



PARTNER COUNTRIES: Cambodia, Laos, Thailand, Vietnam

PROJECT: Stock structure of two important Mekong River carp species (*Henicorhynchus* spp.) (FIS/2003/003)

DESCRIPTION: Using molecular genetics to identify independent gene pools, biologists are tracking the size and health of fish populations

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Tracking fish genes

Urban growth in the Mekong River Basin threatens the fisheries that provide food security. A project aims to identify and strengthen the fish stocks

BY JANET LAWRENCE

Using molecular genetics, researchers are tracking the sustainability of key fish stocks that provide food security to 60 million people across the Mekong River Basin in southern Vietnam.

Rapid urban development in the Basin threatens the fisheries that provide food security, and despite their importance, management of these fisheries is rudimentary at best. Although the Mekong River Commission has initiated studies of a number of important fish species, the task is huge—there are about 1700 species native to the system.

Effective fisheries management requires an understanding of the scale at which fish populations are distinguishable from each other. However, in the first instance discrete breeding units (stocks) need to be identified and information gathered on their individual ecologies and life histories.

This is where researchers, via an ACIAR project, have made a start, using molecular genetics



to identify independent gene pools and therefore discrete stocks of two critical species. Armed with this information, biologists can track the size and health of a population over time and detect when it is under threat from overfishing or environmental changes.

Scientists from the School of Natural Resource Sciences at Queensland University of Technology (QUT) have been working with partners associated with the Mekong River Commission Fisheries Program in Cambodia, Thailand, Vietnam and Lao PDR on this project.

Project leader Dr Peter Mather of QUT says that the genetic methodologies for identifying discrete fish stocks have not been used as widely in the region as elsewhere, and the time is right to test their application for the Mekong. Work has begun to determine the patterns of genetic structure in two carp species, *Henicorhynchus siamensis* and *H. lobatus*, that are difficult to tell apart.

Dr Mather says observations of fish gathered in feeding grounds can easily lead to the misconception that all representatives of one species belong to the same population. Yet distinguishing separate groups within a mass of fish is critical in tracking their movements through the Mekong, he says.

“Two carp species were selected as models for the technology because they represent about half the fish caught in the river system,” Dr Mather says.

“Fisheries biologists have traditionally gathered information about discrete breeding populations by tagging fish and observing their movements. However, the genetic approach allows us to directly establish population boundaries.”

The project is attempting to establish the location, size and distribution of discrete breeding units. Scientists are using mitochondrial-DNA genetic markers—DNA sequences inherited solely from the mother—that can specifically connect a fish with a particular breeding population.

The team has studied populations of the two target species across the natural geographic range in the Mekong River Basin, buying samples from local fishermen and at local riverside markets. Pectoral fin clips taken from both species were prepared for sending to the Ecological Genetics Laboratory at QUT in Brisbane for genetic analysis.

In addition, whole fish were preserved and catalogued for morphometric analysis by collaborators at the Research Institute for Aquaculture No. 2 in Vietnam. This analysis enables the physical features of the fish to be correlated with their genetic make-up.

Dr Mather says that the interaction of the environment with the genotype of the fish can produce individuals with similar characteristics but different genetic make-ups (as had happened with the two species under study). Conversely, environmental differences



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can cause changes within similar genetic make-ups. For example, freshwater prawns can produce different numbers of spines on the rostrum on the head, depending on the level of salinity, he says.

Results for both species reveal population structure to varying degrees. For *H. siamensis* the data suggest that there are two genetic types in the Lower Mekong Basin (below the Khone Falls in Vietnam and Cambodia).

Whether the two genetic types interbreed is still to be determined. However, it is clear that *H. siamensis* individuals do not disperse upstream beyond the Khone Falls, as was thought previously.

In contrast, the Khone Falls do not act as a barrier for upstream dispersal of the other species (*H. lobatus*). The data for this species support recognition of a single stock throughout the main channel of the Mekong River from southern Vietnam to Lao PDR.

A genetically distinct population has been detected, however, in the Mun River. Research has shown that the two *H. lobatus* stocks are separated by the Pak Mun Dam near the confluence of the Mun and Mekong rivers, although the level of genetic divergence between them reflects a much older dispersal than the dam that now acts as a barrier.

Certainly, the genetic differences found there confirm that the scientists are dealing with separate stocks of *H. lobatus*, which therefore need management strategies tailored to their locations above and below the dam. This is the sort of definitive knowledge that scientists were hoping for. The research will help to boost the long-term management of these two Mekong River fish species, and will also be a model for future work on other species. ◀