



# AMERICAN FISHERIES SOCIETY

## MONTANA CHAPTER

5646 Prospect Drive  
Missoula, MT 59808  
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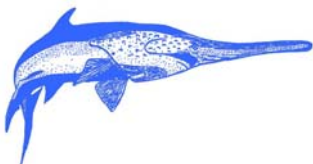
Dale Hall  
U.S. Fish and Wildlife Service  
1849 C Street, NW  
Washington, DC 20242

Dear Mr. Hall,

The Montana Chapter of the American Fisheries Society (MCAFS) is an organization of professional fisheries scientists and students from state, federal, and tribal management agencies, universities, and the private sector across Montana. Our objectives are: conservation, development, and wise use of Montana's fisheries; promotion of the educational, scientific and technological development and advancement of all branches of fisheries science and practice; and exchange and dissemination of knowledge about fish, fisheries, and related subjects. A primary interest to our membership is the long-term conservation of Montana's native fishes.

Given the endangered status of pallid sturgeon, recurrent failure to meet defined RPMA-specific stocking goals, and recent development of reliable genetic "marks," the MCAFS is very concerned with the apparent reluctance of the U.S. Fish and Wildlife Service (USFWS) to authorize stocking of physically unmarked fish. Prior to 2005, hatchery-reared pallid sturgeon that were too small to physically mark (< 70cm) to distinguish between hatchery and wild origin were not released and, as thinning occurred as fish grew to markable sizes, excess fish were destroyed rather than stocked even though defined stocking goals were not being achieved. However, recent findings by DeHaan et al. (2005) indicate that inherent genetic information can be used to reliably distinguish between hatchery and wild origin, which creates the opportunity to stock rather than destroy fish that are too small to physically mark.

We reviewed the report of DeHaan et al. (2005) addressing the use of microsatellite data for parental assignment of pallid sturgeon. Some of the primary objectives of the study were to determine how reliably hatchery produced fish could be assigned to family of origin when information from all possible parents was available and how well released juveniles could be distinguished from naturally produced juveniles using biochemical genetic data. In short, the answer is extremely well.



Dehaan et al. (2005) first determined the genetic characteristics (genotype) at 20 microsatellite loci of all 93 adult pallid sturgeon collected from 2000 through 2004. Based on the information from 17 of these loci, they found the multiple locus exclusion probability to be 0.996. That is, based on these 17 loci, an individual that was not a parent of another would be correctly identified as not being a parent better than 99% of the time.

DeHaan et al. (2005) also investigated how reliably the data could distinguish between hatchery and wild produced juveniles. Since wild juveniles basically do not exist, they used simulated populations produced from the data obtained from the 93 adults to address this issue. They generated three hypothetical populations. In one of these populations, 90% of the adults had been used to produce hatchery fish, in another 50% of the adults produced hatchery fish, and in the final one only 10% of the adults produced hatchery fish. For each of these three hypothetical populations, they assessed the reliability of using microsatellite data to distinguish hatchery from wild fish using a simulated sample of 1,000 juveniles from 100% to 0% hatchery fish in decreasing increments of 20%. The results indicated that in all cases the parents of the hatchery fish were correctly identified and that no wild fish were ever incorrectly assigned to hatchery parents. These simulations, therefore, strongly suggest that hatchery and wild pallid sturgeon can be distinguished and individuals of hatchery origin can very reliably be assigned to families even when a sample contains wild fish of unknown parentage.

Additionally, DeHaan et al. (2005) investigated how well fish could be correctly identified back to family of origin by blindly attempting to assign six individuals from each of six different families back to family. Again, this was accomplished with 100% accuracy.

Finally, the two primary factors that may detrimentally influence assignment accuracy, scoring errors and mutations, were investigated. Scoring errors appeared to exist in the neighborhood of one percent and the mutation rate appeared to be about  $1 \times 10^{-4}$ . Because of these small values, these factors are expected to have minimal overall influence on assignment accuracy for pallid sturgeon.

We strongly agree with the authors' conclusion that microsatellite data can successfully be used to "mark" pallid sturgeon. Results demonstrate that hatchery fish can be accurately assigned to family of origin and that hatchery fish can be distinguished from wild fish with a very high degree of certainty. There is no biological reason why such a marking program should not be adopted. If adopted, however, as the authors point out it will be imperative to continue to collect the microsatellite data from additional parents and before release make sure observed genotypes in families conform to those expected based on the genotypes of the parents. The latter is important to guard against the possibility that a mutation in a family may make a high proportion of individuals in it un-assignable to the

family and that these individuals may thus be incorrectly considered to be of wild origin.

Recent findings indicate that fish stocked as small as fry can contribute to pallid sturgeon recovery efforts (P. Bratten, USGS, Fort Peck, Montana, personal communication) and can be accurately traced back to hatchery origin using microsatellite data (DeHaan et al. 2005). Although USFWS approved the release of hatchery-produced fry into RPMA 1 in 2005, fry were not authorized for release into RPMA 2 because of concern about the reliability of genetic marks, thereby potentially compromising pallid sturgeon recovery efforts. Therefore, in the future, we recommend that excess hatchery-produced fry and fingerlings be made available and authorized for release into both RPMAs 1 and 2 with the understanding that they are genetically marked to distinguish between hatchery and wild origin in accordance with the Upper Basin Pallid Sturgeon Propagation Plan and draft Pallid Sturgeon Stocking and Augmentation Plan.

Thank you for taking our recommendations into consideration and please inform us of your proposed actions in remedying this situation.

Sincerely,

/s/ Kate Walker  
President, Montana Chapter AFS

#### Literature Cited

DeHann, D. W., D. E. Campton, and W. R. Arden. 2005. Genotypic analyses and parental identifications of hatchery-origin pallid sturgeon in the upper Missouri River Phase I: inheritance of microsatellite, nuclear DNA markers. Final Report, United States Fish and Wildlife Service, Abernathy Fish Technology Center.