quality spawning sites using these models, the physical suitability of littoral zones in other lakes with low recruitment can be diagnosed and the need for potential habitat restoration can be determined.

An ichthyofaunal study of Paleocene and Eocene fishes in the Sentinel Butte and Green River Formations

Principal Investigator: Michael Bozek

Funding Source: University of Wisconsin – Stevens Point

We have been conducting paleontological research of Paleocene and Eocene fish from the Sentinel Butte formation in North Dakota and the Green River Formation in Wyoming, Colorado, and Utah. This research elucidates our understanding of the paleozoogeography and paleolimnology of the North American fish fauna and links extinct aquatic systems to extant systems. The identification of new fish species and their localities helps to reconstruct phylogenetic trees, paleoenvironments of aquatic systems, gives us a basis for understanding present fish distribution in North America, and provides data for interpreting population dynamics of extinct fish species. Our work has identified numerous new collection localities and several new species of fish are currently being classified, taxonomically. In addition, we have elucidated growth rates, asymptotic growth, and mortality rates for one species of osteoglossid and we are currently assessing a species of percid. For example, from the Sentinel Butte Formation (Paleocene) in North Dakota, our work has identified seven taxa of fish. Of these seven taxa, we have described a new osteoglossid (*Joffrichthys triangulpterus*) and identified a member of the pike family, *Esox tiemani*. Three new undescribed species of fish have been recovered from the site, one from the family Amiidae, while one new species represents perhaps a new family of the order Percopsiformes. This important find may provide direct physical evidence linking two fish families, Poeciliidae and Cyprinodontidae, which supports *a priori* postulations in the phylogenetic literature.



Cooper's hawk genetic structure and parentage assessment

Principal Investigator: Brian Sloss
Bob Rosenfield
Laura Rosenfield
Ryan Franckowiak

Funding Source: USGS
University of Wisconsin-Stevens Point

The Cooper's hawk (*Accipiter cooperii*) is a medium sized raptor found primarily in deciduous forests across North America. Three discrete populations are thought to occur in Wisconsin, North Dakota, and British Columbia. Migration and suspected gene flow across this range was expected to result in fairly low amounts of divergence between populations. Morphological/ morphometric assessment of hawks from the three populations showed population divergence and differentiation consistent with an east-west cline. Determining if the differences are the result of genetic divergence or the result of non-genetic, environmental influences will provide key information for the management and conservation of this species. To this end, we are conducting genetic research on numerous aspects of the Cooper's hawk's biology. Key issues addressed in this research include: 1) the phylogeography of Cooper's hawk across North America in conjunction with an east-west morphological cline, and 2) parentage assessment of a suspected multiple brood male bird from North Dakota.

Delineation of muskellunge genetic structure in northern Wisconsin

Research Assistant: Ed Murphy and Brandon Spude, M.S. Candidates

Principal Investigators: Brian Sloss

Funding Source: Wisconsin Department of Natural Resources

The muskellunge (*Esox masquinongy*) is a prized sportfish throughout its native range. Wisconsin contains >700 muskellunge populations providing a diverse array of angling experiences from high-density action waters to low-density trophy fisheries. The Wisconsin Department of Natural Resources' (WDNR) muskellunge management goals include maximizing angling opportunities while preserving genetic integrity. Historically, the WDNR has managed musky populations through regulations, such as daily bag limits and length limits, and a prolific stocking program. However, supplemental muskellunge stocking can have strong impacts on the genetic integrity of a population. The use of stocks when managing native populations minimizes risks to genetic integrity including outbreeding depression and introgression. Currently, the WDNR delineates genetic management units based on watershed boundaries and genetic data. The available genetic data showed low variation and little genetic structure resulting in a more-or-less default watershed delineation. To develop a more precise management approach, we used microsatellite genotyping and non-lethal sampling to identify genetic structure among naturally recruiting muskellunge populations in Wisconsin. The WDNR provided non-lethal fin clips from 39 naturally recruiting populations ($n \approx 50$/population) across the native range of muskellunge in Wisconsin. Microsatellite genotyping was conducted using a suite of 14 loci developed in our lab. Genetic stock identification showed an east-west split among populations not stocked since 1990. Two contemporary management units, the upper Chippewa River and the Lake Superior, failed to resolve suggesting historical genetic boundaries and contemporary watershed boundaries are not congruent for these two units. Further delineation and resolution of stock boundaries within the state will provide for more accurate and efficient management of Wisconsin's muskellunge resource.

Development of a habitat quality index for littoral zones of north temperate lakes in Wisconsin

Research Assistant: Sara Schmidt, M.S. Candidate

Principal Investigators: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Littoral zones can be structurally diverse among and within lakes and thus provide a wide array of habitat for a variety of aquatic organisms. However, little work has been done to conceptually integrate littoral zone habitats into generalized management applications. In particular, research on how complex littoral zone habitats are, on typologies to provide management frameworks, and understanding the functional relation between habitat diversity and biotic diversity are lacking. The objective of this study is to explore the concept of creating three-dimensional littoral zone fingerprints of lakes with the goal of exploring how they might be useful in a variety of management applications. We quantified littoral zone habitat in numerous north temperate lakes at using quadrats and transects. Depth, slope, size and percent substrate cover, plant type and cover, and coarse woody structure were visually estimated in square meter quadrats along 100 transects in each lake to a depth of 3m using snorkel and SCUBA. Three dimensional ordination of habitat features of lakes clearly shows the variation in habitat occurring within and among lakes including the abundance of simple, complex, rare, sensitive, and species-specific spawning habitats. Results reveal that patterns in littoral zone habitat are promising toward developing applied management tools for classifying, protecting and restoring littoral zone habitats in lakes.

Effects of managing riparian vegetation to increase the length of suitable trout water

Research Assistant: Benjamin Cross, M.S. Candidate

Principal Investigator: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Summer water temperatures limit the length of streams capable of providing suitable trout habitat in central Wisconsin. The heating of streams is the result of complex interactions of air temperature, relative humidity, wind speed, ground water input, solar radiation, stream width, depth, and velocity. Shade, provided by riparian vegetation, reduces solar radiation and may promote opportunities to decrease water temperatures before water reaches thermally marginal habitats. In fact, one trout stream management technique used in Wisconsin removes riparian trees and shrubs in exchange for managing riparian grasses. This is done presumably to increase primary production, decrease stream width, and increase stream depth. However, these manipulations also increase solar radiation affecting downstream thermal conditions. A key research gap involves understanding how much downstream trout habitat is being lost due to increased summer water temperatures as a result of the loss of riparian canopies. The purpose of this study is to fit a stream temperature model to central Wisconsin streams based on varying riparian vegetation treatments and subsequently use this model to predict the amount of stream capable of supporting trout populations based on known thermal preferences. This model will be used to predict potential trout habitat gains/losses due to manipulation of riparian vegetation and shade.

Estimating strain contribution for lake trout naturally produced at Lake Michigan's mid-lake reef complex

Research Assistant: Meaghan Proctor, M.S. Candidate

Principal Investigator: Brian Sloss

Funding Source: Great Lakes Fishery Commission

Historically, lake trout (*Salvelinus namaycush*) were abundant in Lake Michigan and supported a large commercial fishery. But the introduction of sea lamprey (*Petromyzon marinus*) combined with over-harvest of lake trout and habitat degradation contributed to the lake trout's extirpation from Lake Michigan during the 1950s. Since then, a restoration program has been developed which relies on stocking of multiple strains developed from either native Lake Michigan lake trout collected prior to extirpation or strains that occupy a habitat similar to native lake trout. The most commonly used strains are Seneca Lake (SLW), Lewis Lake (LLW), Green Lake (GLW), and Marquette (SMD). Despite intensive stocking, restoration efforts have shown limited success primarily attributed to minimal natural reproduction. Genetic assessment of lake trout eggs and sac fry has been used to determine the strains of lake trout that are most successfully spawning and hatching under natural conditions. Management agencies can subsequently focus their efforts on stocking the successful strains. Our objective was to determine the strain of origin for eggs and sac fry produced in the Fall 2006 on the Mid-Lake Reef Complex of Lake Michigan. We used seven microsatellite genetic markers and known genetic diversity from the four most common strains stocked in Lake Michigan. Data was analyzed using individual assignment tests, admixture and mixed stock analysis, and hybrid detection methods. Simulations were performed on all measures to assess the usefulness of various algorithms for predicting F_1 and F_x hybrids. The level of genetic diversity among the four strains at seven microsatellite markers appeared to allow moderate confidence in the assignment of lake trout to a single strain and limited accuracy in predicting F_1 or F_x strain hybrids.

Fish community dynamics in Escanaba Lake, Wisconsin

Research Assistant: Jonathan Stoffregen, M.S. Candidate

Principal Investigator: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

North temperate lakes represent a major ecological resource that provides economic benefits in northern Wisconsin. To ensure adequate protection of these resources, it is necessary to manage them using strategies based on scientifically valid information. Natural fish population size, reproduction, and recruitment, are highly dynamic and often fluctuate widely and unpredictably. Such population variability in combination with intensive harvest from state and tribal users greatly increase the risk of overexploitation and possible fishery collapse. The only effective way to measure natural variability in fish populations is by studying them for a long period of time. The Wisconsin Department of Natural Resources (then the Wisconsin Conservation Commission) established the Northern Highlands Fishery Research Area (NHFRA) in 1946. The DNR and the University of Wisconsin have conducted numerous research projects on NHFRA lakes, but the most valuable research has been the maintenance of several long-term databases. Angler harvest on all five lakes has been continuously monitored since 1946 and is thought to be the longest such record of compulsory creel data in the world. Intensive harvest of a key species such as walleye in Escanaba Lake may have significant ramifications on the entire fish community. Because of this, and because of increasing changes in fish habitat and water quality, there is an increasing need for multi-species and ecosystem management in Wisconsin. The joint WDNR-GLIFWC steering committee identified a need to better understand fish species interactions and to assess species other than walleye. Walleye, muskellunge, northern pike, and yellow perch currently comprise the majority of sport fish in Escanaba Lake. Smallmouth bass, largemouth bass, bluegill, and black crappie once major fish in the assemblage are all but absent now and rock bass and pumpkinseed are in a low abundance. Consequently, a high quality sport fishery for bass/panfish species has been lost. Analysis of data collected in this study and historical NHFRA data will be used to address this issue. Analysis of the long-term community dynamics in Escanaba Lake is necessary to improve the understanding as to why these changes have taken place. The objective of this project is to assess the long-term community dynamics of the fish assemblage of Escanaba Lake, Wisconsin. Knowledge gained will be very valuable to managers of sport fisheries and lake-ecosystems.

Forecasting future riparian forest stand characteristics and sustainable contributions of riparian trees to littoral zone woody habitats in developing watersheds

Research Assistant: Benjamin Mann, M.S. Candidate

Principal Investigators: Michael Bozek

Funding Source: US Department of Agriculture - McIntire Stennis

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Resource managers and biologists are beginning to understand the links between terrestrial and aquatic ecosystems and trees provide one important link. When riparian trees recruit into the littoral zones of lakes, they provide habitat for fish, invertebrates, reptiles, amphibians, etc. Natural (e.g. catastrophic wind-throw, disease outbreaks, fire, old age) and anthropogenic (logging, development) processes affect the sustained recruitment of trees to lakes and subsequently their use as habitat by fish and other aquatic organisms. The objectives of this study are to refine a model that forecasts the recruitment of trees to a north temperate lake, and assess how fish utilize these habitats, and assign relative values to these fish habitats. The riparian area and littoral zone around Katherine Lake, Wisconsin will be surveyed to collect data on riparian forest conditions and combine with previously collected data on woody structure in the littoral zone. A dynamic model will be created that integrates riparian forest dynamics with the recruitment of wood to the lake, the rate of wood decay, and use of wood by fish in this lake will be used to forecast tree recruitment and asses its value as habitat. This research will enable biologists and managers to determine if current land uses create conditions for the sustainable recruitment of wood to aquatic systems for animal species that use it.

Genetic concerns and paddlefish propagation

Principal Investigator: Brian Sloss

Funding Source: US Fish and Wildlife Service

The biology of the paddlefish (*Polyodon spathula*), like sturgeon, is not conducive to high levels of exploitation. Nevertheless, a number of small, tightly regulated yet highly popular paddlefish fisheries occur throughout its range. Numerous anthropogenic and biological changes in big river ecosystems over the past 100+ years (i.e., channelization, fragmentation, and introduction of exotics) coupled with current exploitation poses serious threats to the long-term viability of the species as a whole. Because the Missouri River forms a geopolitical boundary, an extensive propagation and management program exists as a cooperative effort between South Dakota Department of Game, Fish and Parks, Nebraska Game and Parks Commission, and U.S. Fish and Wildlife Service. This program is concerned with various factors including genetic implications of propagating cultured fish such as the source of broodfish, mating strategy, and the genetic diversity represented in broodfish and progeny. Our objective is to analyze the genetic diversity of broodfish, the sources of broodfish, and two additional populations of paddlefish from the Upper Missouri River to determine the efficacy of propagation practices. We sampled paddlefish from Lake Francis Case, Lewis and Clark Lake, broodfish used by the Gavins Point National Fish Hatchery in 2005 and 2006, and resulting progeny. All fish were genotyped at five microsatellite loci. Standard genetic diversity measures were calculated and comparisons were made across sample years and between sample sites. Diversity was assessed temporally from broodfish to fry to stocked fish to examine bias in survival due to hatchery conditions. This study will allow more efficient propagation of paddlefish in the Upper Missouri River system thus, improving our efforts to conserve this unique resource.

Genetic analysis of North American yellow perch strains

Research Assistant: Rachel Koehler, Undergraduate Research Assistant

Principal Investigator: Brian Sloss
Chris Hartleb

Funding Source: UW-Stevens Point
USGS

The North American yellow perch (*Perca flavescens*) has a wide distribution across the United States and is a commercially valuable species that is common in aquaculture settings. Within the aquaculture community it is believed there are northern and southern strains of perch differing in growth rate and, potentially, maximum size. It is unknown if this difference in growth is due to a longer growing season in the southern U.S. or to genetic differences between northern and southern fish. If differences in growth performance have a genetic basis, the use of the southern strain may help maximize the economic potential of northern perch culture. As a precursor to a garden-type experiment to evaluate growth rate, we assessed the genetic diversity of 14 yellow perch populations for genetic evidence of strains. Genetic variability was examined at six microsatellite loci for the different populations. Allelic diversity was significantly different between yellow perch populations from different geographic regions with southern yellow perch having significantly greater diversity. Measures of genetic differentiation between the populations suggest significant divergence between the northern populations and southern populations consistent with *a priori* geographic expectations. The observed divergence is consistent with the anecdotal evidence of strain differences in yellow perch.

Genetic assessment of the Humboldt River Lahontan cutthroat trout distinct population segment

Principal Investigator: Brian Sloss

Funding Source: US Fish and Wildlife Service

Lahontan cutthroat trout (LCT; *Oncorhynchus clarki henshawi*) is a federally-threatened species protected by the Endangered Species Act of 1973, as amended. A 1995 Recovery Plan developed by the USFWS has identified a goal of maintaining and enhancing existing populations in the Humboldt River Distinct Population Segment (DPS) in northern Nevada. The Humboldt DPS Team, consisting of fishery experts from federal and state agencies, has determined that this requires the establishment of functional metapopulations within each of nine subbasins in the upper Humboldt River. A major threat to this objective is the presence of non-native salmonids, which displace and hybridize with LCT. Many LCT-containing streams have evidence of hybridization between rainbow trout (*O. mykiss;* RBT) and LCT. However, the geographic extent of the problem is not known and isolated populations of pure LCT might exist in headwater areas. As these streams are targeted for lethal treatment (i.e., rotenone), which is the first step in LCT recolonization, genetic information linked to specific sampling locations are needed to determine treatment areas and avoid take of a listed species. The goal of this project to assess and map the genetic composition of LCT and LCT-hybrids in Segunda and Stewart creeks. Specific objectives include: 1) to determine the genetic purity and extent of putative introgressive hybridization within LCT populations from Segunda and Stewart Creeks using a combination of nuclear and mitochondrial genetic techniques, and 2) to develop a GIS-based distribution of genetic purity and potential hybridization within LCT populations from Segunda and Stewart Creeks. Management of genetically-pure LCT populations, if found, will include expanding current distributions throughout the remainder of these streams. Otherwise, LCT supplementation from donor streams will be necessary.

Genetic stock structure and genetic diversity of Wisconsin walleye

Research Assistant: Jeremy Hammen, M.S. Candidate

Principal Investigators: Brian Sloss
Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Maintaining genetic integrity in naturally recruiting walleye (*Sander vitreus*) populations is an explicit goal of the Wisconsin Walleye Management Plan. Genetic integrity implies a stability of temporal and spatial genetic characteristics of a population. To maintain the genetic integrity of walleye, it is necessary to understand the distribution of genetic diversity across the landscape. Our objectives are to: 1) assess the genetic diversity of 25-35 naturally recruiting walleye populations throughout the ceded territory of Wisconsin and 2) develop a stock structure model for the state based on this genetic diversity. Genetic diversity and population structure will be assessed through multi-locus, microsatellite genotyping of 50 fish per population. Subsequent genetic structure and stock assessment will follow a hierarchical approach known as genetic stock identification. Success in meeting these objectives will give managers a quantitative evaluation of genetic diversity within populations and allow better understanding of the spatial component walleye genetic integrity. Estimation of population genetic structure and the development of a genetic stock model for the ceded territory will provide a framework for efficient stock management of walleye populations. The continued implementation of walleye stock management coupled with well-defined genetic stock boundaries will provide for long-term maintenance of walleye genetic integrity.

Lake sturgeon rehabilitation using stream-side rearing facilities

Research Assistant: Luke Roffler, M.S. Candidate

Principal Investigators: Bradley Eggold, Steve Fajfer, Ed Baker, Robert Elliott, Steve Holger, Brian Sloss, Marty Holtgren, Marc White

Funding Sources: Great Lakes Fishery Trust
Wisconsin Department of Natural Resources

Lake sturgeon rehabilitation is currently a focus of many Great Lakes agencies. Strategies to increase their population have been identified because lake sturgeon populations are extremely small and believed to be a fraction of their historical abundance. Stocking of fish has traditionally been conducted in a manner where gametes are collected, hatched and reared at a hatchery and stocked into selected rivers. However, at the Great Lakes Lake Sturgeon Coordination meetings concerns were raised about straying and spawning site fidelity associated with traditionally raised lake sturgeon. Streamside rearing facilities (SRFs) have been identified as a method that may maximize the likelihood of imprinting and thus minimize the risk of straying of stocked fish. The main focus of this project is to expand our current knowledge and expertise on rearing lake sturgeon in SRFs. Four streamside rearing units will be built and deployed at four sites in the Lake Michigan basin: the Milwaukee and Manitowoc Rivers in Wisconsin and the Cedar and Whitefish Rivers in Michigan. The long-term goal of this project is to test the following hypothesis that is related to the usefulness of implementing SRFs for lake sturgeon rehabilitation: (1) streamside rearing facilities can be effectively used to rear lake sturgeon of suitable numbers, quality and size, and in a manner expected to facilitate their imprinting to the target waters, so that when used as part of a long term stocking program, will result in the successful rehabilitation of this species to tributaries of Lake Michigan; (2) production capabilities of the streamside rearing facilities (SRFs) are not significantly different than hatchery capabilities and are capable of rearing lake sturgeon that are suitable for reintroduction and rehabilitation of the species in tributaries of lake Michigan; and (3) SRF-reared lake sturgeon growth rates and condition factors are similar to those observed for hatchery raised and wild lake sturgeon so that fish reared in SRFs would be expected to survive in sufficient numbers after stocking to establish successful year classes that will mature and return to spawn naturally in the target rivers.

Spawning habitat selection of sympatric smallmouth bass and rock bass in two north temperate lakes: habitat segregation in space and time

Research Assistant: Andrea Musch, M.S. Candidate

Principal Investigators: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Smallmouth bass and rock bass co-occur throughout much of their range and are believed to be ecologically similar. As a result, they are often placed into the same functional guild in ecological analyses. However, no such formed analysis of their relationship has been conducted. Smallmouth bass and rock bass spawn in shallow water in the spring. Timing of spawning along with habitat used and relative availability of spawning habitat could create competition while spawning. This study evaluated the spatial and temporal overlap during spawning by sympatric smallmouth and rock bass in three north temperate lakes that have distinctly different littoral zone habitat compositions. The objectives of the study were to assess spawning habitat in relation to available habitat for smallmouth and rock bass, and to assess the degree of spawning separation occurring between rock bass and smallmouth bass. Spawning separation was evaluated in terms of timing of spawning, habitat used by both species, and habitat available relative to nest densities of each species for each lake. Locations of smallmouth bass and rock bass nests in lakes were surveyed every other day during the spawning season using snorkel and SCUBA gear. Initial date of egg placement was recorded for nests of both smallmouth bass and rock bass. Nest site characteristics were then quantified for nests. Littoral zone habitat was characterized along 100 randomly placed transects. Logistic regression was used to compare sites where nests of either species were found to random sites in the different lakes. Linear discriminant analysis was used to assess degree of habitat overlap between smallmouth and rock bass nest use. Both species tend to overlap in spawning time while some separation of spawning habitat has been observed based on microhabitat use.

Spawning strategies and impacts on the maintenance of genetic diversity in lake sturgeon propagation

Principal Investigator: Brian Sloss
Ron Bruch

Funding Source: Wisconsin Department of Natural Resources

Sustainable propagation and rehabilitation of lake sturgeon populations relies on the implementation of sound genetic principles in any broodstock management program. A central issue with genetic considerations of hatchery production is the mode and strategy of crossing males to females. Key questions in lake sturgeon propagation include: (1) how many adults need to provide gametes to ensure a reasonable level of genetic diversity; (2) what gamete fertilization strategy will produce the most diverse offspring; and (3) what are the segregation patterns of the standard mitochondrial and microsatellite markers used in lake sturgeon genetics analysis. Of central concern for lake sturgeon is a phenomenon known as sperm competition. When milt from multiple males is mixed prior to fertilizing the eggs from a female, the possibility exists that not all males will equally fertilize the same number of eggs. This disproportionate fertilization, sperm competition, is a major impediment to maximizing the effective population size and, subsequently, the genetic resources of lake sturgeon hatchery products. We are assessing the genetic contribution of three mixed milt families compared to *a priori* expectations of 20% fertilization by all males. The results of this study will be used to adapt the State of Wisconsin's standard protocols for fertilization.

The genetic impact of broodstock selection strategies in Wisconsin's wild trout stocking program

Research Assistant: Mike Hughes, M.S. Candidate

Principal Investigators: Brian Sloss

Funding Source: Wisconsin Department of Natural Resources

The popularity of native brook trout (*Salvelinus fontinalis*) among anglers has led to the development of an extensive management program by the Wisconsin Department of Natural Resources (WDNR). In 1995, WDNR began a wild trout stocking program aimed at improving the quality of hatchery-reared trout in southwestern Wisconsin. Ripe feral brook trout are removed from a stream, spawned at the hatchery, and then returned to their source waters. The hatchery-produced 'wild' progeny are subsequently stocked to support trout fisheries within the region. Ash Creek (Richland Co.) currently serves as the single source of broodstock for this program and was selected because it contains a healthy, naturally reproducing population. The large proportion of spawning fish, perhaps >50%, removed annually to support this program has raised concerns regarding the impacts on the viability of Ash Creek's trout population. Furthermore, previous genetic research has raised concerns as to whether the Ash Creek population is representative of southwestern Wisconsin populations. The three objectives of this study are: 1) Evaluate genetic and demographic impacts of Wisconsin's feral broodstock sampling strategy by comparing genetic diversity, and size distribution of Ash Creek brook trout with selected hatchery broodstock. Levels of genetic diversity will be measured and compared among hatchery-reared progeny and wild progeny to assess the impacts of differential reproduction to year-class production; 2) Evaluate the suitability of Ash Creek's population as a representative broodstock by characterizing regional patterns of genetic variation; and 3) Identify and evaluate alternative broodstock selection strategies to optimize diversity levels in stocked fish based on the proportion of the source population used as broodfish. Microsatellite DNA analysis will be used to assess levels of genetic diversity within and between the populations. The long-term value of the wild trout program is predicated on the production of trout that are healthy and vigorous. Loss of genetic diversity in the sole broodsource stream could threaten this health and vigor resulting in the eventual collapse of the program. The genetic data collected in this study is aimed at preventing such a collapse.

Tournament-associated mortality and the effects of culling in Wisconsin black bass tournaments

Research Assistant: Craig Williamson, M.S. Candidate

Principal Investigators: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Culling, or continuing to fish after reaching a creel limit is a common practice in bass fishing tournaments that occur in most states. In contrast, current Wisconsin fishing regulations state that any fish taken into an angler's possession and not immediately returned must be considered part of that angler's daily creel limit; the rule applies even to tournament anglers. In 2004, the Wisconsin legislature passed Act 249 which requires the Wisconsin Department of Natural Resources to establish a bass fishing tournament pilot program to evaluate the economic, sociological and biological impacts of culling in bass tournaments. The objective of this study is to quantify mortality rates (initial and 5 day-delayed) occurring as a result of tournament-induced stress and culling in particular. Two parallel studies will be conducted. The first study will quantify general characteristics of tournament angling, including angler catch demographics (e.g., live well characteristics/conditions, fish catch rates and times, degree of culling and holding times), tournament conditions (e.g., water temperature, pathogens, and weigh-in procedures), and subsequent mortality. The second study directly targets the effects of culling on mortality rates. This aspect of the project will be evaluated using simulated (i.e., controlled) angling and culling activities by volunteer anglers simulating culling that occurs during a tournament. Anglers will be given 5 bass to hold in their live wells and then will "cull" a bass at two hour intervals throughout the day. The "culled" bass will be held in holding pens based on the length of time they were held in a live well. These bass will be evaluated for initial and 5-day delayed mortality. We expect to find mortality rates of tournament-caught and tournament-culled bass to have a strong correlation with water temperature and presence or absence of largemouth bass virus (Family Iridoviridae) as has been seen in previous studies. Because peer reviewed tournament-associated mortality studies in the northern United States are scarce in literature, this study will help fishery managers better understand the biological impacts of bass tournaments held in the northern United States. Moreover, this study will also provide information to the Wisconsin Department of Natural Resources about effects of culling and bass mortality which can be used in any fishing regulation changes which may be implemented.

COMPLETED PROJECTS

Determining the response of macrophytes to human perturbation in the watersheds and along the lakeshores of small Wisconsin lakes

Research Assistant: Laura Canny

Principal Investigators: Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Some changes to aquatic plant communities have been attributed to the effects of human perturbations including agriculture, urban development, and direct removal of the plants. However, more research is needed to understand specifically how human perturbation affects macrophyte communities and to evaluate the effectiveness of using macrophytes as bioindicators. The objectives of this study are (1) to determine the effects human perturbations have on the distribution, diversity and density of aquatic macrophytes and (2) to quantify the environmental gradients and tolerance levels of individual macrophyte species. Macrophyte communities in approximately fifty Wisconsin lakes will be surveyed to determine species occurrence and relative abundance in the littoral zone. To determine the extent of regional variation, lakes will be chosen from two different ecoregions (Omernick et al. 2000): the Northern Lakes and Forests region and the Southeastern Till Plains region. Within these ecoregions, drainage, seepage and spring-fed lakes will be chosen along a gradient of development ranging from low (i.e. forested), to agricultural, to urban development at the watershed scale, and house density at the lakeshore development scale. Percent cover of each macrophyte species will be sampled using snorkel and SCUBA within 18 equally placed 0.25m^2 quadrats along 14 randomly placed transects. Half the transects will be placed at developed sites and half will be placed at undeveloped sites to determine effects of site-specific perturbations. The effects of watershed development (e.g. agriculture, urban), shoreline development, and direct removal of plants or plant communities from near-shore transects will be analyzed using regression analysis; analyses will assess effects human perturbation has on plants at the lakeshore and watershed levels. Macrophyte community data will also be compared to water chemistry data using regression analysis, resource selection functions, and canonical correspondence analysis (CCA) to determine environmental tolerance levels. It is expected that plant community structure will be significantly related to watershed development. Water quality data will be used to determine sensitivity of individual species across lakes to assess the value of individual species as bioindicators. The results of this study will be used to develop techniques that better protect our lake ecosystems.

Genetic and demographic analyses of remnant Menominee River lake sturgeon: implications for rehabilitation and reintroduction

Research Assistant: Todd Kittel, M.S. Candidate

Principal Investigators: Brian Sloss

Funding Source: WE Energies
Wisconsin Department of Natural Resources

Impoundments on large rivers fragment and impede fish populations, especially potamodromous fish such as lake sturgeon (*Acipenser fulvescens*). Fragmentation can result in numerous viability concerns regarding genetic and demographic issues. The remnant Menominee River lake sturgeon populations are the second largest conglomerate in Lake Michigan. River-locked populations spawn below White Rapids (WR) and Grand Rapids (GR) dams while the parental lake-run population spawns below the Menominee Dam (MD). These populations likely have small numbers of spawning fish dominating a given year's reproductive effort potentially resulting in the majority of offspring being related. Small, isolated populations lose genetic diversity through genetic drift and inbreeding. Compounded by lake sturgeon life-history (late maturity, intermittent spawning, and polygamous), loss of genetic diversity threatens short-term productivity and long-term viability. There are two objectives of this study: (1) characterize population structure and the distribution of genetic variation within and among river reaches and estimate gene flow between populations thereby assessing the effects of fragmentation and (2) determine the impact of fragmentation and small population size on viability and sustainability by assessing life-history measures of the river-locked Menominee River populations. A total of 678 lake sturgeon were captured during the 2005 spawning season via electrofishing and gillnetting. Length, weight, girth, sex, and a tissue sample were taken from each fish and then tagged with a passive integrated transponder (PIT tag) for recapture identification. Population estimates were calculated using the Schnabel method. Drift nets were deployed to collect larval sturgeon. Microsatellite genotyping was performed on 12 standardized loci. Analysis of genetic diversity and gene flow are underway. A low number of sampled larvae in 2005 (0 and 87 for WR and GR, respectively) may limit analyses of parental contribution. Efforts to identify other potential spawning sites are planned for 2006. Additional samples of age +1 individuals and larvae (2006 spawning season) as well as archived spine samples taken in 1978 (WR and GR) and 2001 (MD) will be added to the genetic dataset. This research will assist efforts to conserve genetic diversity and long-term viability of Menominee River populations and address immediate management concerns regarding fish passage.

Stock structure identification of Lake Michigan lake whitefish using microsatellites and mitochondrial DNA

Research Assistant: Justin VanDeHey

Principal Investigator: Brian Sloss

Funding Source: Great Lakes Fishery Commission

The lake whitefish (*Coregonus clupeaformis*) has comprised an important commercial fishery on Lake Michigan since the early 1800's. In 2000, lake whitefish was the leading Lake Michigan fish in total pounds harvested (4,793,087 lbs), and dollar value ($5,152,409 US). The lake whitefish commercial fishery is managed through the use of quotas and management units or zones rather than on a stock basis. There are concerns regarding the management of potentially shared stocks being commercially harvested by Michigan and Wisconsin state-licensed and native commercial fishing operations. Stocks represent the basic biological unit of focus for fish management efforts and, subsequently, stock discrimination is an integral part of sound, science-based, fisheries management programs. Previous studies indicated potential stock structure; however, questions still exist regarding the number, distribution, and discreteness of lake whitefish stocks in Lake Michigan. The first objective of the project is to determine the extent of lake whitefish microsatellite and mitochondrial DNA genetic diversity within and among putative lake whitefish spawning aggregates and determine the utility of these markers to discriminate among spawning stocks of lake whitefish. The second objective of the project is to describe the genetic population structure of spawning lake whitefish aggregates in northern Lake Michigan and Green Bay in terms of genetic stock identification and degree of stock isolation. I will be assessing the level of polymorphism of microsatellites and mitochondrial DNA to determine a combination of genetic markers adequate to delimit potential stocks. These genetic markers will be used to describe the genetic structure among spawning lake whitefish aggregates ($N \geq 4$) in northern Lake Michigan, Green Bay and several smaller spawning groups throughout Lake Michigan. Evidence of genetic stock identification and the degree of stock isolation in the form of genetic diversity, heterogeneity, and genetic divergence between the putative stocks will be determined. Identification and delineation of lake whitefish stocks in and around Lake Michigan will allow more efficient and effective management of this shared resource.

The impact of stocking on the genetic integrity of the walleye population in Escanaba Lake, Wisconsin

Research Assistant: Ryan Franckowiak

Principal Investigators: Brian Sloss
Michael Bozek

Funding Source: Wisconsin Department of Natural Resources

Supplemental stocking is a common fisheries management technique used to enhance self-sustaining walleye (*Sander vitreus*) populations by compensating for low or variable recruitment. The effectiveness of supplementation efforts for augmenting naturally recruiting populations has been questioned and concerns have been raised regarding the potential genetic impacts associated with these efforts. It has been argued that poor survival and relative fitness of introduced fish presents minimal risk to the genetic integrity and long-term viability of the recipient population. Few supplementation efforts, however, have been evaluated in terms of the genetic implications associated with the naturalization and successful reproductive recruitment of stocked fish. We used microsatellite DNA isolated from archived scale samples to determine the impact(s) supplemental stocking had on the genetic composition of the Escanaba Lake walleye population. Between 1954 and 1962, approximately 145,000 walleye fingerlings were stocked into the lake as part of a study to assess the feasibility of creating or enhancing a walleye year class. These supplementation efforts did not greatly augment walleye abundance in Escanaba Lake. Nevertheless, we observed a significant increase in allelic diversity (Wilcoxon signed-rank, $p < 0.05$) following supplementation resulting from the apparent influx of 18 alleles. The appearance of novel alleles is a strong indicator that introgression occurred between stocked and resident fish. Significant genetic divergence observed between samples collected pre- and post-stocking suggest that the supplementation efforts had a significant influence on the genetic composition of the Escanaba Lake walleye population despite minimal demographic impacts. Because of the potential genetic consequences associated with supplemental stocking, management initiative prescribing the use of supplemental stocking to achieve management objectives need to be critically evaluated.

PEER-REVIEWED PUBLICATIONS

Catalano, M.J., M.A. Bozek, and T.D. Pellett. 2007. Effects of dam removal on fish assemblage structure and spatial distributions in the Baraboo River, Wisconsin. North American Journal of Fisheries Management. 27:519-530.

Probst, J.R., D.M. Donner, and M.A. Bozek. 2007. Continuous, age-related plumage variation in male Kirtland's Warblers. Journal of Field Ornithology. 78(1): 100-108.

Rosenfield, R.N., J. Bielefeldt, L.J. Rosenfield, A.C. Steware, M.P. Nenneman, R.K. Murphy, and M.A. Bozek. 2007. Variation in reproductive indices in three populations of cooper's hawks. Wilson Journal of Ornithology. 119:181-188.

Rosenfield, R.N., T.G. Driscoll, R.P. Franckowiak, L.J. Rosenfield, B.L. Sloss, and M.A. Bozek.
2007. Genetic analysis confirms first record of polygyny in Cooper's Hawks. Journal Raptor Research 41(3):230-234.

Schrey, A.W., B.L. Sloss, R.J. Sheehan, R.C. Heidinger, and E.J. Heist. 2007. Genetic discrimination of Middle Mississippi River *Scaphirhynchus* sturgeon into pallid, shovelnose, and putative hybrids with multiple microsatellite loci. Conservation Genetics. 8:683-693.

Goerlitz, L.M. and M.A. Bozek. IN PRESS. The influence of ecoregion classification on fish species-area relations in inland Wisconsin lakes. The American Midland Naturalist.

Sloss, B.L., M.J. Jennings, R.P. Franckowiak, and D.M. Pratt. IN PRESS. Genetic identity of brook trout in Lake Superior south shore streams: potential for genetic monitoring of stocking and rehabilitation efforts. Transactions of the American Fisheries Society.

Sloss, B.L., R.P. Franckowiak, and E.L. Murphy. IN PRESS. Development of new microsatellite loci and multiplex reactions for muskellunge (*Esox masquinongy*). Molecular Ecology Notes.

Jennings, C.A., B.L. Sloss, B.A. LaSee, G.J. Burtle, and G.R. Moyer. ACCEPTED. Care, Handling, and Examination of Sampled Organisms and Related Tissues. In: A. Zale, D. Parrish, and T. Sutton, eds. Fisheries Techniques 3rd Edition. American Fisheries Society. Bethesda, Maryland.

TECHNICAL REPORTS

Bozek, M.A., and C.W. Williamson. 2006. Tournament-associated mortality and the effects of culling in Wisconsin black bass (*Micropterus* spp.) tournaments. Final Report to Wisconsin Department of Natural Resources. 67pp.

Sloss, B.L., and T. Kittel. 2007. Genetic analysis of remnant Menominee River lake sturgeon (Acipenser fulvescens) populations: implications for rehabilitation and reintroduction. Final Report to WE Energies Mitigation and Enhancement Fund. 39 pp.

Sloss, B.L., J.A. VanDeHey, T.M. Sutton, P. Peeters, and P. Schneeberger. 2007. Genetic structure among Lake Michigan's lake whitefish spawning aggregates. Final Report to Great Lakes Fishery Commission. 118 pp.

SCIENTIFIC MEETING PRESENTATIONS

Rosenfield, R.N., L.J. Rosenfield, R.K. Murphy, A.C. Stewart, W.E. Stout, and M.A. Bozek. October 2006. Comparative morphometry among three northern populations of breeding Cooper's Hawks. IV North American Ornithological Conference, Veracruz, Mexico.

Sloss, B.L. 2006. Fish propagation and genetic integrity: establishing realized impacts through historical DNA analysis. Seminar presented to the Department of Biological Sciences, Western Illinois University, Macomb, Illinois. INVITED

Sloss, B.L. 2006. Conservation genetics of propagation: examining impacts using historical DNA analysis. Seminar presented to the Department of Natural Resource Ecology and Management, Iowa State University, Ames, Iowa. INVITED

Franckowiak, R.P., N. Billington, R.N. Koigi, B.L. Sloss, J. Xiong, and W. Gardner. December 2006. Genetic structure of Upper Missouri River sauger (Sander canadensis). 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Hammen, J.J., B.L. Sloss, and M.A. Bozek. December 2006. Genetic diversity and recruitment dynamics of Wisconsin walleye. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Hughes, M.S., B.L. Sloss, and M.G. Mitro. December 2006. Genetic evaluation of broodstock selection and collection strategies for Wisconsin's wild trout stocking program. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Kittel, T.A., B.L. Sloss, J. Schenk, and A. Larsen. December 2006. Genetic and demographic analyses of remnant Menominee River lake sturgeon populations. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Koehler, R.A., C. Hartleb, B.L. Sloss, and R.P. Franckowiak. December 2006. Genetic analysis of North American yellow perch strains. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Mann, B.M., and M.A. Bozek. December 2006. Microhabitat use of submerged trees as fish habitat in a north temperate lake. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Murphy, E.L., B.L. Sloss, and M.J. Jennings. December 2006. Contemporary genetic stock structure of muskellunge in northern Wisconsin. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Murphy, E.L., B.L. Sloss, and M.J. Jennings. December 2006. Impacts of supplemental stocking in Wisconsin's muskellunge propagation program. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Raabe, J.K., M.A. Bozek, and S.P. Newman. December 2006. Spring wind and wave dynamics on a walleye spawning reef in a north temperate lake. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Sloss, B.L., R.P. Franckowiak, and R. Klumb. December 2006. Genetic management and paddlefish propagation in the Upper Missouri River. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

VanDeHey, J.A., B.L. Sloss, T.M. Sutton, P.J. Peeters, and P.J. Schneeberger. December 2006. Lake Michigan lake whitefish stock structure. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Williamson, C.W., M.A. Bozek, and M.J. Jennings. December 2006. Tournament-associated mortality and effects of culling in Wisconsin black bass tournaments. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Williamson, L.E., and M.A. Bozek. December 2006. Predicting walleye spawning potential in a north temperate lake. 67th Annual Midwest Fish and Wildlife Conference. Omaha, Nebraska.

Hughes, M., B.L. Sloss, and M. Mitro. January 2007. The genetic suitability and long-term viability of Ash Creek's brook trout population as a regional brood source for Wisconsin's wild trout stocking program. Wisconsin Chapter of the American Fisheries Society Annual Meeting. Milwaukee, Wisconsin.

Murphy, E., B.L. Sloss, and M. Jennings. January 2007. Impacts of supplemental stocking in Wisconsin's muskellunge propagation program. Wisconsin Chapter of the American Fisheries Society Annual Meeting. Milwaukee, Wisconsin.

VanDeHey, J., and B.L. Sloss. January 2007. Genetic structure among Lake Michigan's lake whitefish spawning aggregates. Wisconsin Chapter of the American Fisheries Society Annual Meeting. Milwaukee, Wisconsin.

Williamson, C., M.A. Bozek, B.L. Sloss, and M. Jennings. January 2007. Tournament associated mortality and the effects of culling in Wisconsin black bass (*Micropterus spp*) tournaments. Wisconsin Chapter of the American Fisheries Society Annual Meeting. Milwaukee, Wisconsin.

Williamson, L., and M.A. Bozek. January 2007. Assessing quality of spawning habitat for walleye (*Sander vitreus*) based on habitat characteristics in two northern Wisconsin lakes.
Wisconsin Chapter of the American Fisheries Society Annual Meeting. Milwaukee, Wisconsin.

Billington, N, R. N. Koigi, R. P. Franckowiak, B. L. Sloss, J. Xiong, and W. Gardner. March 2007. Population genetic structure of sauger in the upper Missouri River system. 68th Annual Meeting of the Association of Southeastern Biologists. Columbia, South Carolina.

Koigi, R. N., N. Billington, J. Xiong, B. L. Sloss, R. Francowiak, and W. Gardner. March 2007. Genetic structure of Montana sauger populations. 84th Annual Meeting of the Alabama Academy of Science. Tuskegee, Alabama.

Hammen, J.J., B.L. Sloss, and M.A. Bozek. June 2007. Genetic diversity and recruitment dynamics of Wisconsin walleye. North Central Division of the American Fisheries Society's Walleye Technical Committee Annual Meeting. Cloquet, Minnisota.

Sloss, B.L. and E.L. Murphy. July 2007. Muskellunge genetics research in Wisconsin: An update. North Central Division of the American Fisheries Society's Esox Technical Committee Annual Meeting. Woodruff, Wisconsin.

VanDeHey, J.A., B.L. Sloss, T.M. Sutton, P.J. Peeters, and P.J. Schneeberger. July 2007. Genetic structure among Lake Michigan's lake whitefish spawning aggregates. Lake Michigan Technical Committee Summer Meeting. Marinette, Wisconsin.

Billington, N., R. N. Koigi, B. L. Sloss, R. Francowiak, J. Xiong, and W. Gardner. September 2007. Genetic structure of Upper Missouri River sauger populations. 137th Annual meeting of the American Fisheries Society. San Francisco, California.

COMPLETED GRADUATE THESES

Canny, L.L. 2007. Determining aquatic macrophyte response to human perturbation in watersheds and along lakeshores of Wisconsin lakes and the tolerance levels of individual species to environmental gradients. M.S. Thesis. University of Wisconsin Stevens Point. 182pp.

Raabe, J.K. 2006. Walleye (*Sander vitreus*) spawning habitat selection and dynamics in a north temperate Wisconsin lake. M.S. Thesis. University of Wisconsin Stevens Point. 182 pp.

VanDeHey, J.A. 2007. Genetic structure among Lake Michigan's lake whitefish spawning aggregates. M.S. Thesis. University of Wisconsin Stevens Point. 118 pp.

COURSES/LECTURES PRESENTED BY COOPERATIVE UNIT STAFF

COURSES

Bozek	Fish Management Fish Habitat Analysis, Design, and Modeling Applied Multivariate Statistics in Fish and Wildlife Research Paleolimnology Field Course International Environmental Studies Seminar
Sloss	Ecological Genetics

GUEST LECTURES

Sloss	Conservation Genetics and Invasive Species, NRES/Water 324 – Invasive and Exotic Species; University of Wisconsin Stevens Point Conservation Genetics and Resource Management NRES 462/662 – Adaptive Resource Management; University of Wisconsin Stevens Point Metapopulations, Fragmentation and Genetic Diversity WL 840 – Metapopulations and other advanced topics; University of Wisconsin-Madison

PROFESSIONAL AND FACULTY SERVICE BY COOPERATIVE UNIT STAFF AND FACULTY COOPERATORS

BOZEK

American Fisheries Society—Resolutions Committee
University of Wisconsin-Stevens Point, College of Natural Resources—Graduate Committee
North American Black Bass Coalition Steering Committee

SLOSS

Genetics and Biodiversity Tech Committee, North Central Division of the American Fisheries Society 2002-Present. - Chair
North Central Division of the American Fisheries Society, 2004-2006 - Education Section Representative (elected)
Lake Michigan Lake Sturgeon Technical Committee - Member
University of Wisconsin-Stevens Point, College of Natural Resource Graduate Committee - Member
North American Journal of Fisheries Management - Peer Reviewer
Environmental Biology of Fishes - Peer Reviewer
Journal of Great Lakes Research - Peer Reviewer
Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative - Peer Reviewer

SCHOLARSHIPS AND AWARDS

Jeremy Hammen	2007	Worth Fisheries Scholarship
Mike Hughes	2006	UPDC Travel Grant
Luke Roffler	2006	Musky Alliance Scholarship
Justin VanDeHey	2006	UPDC Travel Grant
	2007	UPDC Research Grant
Lauren Williamson	2006	UPDC Travel Grant