Gene pool management of hatchery Barramundi *Lates calcarifer* for production and stock augmentation programmes

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**INTRODUCTION**

The depletion of Australia's wild Barramundi *Lates calcarifer* fishery pre-empts two future roles for Barramundi aquaculture in Australia: first, the industry is primarily intended to supply meat upon a sustained basis; and second, it will probably serve as the predominant source of genetic material for the augmentation of those wild populations that have been depleted, and in that sense the process becomes somewhat circular and interdependent. This paper considers this relationship in the context of captive gene pool management and suggests an alternative method of conserving Barramundi genetic resources to be used to provide genetically "compatible" stocks for the two activities in conjunction with genetic improvement for commercial operations.

An understanding of the genetic structure of exploited fish species like Barramundi is essential for the development of appropriate fisheries management and the conservation of genetic resources. Strategies of gene pool management vary, depending on the biology of the species concerned and [particularly] the overall aim of the management programmes. For example, management of wild Barramundi fisheries should aim to maintain the genetic diversity of natural populations, whereas the aquaculturalist restricts the captive gene pool by selecting for favoured production traits. An immediate corollary appears to be that the management of wild and captive Barramundi populations cannot achieve satisfactory endpoints without detriment to one or the other, or perhaps both.

However, this is not necessarily the case; a diversified Barramundi aquaculture industry can serve as a provider of Barramundi flesh and of genetic material similar to those wild populations intended for replenishment, thus contributing to the conservation of the genetic diversity of wild Barramundi populations. Such gene pool management strategies represent an investment in a more diverse and sustainable future for both the wild fishery and aquaculture.

**MEASURING GENETIC VARIATION**

There are two primary methods of measuring genetic variation: one method is to begin with those physical characteristics that aquaculturalists consider important (e.g., growth rate, disease resistance, "meatiness", etc.), and to work backwards to determine if those phenotypes have a genetic basis (i.e., are heritable). The heritability of a trait is the proportion of variation in that trait which is due to genetic differences [more strictly additive genetic differences] between individuals. Identifying the heritability of quantitative traits has been sought for some time (e.g., Kinghorn 1983; Allendorf *et al.* 1987; Storfer 1996) and remains an urgent challenge.

The second method of measuring genetic variability goes directly to individual genes (segments of DNA) or their protein products. These gene "markers" do not usually influence quantitative traits of any importance, but are simply convenient to access by molecular genetic techniques. One of the most popular of these markers is mitochondrial DNA (mtDNA). Because it is rapidly evolving and maternally inherited, mtDNA can be very useful for identifying relatives of individuals and monitoring levels of inbreeding by determining the numbers of lineages (genotypes) in a population.

For the purpose of demonstration, tissue samples were collected from five fish from a Barramundi hatchery in Cairns and ten from a hatchery in Darwin. These fish were all first generation (F1) hatchery stock representing local wild fish. Fourteen wild fish were sampled from each of the Ord and Fitzroy Rivers in the Kimberley region of Western Australia. The results of direct DNA sequencing of a section of the mitochondrial genome (details are given in Doupê and Chandler 1998) of these fish are summarized in Table 1.

A total of 25 individual mtDNA genotypes among 43 fish were counted. Twenty genotypes were detected between the 28 Kimberley fish, whereas ten Darwin fish displayed only four...
genotypes, and the Cairns fish were genetically identical. This lack of genetic variation in the hatchery fish is also reflected in calculations of within-population nucleotide diversity, \( \pi \) (see Nei 1987), and shown in Table 1. The single genotype representing Cairns fish resulted in a diversity index of nil. The genetic diversity for Darwin fish was 0.005, which is three times less than the Fitzroy River samples and about 10 times less than samples from the Ord River (Table 1) (note, however, the large standard errors of the Kimberley samples).

Because Barramundi are highly fecund and protandrous hermaphrodites, aquaculturalists typically use very few broodfish (often 10 or less; Keenan 1995). A mature female can be expected to produce many millions of eggs each year (Davis 1984). Similarly, the highest performing males and fastest growing fish from production runs are often retained as eventual broodstock. Hatcheries are therefore practising phenotypic rather than genetic selection to provide the genetic basis for fingerling production. This results in comparatively few individuals "founding" the hatchery population and may explain the lack of diversity in fish from Cairns and Darwin.

### EFFECTS OF INBREEDING ON GENETIC VARIATION

A widely used measure of genetic variation is heterozygosity; the likelihood that a genetic locus contains different alleles in a diploid individual. Heterozygosity is decreased by inbreeding, or mating with relatives. Inbreeding increases with a small effective population size, as individuals are more likely to mate with a relative by chance. It has been demonstrated that the increase of inbreeding typically achieved by fish farmers is about 3-5% per generation, sufficient to counteract the benefits of mass selective breeding programmes (Tave 1989). The loss of heterozygosity by maintaining small effective population sizes in founding hatchery populations has long been thought a major contributor to the problems of propagating populations in artificial environments. Such problems include a reduction in fitness through inbreeding, and are often measured by a decrease in desired production traits like fertility or progeny viability, or by the poor performance of hatchery fish used to stock impoundments. Even where the F1 generation has displayed increased fitness, the available data invariably show a decrease in fitness in the following (F2) generation (Endler 1977). Periodic mixing of only 5-10% of populations in a salmon hatchery have shown that reductions of fitness might take many generations to recover (Emlen 1991). Recovery of genetic diversity would be expected to occur relative to the origins and amounts of new genetic material introduced to the population. The immediate remedy appears to be in selecting from larger numbers of periodically replaced broodstock.

### MANAGING GENETIC VARIATION: A ROLE FOR AQUACULTURE

Although the selection of superior traits in captive breeding and artificial selection by outcrossing has been accomplished in other forms of agriculture for many years, in fisheries aquaculture this has generally not been the case. This may be partly due to the high fecundity of most species. Beginning a selection programme with only a few broodstock and therefore a small effective population size does not provide the initial genetic diversity which is necessary to select for improved production traits. Hatcheries for aquaculture production should therefore start with a large number of broodstock to reflect the diversity of natural populations; selection among this diverse array of genotypes can then be made to genetically improve production traits (see for example, Engström et al. 1996; Gjerde et al. 1996).

The selection lines where genetic diversity is being decreased should be maintained separately from the genetically diverse nucleus broodstock for at least two reasons: first, the diverse nucleus broodstock can be used for periodic outcrossing with those selection lines to prevent a greater than anticipated rate of inbreeding, and hence a loss of productive fitness for desired food production traits; and second, the genetically diverse nucleus broodstock can be used as a basis to replenish wild stocks and for fishery enhancement programmes. This provides a secondary, but equally important role for the Barramundi captive breeding programme.

Hatchery-reared fish have been used to replenish the wild Barramundi fishery in the Cairns region for some years now, and if this sample reflects that practice, then the perception that aquaculture will offset the depletion of wild stocks is flawed if the populations that are used for these initiatives are genetically impoverished in the first instance [i.e., being the product of artificial selection
programmes using the same broodstock for successive generations]. Without redress, the genetic homogenization of the wild fishery is perhaps inevitable in the long term, with the hatchery acting as a genetic sink for wild broodstock, thus reducing by attrition the very population it was designed to enhance. Further, there are also implications for hatchery production, as the opportunity for prospecting alternative genetic material from local wild stocks must also be diminished.

CONCLUSION

Barramundi is a highly regarded sport and tablefish, and the recreational popularity of the species is expected to increase. The rise in northern Australian tourism, and the significant economic benefits of the recreational fishery across the region (see Griffin 1979; Rutledge et al. 1990; West et al. 1996) indicate that stopping the augmentation of wild Barramundi fisheries is not an option; it is likely to become a common management practice in many waterways as fishing effort increases. The alternative role for aquaculture is in providing genetically “compatible” stocks for these activities, and this role could be integrated with the provision of improved genetic stock for commercial farming operations.

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REFERENCES


