



Using Rainforest Research

Fishy genes tell us about the past

August 1999

Freshwater fish are restricted to streams, rivers, lakes and small bodies of freshwater, offering scientists opportunities to investigate the effects of long-term isolation on the process of evolution. In the rainforests of north Queensland populations of fish in streams can be extremely isolated, due to physical barriers such as waterfalls, or highly connected where stream structures run continuously. In situations where fish are isolated there are opportunities over time for these populations to change and even become new species. The extent to which populations diverge is the result of a mosaic of evolutionary, ecological and genetic forces. How these forces interact is reflected in the genetic structure of populations, something which scientists can analyse.

Rainforest CRC PhD student, Dugald McGlashan is using genetic techniques to infer how evolutionary forces have determined population structure in three freshwater fish that inhabit north Queensland river systems. Dugald and his assistants capture fish from upland and lowland streams. At each site 30-40 fish are captured and frozen for transport back to the laboratory. By determining the differences in proteins and DNA they are able to assess variation within a particular population of fish as well as the variation between separate populations of fish.

Investigating the genetic patterns of fish in the streams of north Queens-

land's rainforests is useful on several counts: it helps us to unravel the complex geological events that have occurred in the region; it enables natural resource managers to understand the conservation of fish stocks and to make decisions when particular species suffer from local extinctions. It also enables other scientists to compare these results with similar research in other regions.

The hardyhead story

The flyspecked hardyhead (*Craterocephalus stercusmuscarum*) was one of the species chosen because it is small, plentiful and unlikely to have been transferred too often by humans—an activity which would obscure natural patterns of variation. They commonly occur above discontinuities

in the river profile such as waterfalls. The focus of this study was the Johnstone River system. Its headwaters are on the Atherton Tablelands west of Cairns running east towards the coast on either side of an old lava flow and exits at Innisfail, south of Cairns. Fish samples were taken throughout the Johnstone system, and also from other rivers in the area: the Barron, Russell-Mulgrave, Liverpool and Herbert.

At least three distinct groups of hardy-heads were found within the Johnstone River that had genetic similarities to populations from the other river systems in the study. Although they look very similar, there are huge genetic differences, equivalent to differences between *species* in some other animals.

How DNA Analysis helps determine evolutionary patterns

Dugald uses tail muscle from the fish to extract proteins and DNA from the mitochondria. He then analyses the protein from all samples and each capture site using special gels to which he applies an electric current. Since proteins have an electric charge they move through the gel, with different proteins moving at different rates. From the patterns of specially stained proteins, he can determine how many variants of a particular protein there are within and between the populations of fish he has collected.

The mitochondrial DNA extracted from the fish tail muscle provides the basis of another useful technique to examine genetic variation among the fish populations. Mitochondria are tiny organs found within every cell - they are the powerhouses of cells. Because they are inherited through the mother, mtDNA provides a more accurate picture of ancestry.

Dugald uses the mtDNA to determine how much change there has been in the order of the building blocks of DNA, specifically the ATCG bases which determine the unique character of each DNA strand. This helps to determine how long ago the changes took place, and how closely a population is related. The greater the change, the longer ago the populations separated.

Providing science for the conservation and management of Australia's World Heritage tropical rainforests.



COOPERATIVE RESEARCH CENTRE
FOR TROPICAL RAINFOREST
ECOLOGY AND MANAGEMENT





The Rainforest CRC is a research partnership involving the Commonwealth and Queensland State governments, the Wet Tropics Management Authority, the tourism industry, Aboriginal groups, CSIRO, James Cook University, Griffith University and The University of Queensland

How did this come about? Since fish populations from the Atherton Tablelands had very little in common genetically with those from lowland populations near Innisfail, it is unlikely they travel up waterfalls. Also, fish in lowland streams of the Johnstone River were genetically similar to other populations in adjacent lowland rivers, suggesting that coastal fish have a more recent common ancestor than upland fish. A startling discovery was the presence of two very different groups on the Atherton Tablelands. One of these groups was similar to fish living in the upper reaches of the Barron River, while the other group was very similar to populations in the upper Herbert River.

The implication is that although some populations are only kilometres apart geographically, they are millions of years apart in evolutionary terms. Conversely, while some populations are geographically separated in different river systems, we can use the genetic similarity of these populations to infer that they were once joined, meaning that some rivers used to flow in vastly different patterns to those of the present.

Conservation management implications

Management of any animal species or population attempts to ensure that natural processes which have occurred in the past to sustain that species or population can still occur. Also, it is generally agreed care

must be taken to avoid the unnecessary mixture of populations that have been separated for long periods of time. This is because isolated populations are evolving independently and become adapted to the conditions in which they live.

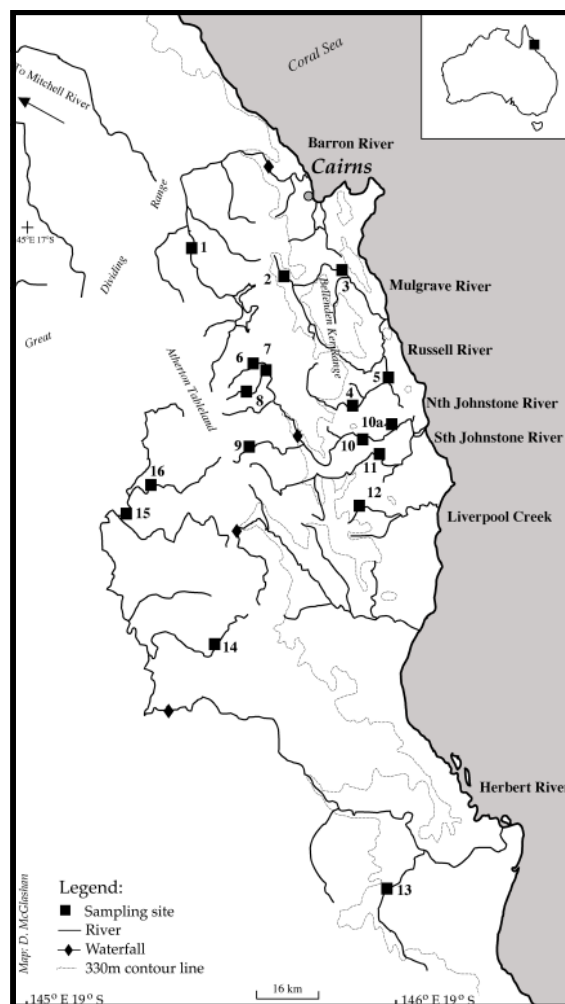
This study has shown that there are at least three independently evolving hardyhead groups within the Johnstone River, implying that there is no migration of individuals between the groups. Any local extinction of hardyheads in a section of the Johnstone River would probably result in them never returning to that particular stretch of river. However, areas have been identified that should be used in any restocking program, if it was ever necessary. The study also reveals that extreme caution should be taken to avoid any unnecessary movement of hardyheads, even between streams within the same catchment.

The Johnstone River of the Wet Tropics has a remarkable mix of hardyheads that have been evolving independently, probably for millions of years. Such divergences within the same system have rarely been documented, and these results suggest that the Johnstone River would be a vital cog in any conservation efforts of the Wet Tropics

aquatic fauna.

For more information about fish evolution, please contact:

Dugald McGlashan
Australian School of Environmental Studies, Griffith University
Nathan, Queensland 4111
Ph: 07 3875 3601 / 6660
Fax: 07 3875 7459 or E-mail:
D.McGlashan@mailbox.gu.edu.au



P.O. Box 6811, Cairns, Queensland, Australia 4870 • PHONE: (07) 4042 1246 • FAX: (07) 4042 1247
EMAIL: rainforestcrc@jcu.edu.au • WEBSITE: rainforest-crc.jcu.edu.au

