Topical issues in genetic diversity and breeding

Genes and Fish

Genetic impacts of translocations on biodiversity of aquatic species with particular reference to Asian countries

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Long term damage could result to aquaculture and to fisheries when translocations (or transfers or introductions) of aquatic species are haphazard. This article by Dr Nguyen T. T. Thuy and Professor Uthairat Na-Nakorn, explores some past and potential influences on the genetic diversity of aquatic fauna from translocations, focusing on genetic interactions that could be brought about. Some 30 years ago, Dr T.V.R. Pillay suggested that the era of haphazard translocations was over and that any future translocations will be better planned and evaluated. This has not yet happened; many nations and countries, signatories to international conventions included, continue to indulge in translocation of aquatic species for aquaculture and the pet trade, often based on the narrow objective of increasing production.

Fish species translocations, inadvertently or otherwise, have been taking place ever since humans started large-scale migrations. Most major human migrations were associated with movement of plants and animals that were familiar to the migrating communities. In the modern era, translocations of fish and other aquatic animals (as well as plants) has become more deliberate, carried out mainly for purposes of food production, as pets or for ornamental value, and even for control of noxious weeds and the like (Welcomme 1988). In addition to apparently purposeful translocations, unintentional and accidental translocations occurred and continue to be so even today. A major problem facing most maritime countries is translocations or accidental introductions associated with the discharge of ballast water, which is a subject on its own right (Crossman and Cudmore 2000)

Translocation is defined as the transfer of an organism, by human agency, from one place to another (Hodder and Bullock 1997). A number of synonyms are also commonly used, these being “introduction” or “transfer”. Translocation therefore includes the introduction of species into areas where they did not previously exist, and the movement of individuals or populations from one locality to another within the natural distributional range of the species (Doupé and Lymbery, 2000). The introduced species/populations are then referred to as exotic or alien species/populations. The use of the term “alien” came into prominence since its adoption by the Convention on Biological Diversity (CBD) (Convention on Biological Diversity, 1994), and is the preferred term of some international and national agencies.

The bulk of translocations of aquatic species have been primarily associated with fish food production. The overall success of such translocations as well as the impacts of translocations on native fauna have been reviewed by Welcomme (1988) and De Silva (1989). In general, most of these translocations have been a post World War I phenomenon and have been associated with aquaculture development in the world and the commercial pet trade. In 1977, Pillay suggested that the era of haphazard translocations was over and that any future translocations will be better planned and evaluated. This is still a long way from being realised; many nations, even though they are signatories to international conventions, continue to indulge in translocation of aquatic species for aquaculture and the pet trade often based on the narrow objective of increasing production.

In general, analyses and evaluations of translocation have been confined to direct, visible affects on the diversity of native flora and fauna. These include specific influences on the status of individual native species such as whether an alien species/ populations has affected the vulnerability of a species or a flock of species, such as for example the effects of the introduction of Nile perch (*Lates niloticus*) on the Haplochrominid cichlid species in Lake Victoria, Africa (Leveque, 1995). In addition, disease and parasite transmission associated with translocations also have been well documented (Dobson and May, 1986) and indeed in the recent times this aspect has been given much prominence particularly in respect of disease transmission associated with the shrimp aquaculture industry (Bondad-Reantaso, 2004). On the other hand, relatively unnoticed and paid scant attention to are the effects of translocations on the genetic make up of indigenous species/populations.

This article explores and documents some past and potential influences on the genetic diversity of the aquatic fauna, with particular reference to Asian countries, as wherever appropriate, resulting from translocations. It makes no attempt to evaluate ecological impacts of introductions apart from indirect genetic impacts on the native gene pools. Although generally not evaluated, in some areas these aspects have been dealt with (eg. Beverton, 1992; De Silva et al., 2004; Guerrero, 1999; Kudhongania et al., 1992; Welcomme and Vidthayanon, 2003, amongst others). The major focus here will be on genetic interactions that could be brought about through translocations.

Potential genetic effects of translocations

Genetically, translocations can be considered in two ways: (1) the introduction of an entirely new species into a new location/habitat, and (2) the introduction of new populations/ strains of species already present in that locality. The former is relatively easy to detect and the effects are generally more obvious (Beverton, 1992; Kudhongania et al., 1992; Welcomme and Vidthayanon, 2003). In contrast, the latter event is often difficult to recognise due to the lack of morphological differentiation between populations/strains within species. Also, more often than not, genetic data regarding population structure prior to translocations are not available and this makes it difficult, if not impossible, to conduct comparative studies on the changes brought about as a result of the translocation.

Introduction of exotic species/ populations into a new environment can alter the genetic composition of the native fauna in many different ways. Direct effects include reduced genetic diversity and outbreeding depression by hybridisation/introgression, and indirect effects are those related to reduced population size and changes of selective pressure due to ecological interactions such as competition, predation and disease transmission (Waples, 1995). Domestication for aquaculture can alter allele frequencies and reduce genetic variation and therefore also contribute significantly to the modification of genetic composition of the native fauna if these stocks are released for stock enhancement and/or escape from aquaculture operations.

Hybridisation and introgression

Hybridisation is interbreeding of individuals from genetically distinct populations, regardless of the taxonomic status of such populations (Harrison, 1993). Introgression is gene flow between populations whose individuals hybridise, and occurs when hybrids backcross with one or both parental populations. Hybridisation, however, need not necessarily be accompanied by introgression. For example, offspring of hybrids might all be sterile. Introgression can also be unidirectional, with backcrossing with one parental population only, but hybridisation can pose a threat to small populations even if gene pools do not mix. Hybridisation and introgression can be especially problematic for rare species when they are forced to interact with more abundant and dominant ones.

An example of loss of diversity of native species due to massive introgression has been reported for a number of trout species in Western US watersheds (Allendorf and Leary, 1998; Dowling and Childs, 1992; Leary et al., 1993). For example, rainbow trout (*Oncorhynchus mykiss*) hybridise easily and extensively with threatened Apache trout (*O. apache*) and endangered Gila trout (*O. gilae*). Now it is known that 65% of Apache trout have rainbow trout alleles and one native population is completely composed of rainbow trout. Comparable molecular studies are also available from Northern Italy with regard to domestic forms of brown trout (*Salmo trutta*), as well as from Poland with regard to *Coregonus pele* that have affected the native *C. lavaretus* in about 70% of lakes.

Although Asia has experienced a large number of translocations of aquatic species since the World War I (Welcomme, 1988; De Silva, 1989; Welcomme and Vidthayanon, 2003), and it is the leading continent in aquaculture production in the world, there is very little information available on Asian fish species with regard to genetic effects arising from hybridisation and introgression. To date, there is only limited numbers of genetic studies in this regard. Based on diagnostic alleles at six allozyme loci and one microsatellite locus, the study by Senanan et al. (2004) demonstrated that introgression of African catfish (*Clarias gariepinus*) genes into native *C. macrocephalus* has occurred in four wild and two broodstock populations in central part of Thailand. Later, Na-Nakorn et al. (2004) reported such introgression in 12 natural populations of *C. macrocephalus*; nine from Chaophraya river system, one from Mekong river system, two from the south; and a hatchery population. These observations indicate that the native gene pools of *C. macrocephalus* have been diluted and are threatened if no appropriate management strategies are undertaken. Similar problems may arise in Bangladesh through the use of hybrid *C. batrachus* x *C. gariepinus* for aquaculture (Rahman et al., 1995).

Hybridisation can also have a variety of effects on fitness of the resulting mixture of gene pools. Although hybridisation is known to produce heterosis this is more likely in the case of the two parental stocks that are not too different genetically. If genetic distance between the two parental stocks increases, genetic incompatibilities become more likely and fitness (usually in either fertility or viability) of hybrids declines (Waples, 1991). The assumption is that local adaptation leads to the possession by members of a population of a particular arrangement of alleles at different loci, called co-adapted gene complexes.

Hybridisation between two populations may lead to the breakdown of these complexes, resulting in reduced fitness. This effect has been demonstrated in pink salmon *Oncorhynchus gorbuscha* by Gharret and Smoker (1991) and little is known in the Asian context.

Indirect genetic effects

Any factors such as predation, competition and disease transmission from exotic species/populations can reduce population size of native species and would eventually lead to inbreeding and as a consequence result in loss of genetic diversity. Although inbreeding can only happen when the bottleneck is severe and lasts for many generations it has important long-term effects. In the short-term a significant reduction in population size can disrupt various demographic features of a population and may lead to extinction from severe perturbation in environmental conditions (Waples, 1991). One of the classic examples in this regards probably the introduction of the Nile perch, *Lates niloticus* into Lake Victoria in the 1950s. This introduction may have contributed to the extinction of up to 260 endemic fish species (Leveque, 1995).

In Asia, one of the worst documented negative effects on fish biodiversity has resulted from within country translocations, for example in Donghu Lake, Wuhan, China when the introduction of grass carp resulted in the decimation of submerged macrophytes and the consequent ecological changes brought about an upsurge of bighead (*Aristichthys nobilis*) and silver carps (*Hypophthalmichthys molitrix*) but also the disappearance of most of the 60 fish species native to the lake (Chen, 1989). The introduction of the Nile tilapia (*Oreochromis niloticus*) was also blamed to be the cause of the disappearance of the endemic species sinarapan (*Mistichthys luzonensis*) from Lake Buhi, Philippines (Gindelberger, 1981), although a recent analysis of the available evidence does not suggest so (De Silva et al., 2004). Also, there are anecdotal and unconfirmed evidence that tilapia (*O. mossambicus*) is a nuisance species in many countries. However, more recently, De Silva et al. (2004) evaluated the current status of tilapia introductions into the Asia-Pacific region and concluded that that there is no scientific evidence to confirm that tilapias have negatively influenced fish biodiversity in the region.

The presence of exotic species may also alter the genetic composition of native ones via the change in selective pressures, for example predation on certain phenotypes or competition on a certain kind of food. These changes are difficult to demonstrate. However, the potential for deleterious effects on native stocks is real and needs to be considered in the planning stages of any translocation events.

Effects of cultured stocks on wild populations

Genetic effects of translocations involving the movements of genetically distinct conspecific individuals, including the release/escape of cultured fish into wild populations have been well documented in the last decade, particularly in respect of salmonids in North America (Hindar et al., 1991). It is noted that the genetic make up of most cultured populations has often been altered through inbreeding, selective breeding, domestication and more recently through genetic modification such as transgenic (Beaumont and Hoare, 2003; Gjedrem et al., 1988) and all of these may affect gene pools of the corresponding wild populations.

When fish are removed from the natural environment and placed in a cultured environment, random genetic drift and domestication effects (new and greatly different selective forces act upon fish in the domestic environment compared to the natural environment) alter the gene frequencies and reduce genetic variation. Domestication reduces genetic variability in fish through both selective processes and random genetic drift.

One of the primary reasons for the large increases in Asian aquaculture production over the past two decades was the ready availability of artificially propagated seed stocks of major cultured species, such as of Chinese and Indian major carps, thereby enabling culture of these species to be independent of the wild seed supplies. The technical developments in artificial propagation led to the establishment of a specialised hatchery sector in the leading aquaculture production nations, include the establishment of backyard hatcheries that use simple technology but have been very successful. However, most of these hatcheries did not practise or rarely practised a turn over of the broodstock(s) from the wild. Poor management of breeding practices potentially lead to the reduction of genetic diversity of cultured stocks.

The limited number of studies available seems to indicate that extensive inbreeding has been occurring in hatchery-produced seed of major cultured species in Asia. Frequently, broodstock are derived from a small founding number and the number of broodstock kept is relatively small. In the Philippines, the commonly cultured "Israel" strain of Nile tilapia (*Oreochromis niloticus*), which is a major contributor to the annual production of over 90,000 tonnes, is derived from a single introduction of 100-200 fry, possibly from a single family, and this situation is similar in many countries in Asia (Pullin, 1988). Eknath and Doyle (1990) based on a study of 18 hatcheries in India demonstrated that there had been rapid inbreeding of stocks of six carp species (catla, rohu, mrigal, common carp, silver carp and grass carp). They estimated that the annual rate of inbreeding was from 2 to 17% per year. In a recent study by Deepak et al. (2004) the above observations were reinforced by a detailed analysis of hatchery stocks of three Indian major carp species. In Vietnam there is also evidence of inbreeding of grass carp. In a recent allozyme study on grass carp in Vietnam, collected from four major hatcheries, only one variable allozyme locus was observed out of 25 loci screened, thereby indicating low levels of genetic variability of the hatchery stocks (pers. obs.).

Increasing release of hatchery-bred individuals into the natural environment could bring about dilution of the native gene pools. In this regard, there appears to be emerging evidence in respect of Barbodes gonionotus in Thailand. A study of 12 natural populations and 29 hatchery stocks of *B. gonionotus* indicated that the natural variability was high (Kamonrat, 1996). Although there was high genetic variability within populations and significant genetic differentiation between populations of both wild and hatchery stocks there was evidence to indicate the possibility of loss or alteration of genetic integrity of both groups. For example, mixed stock sampling indicated that 75 to 96% of river samples were from hatchery populations, possibly resulting from consequences of restocking or stock enhancement programs. In this regard there was also evidence of reduction of genetic integrity between regions and it has been suggested that genetically based stock management policies are needed urgently.

Conclusion

It is clear that translocations have impacted on the aquatic fauna in Asia. The few studies done to date have provided significant warnings of the genetic effects of translocations of aquatic animals within the region. Any translocation event should be well planned with proper risk assessments. In the present context of development, ecology, disease aspects and management implementations that could arise from translocations need to be supplemented with genetic considerations of the particular translocation or stocking plan before embarking on a decision. In order to achieve this there is an urgent need to increase human capacity in molecular genetic techniques and their usage and application, and awareness building in the region on the issues discussed to help sustain the aquaculture industry and in aquatic resource management. Genetic information will provide an additional and a useful tool to ensure that environmental integrity and biodiversity are sustained in the long term.

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