

# MICRA Paddlefish Genetics Plan

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## Recommendations for Paddlefish Propagation and Stocking in Accordance with Conservation Genetics Principles

### Executive Summary

It is likely that for the near future, paddlefish will be stocked to preserve some fisheries in the Mississippi River basin and other selected adjacent river basins, as well as to preserve the species itself. Potentially, stocking can sometimes cause problems, the most serious of which are (1) the impact that stocking can have on the genetic make-up of recipient populations, and (2) the substitution of stocking for amending habitat degradation. It is the intent of this plan to set forth some recommendations that will allow management agencies to accomplish their stocking goals while protecting the species and its component genetic groups. Agencies do not have to go to extreme lengths to culture and stock paddlefish in an accepted manner that is best for the resource. **The common-sense approach is to use a local source for local stocking.** In the absence of a source large enough to culture the often-cited minimum of 25 adult pairs, the next step is to select the location of paddlefish that are expected to be genetically similar. Therefore, it is desirable to conduct an examination of the genetic variability at both mtDNA and nuclear gene loci in obviously different geographic sources of paddlefish. This method will provide a description of population distributions and allow us to devise management units for the species. Recommendations in this plan are designed to ensure that stocking preserves the species' remaining genetic diversity while providing for paddlefish fisheries at the same time.

### Introduction

#### Paddlefish Distribution

Paddlefish occupy a large range in the United States, occurring throughout the large river systems of the Mississippi River Basin and in other rivers emptying into the Gulf of Mexico in Texas, Mississippi, and Alabama. The native distribution of paddlefish has been reduced, although the species still occupies most of the historical range. However, paddlefish are no longer abundant in drainages other than those of the Mississippi River system. Studies of paddlefish movement have documented large spawning runs of 100 miles or more, indicating that fish exhibit a behavior that would eventually lead to genetic divergence among fish from different spawning sites. Genetic divergence endows each spawning unit with genetic variability that gives those fish the ability to adapt

to environmental conditions throughout a fish's life. It is logical that any stocking practice must consider the consequences of diluting or deleting a genetically unique source of variability.

The existence of demographically independent populations, or management units (MUs; see *Nielsen, J. L., editor. 1995. Evolution and the aquatic ecosystem: defining unique units in population conservation. American Fisheries Society Symposium 17, Bethesda, Maryland*), has been demonstrated for many fish species, but paddlefish population genetics studies have not been refined enough to identify MUs for that species. A management unit can be defined as a set of populations that exchange enough individuals between them to keep them statistically homogeneous but are functionally separable from other MUs. This term was developed to establish the appropriate geographic scale for managing populations. The suitability of this term may be debatable considering the geographic scale within which paddlefish exist. Paddlefish occupy a large-scale geographic range, at least in terms of North American freshwater fish. Sampling for genetic analysis may be difficult due to the continuity of habitat, making it hard to draw a line between individual MUs. There are dispersal barriers between the Gulf of Mexico tributaries, although paddlefish have migrated between drainages via brackish water. The best genetic data available for paddlefish (Epifanio et al., 1996, TAFS 125:546-561) indicate that there are two main genetic groups, the Alabama River drainage and the Mississippi River and Pearl River drainages. Those two groups could have been predicted without the genetic data, given that they are geographically separated. Detecting MUs within those two groups, however, can only be accomplished with a broadscale genetic study.

#### Examination of mtDNA and Nuclear Loci Variation

Migration between adjacent habitats is likely to be great enough to overcome local population declines but too low to compensate for widespread population reductions. For management purposes, this critical geographic scale can be defined as the distance over which genetic homogeneity is maintained and beyond which significant genetic heterogeneity is detected in either nuclear or mtDNA alleles. Population bottlenecks in recent years may have changed the allelic nature of some smaller populations. The intent of MU identification, however, is to allow us to draw lines between brood sources, and ample genetic information will still allow us to achieve that goal, despite recent changes in population structure.

#### Hatchery Input

The use of hatcheries to reduce population declines is not a substitute for solving the causes of declines. In addition to genetic considerations, stocking presents additional problems:

- (1) If budget constraints reduce stocking, the species will suffer without immediate relief of harvest pressures;
- (2) More wild fish are harvested when stocking increases fish available, unless only stocked fish are eligible for harvest;
- (3) Removing brood stock from small populations and stocking their offspring elsewhere when population levels are already dangerously low causes friction between management agencies and the public;
- (4) Protecting fish from selective forces by culturing young in a protected hatchery environment;
- (5) Altered hatchery fish can pass those alterations to closely related wild fish, diluting favorable traits;

- (6) Delaying habitat restoration, which may be the worst consequence of relying on stocking.

Stocking may give the impression of a suitable substitute for habitat management. Currently, at least nine state or federal stocking programs exist, and there likely will be no change to that trend in mitigating environmental problems by increasing organism numbers. If we continue to build hatcheries and stock fish to avoid changing what people do to destroy habitat or overharvest fish, we are essentially boosting abundance of commercial and recreational fishing after catastrophe has eliminated them from it.

There are considerations that can reduce the potential for negative interactions between hatchery-supported populations and native remnant populations. In the past, paddlefish hatchery programs overlooked the effects that human intervention in paddlefish reproduction could cause. To be successful, a stocking program must provide fish for an area or population, have a positive return for the money invested, and have as few negative impacts on the native population or residents as possible. This starts with maintaining as much of the natural genetic variation in a population as possible. Before the onset of any broodstock capture, several questions about the intentions of a propagation program must be answered in order to maximize success. The answers will determine the amount of emphasis that should be placed on broodstock sources, numbers, and genetic characteristics.

- (1) Is stocking intended to restore a native population or to supplement a recreational and/or commercial fishery?
- (2) Is there a reasonable chance that stocked fish will reproduce with remnant native fish?
- (3) Should these fish be genetically identifiable so that any gene flow to natural populations can be monitored?
- (4) Will there be a captive brood stock, or will adults be collected from the wild annually?

### **Recommendations**

The following are priorities for genetic conservation in paddlefish stocking:

1. Identify gene diversity using both mtDNA and nuclear loci. It is desirable to first identify gene diversity, and then to monitor hatchery and habitat effects on that structure. It is critical to design a genetic study that will likely be successful in diagnosing MUs but that will avoid over-sampling. By sampling an excessive number of individuals, or by sampling continuous habitat reaches, it becomes difficult to identify MUs at a level that is practical for hatchery practices. As a start, it is recommended that the following geographic localities are sampled. These sites correspond to those sampled in a previous genetic study. Additional localities can be sampled later if refinement in MU boundaries is required. It is also important to avoid oversampling in order to get a representative sample. Oversampling results from a non-random sample that may include a high number of family members, leading to a misidentification of localities as separate units when in fact they may be highly related. Tissue samples from fin should be preserved in a solution of 75% ethanol and 10% EDTA (0.5M, pH 8.0). Samples can be taken as fish are encountered, preferably during the spawn-

ing season. The samples can be kept in a normal freezer. It would be ideal to have 30 to 40 individuals from each locality.

**Table 1. List of potential collection localities for an in-depth study of mtDNA and nuclear DNA variation. River systems were selected using historic and geographic information.**

<u>Drainage</u>	<u>State</u>	<u>Location</u>
Alabama River	Alabama	Mouth of the Tombigbee River
Arkansas River	Arkansas	Lake Dardanelle
Ouachita River	Arkansas	
White River	Arkansas	Below Batesville
Neches River	Texas	
Mermentau River	Louisiana	
Red River	Louisiana	
Lower Mississippi River	Louisiana	Mouth of Red River
Upper Mississippi River	Iowa	Lock and Dam 14
Lower Missouri River	Missouri	Mouth of Osage/Below Bagnell Dam
Osage River	Missouri	Lake of the Ozarks
Ohio River	Ohio/Kentucky	Mouth of Kentucky River
Neosho River	Oklahoma	Miami to Chetopa, KS
Pearl River	Mississippi	Columbia
Pascagoula River	Mississippi	
Upper Missouri River	Montana North	Above Fort Peck Lake
Upper Missouri River	Dakota South	Above Lake Sakakawea
Middle Missouri River	Dakota	Lewis and Clark Lake to Chamberlain
Chippewa River	Wisconsin	Eau Claire
Wisconsin River	Wisconsin	Prairie du Sac

2. Use the allele frequency differences to establish MUs that are composed of similar populations showing nuclear or mtDNA divergence from other populations. It is likely that each of the above sampling locations will have a reasonably unique genetic structure (except for the proximal upper Missouri River locations), and each likely should be handled as a distinct MU. One way to check on the accuracy of MU identification is to resample localities in subsequent years. It may be difficult to verify disparate results between sample years at a given locality if stocked fish are sampled. The presence or absence of rare alleles provides a marker for verification.

3. Identify broodstock populations using genetic data or, in its absence, watershed boundaries, to be used for artificial propagation purposes. Broodstock handling procedures are as follows:

- (1) use proximal sources that are within identified MUs;
- (2) maximize the preservation of genetic variation by using the widely accepted minimum of 25 pairs of adults for a founding population (for restoration), although as few as 2-5 pairs can be used for supplemental stocking;
- (3) do not spawn individual fish more than once in 5 years; and
- (4) return brood fish to the wild.

It is recognized that most stocking is supplemental and will not require, on an annual basis, a large

number of adults. However, multiple year classes should comprise a large number of adults, on the order of 25 pairs over 5 years, for populations largely consisting of stocked fish. Equalizing the contribution of gametes from females can increase the effective number, so it is desirable to discard disproportionate surplus eggs from individual females. Avoid removing brood fish from small, remnant populations that will be supplementally stocked in order to maintain natural variability in years when the populations are not stocked.

4. Until MICRA has funds for genetic testing that can be used to adequately describe management units, do not stock outside of watersheds.

### **Summary**

Because of the decline of paddlefish populations in some portions of the native range, and because of renewed interest in preserving and restoring populations, MICRA recommends the following actions regarding paddlefish conservation:

- Conduct a population genetics study to define gene diversity within the species.
- Use results of the genetics study to define Management Units for the species.
- Identify broodstock populations to be used for artificial propagation purposes.