

## Genetic diversity of common carp (*Cyprinus carpio* L.) in Vietnam using four microsatellite loci

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### Abstract

Four highly variable microsatellite loci were used to investigate genetic diversity and population structure of common carp in Vietnam. A total of 968 fish were genotyped representing three groups comprising: three experimental lines from the Research Institute for Aquaculture No 1 (Bac Ninh); 11 hatcheries; and six wild populations from rivers and reservoirs giving 72 alleles over all loci. The mean number of alleles, per locus per population ranges from 4.25 to 11.00 and the mean observed heterozygosity at the four loci ranges from 0.40 to 0.83. An analysis of the distribution of genetic variation indicated within population variation is very high (90.6%), while among populations within groups and among groups is low (5.0% and 4.5% respectively). Highly significant deviations from Hardy–Weinberg, mostly due to deficits of heterozygotes, were found in both experimental and hatchery groups suggesting either inbreeding or recent stock mixing. Wild common carp populations exhibited more genetic diversity than cultured populations in term of allele richness and observed heterozygosity. Results from assignment tests for the 20 populations of carp indicated that the experimental common carp lines can be largely distinguish from one another and that mixing between indigenous and introduced carp is occurring in hatcheries and possibly also in wild populations. Multidimensional Scaling (MDS) and UPGMA analyses show that the experimental Vietnamese white carp line is closely related to wild common carp populations; the hatchery stocks are mostly closely related to the experimental Indonesian yellow carp line but with evidence of some mixing; and the domesticated Hungarian population is highly divergent and not closely related to any other carp populations. © 2007 Elsevier B.V. All rights reserved.

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### 1. Introduction

The understanding of genetic diversity is one of the most important steps in managing fisheries resources and aquaculture selective breeding programs (Beaumont and Hoare, 2003; Dunham, 2004; Ward and Grewe, 1995).

Aquaculture practices may inadvertently decrease the genetic variability present in farmed stocks by breeding among related individuals or by the use of small numbers of founding broodstock. Selective breeding programs can also lead to decreased diversity when they utilize only a small number of “superior” families that may be related or use a mass selection approach with high selection intensities. Unless pedigree records are maintained, there is often a probability of selecting related individuals as parents for

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constructing the next generation and thereby increasing inbreeding (Norris et al., 1999).

Conversely, breeding programs may deliberately introduce divergent stocks and utilize crossbreeding programs to increase diversity and productivity (Hulata, 1995). However, the extent of stock mixing, the relative survival of the different stocks and the extent to which they are disseminated are important issues that frequently need to be addressed for effective management of aquaculture species (Dunham, 2004). There is also often a need to evaluate the status of wild stocks in aquaculture species as escapes of aquaculture stocks are common and these fish can have negative effects on resident indigenous forms (Cross, 2000).

Many of these issues apply to the common carp, *Cyprinus carpio* L., arguably the most important and oldest cultured fish species in the world, and providing a valuable source of protein especially in rural communities in many developing countries. The species has been widely translocated both within and outside its natural range leading to uncertainties concerning the genetic quality and origin of domesticated stocks and the status of wild populations (Kohlmann et al., 2005; Lehoczy et al., 2005).

In Vietnam, common carp has a natural distribution restricted to the north but is now distributed throughout the country as a result of translocations for aquaculture (Nguyen and Ngo, 2001). Enhancement of common carp production in Vietnam has focused substantially upon the development of genetically improved strains (Thien and Trong, 1995). For this purpose, Hungarian and Indonesian yellow carp strains were imported into Vietnam almost 30 years ago for crossbreeding and mass selection programs with local Vietnamese white carp. The genetic improvement strategy adopted for common carp in Vietnam involved the development of hybrid common carp by crossbreeding among three genetic lines (Vietnamese white, Hungarian scale and Indonesian yellow common carp) coupled with mass selection (Dan et al., 2005; Thien and Thang, 1992). Aquaculture trials have demonstrated that hybrid common carp grew much faster than Vietnamese common carp (Thien and Thang, 1992). However, experimental lines of common carp are thought to have lost their purity, due to inadvertent mixing (Dan et al., 2005).

The ongoing development of common carp farming in Vietnam requires greater understanding of the genetic status of domesticated stocks. To this end an initial study of genetic variation within and among populations using mitochondrial markers was undertaken (Thai et al., 2006). While this study provided useful insights into variation within and between wild and hatchery stocks

Table 1

Locations, code and sample size for 20 populations of common carp sampled in this study

Population	Code	Sample location	Population type
Hungarian-RIAI <sup>a</sup>	HUS	Tu Sori, Bac Ninh	Experimental
Indonesian yellow-RIAI	IDY	Tu Son, Bac Ninh	Experimental
Vietnamese white-RIAI	VNW	Tu Son, Bac Ninh	Experimental
Vinh Phuc	VIP	Me Linh, Vinh Phuc	Hatchery
Thai Nguyen	THN	Cu Van, Thai Nguyen	Hatchery
Son La	SQL	Son La town, Son La	Hatchery
Bac Kan	BAK	Bach Thong, Bac Kan	Hatchery
Tuyen Quang	TUQ	Hoang Khai, Tuyen Quang	Hatchery
Yen Bai	YEB	Van Chan, Yen Bai	Hatchery
Hoa Binh	HOB	Hoa Binh town, Hoa Binh	Hatchery
Ha Tinh	HAT	Duc Long, Ha Tinh	Hatchery
Can Tho	CAT	Cai Rang, Can Tho	Hatchery
Sai Gon	SAG	Binh Chanh, Sai Gon	Hatchery
Thac Ba Reservoir	TBR	Yen Binh, Yen Bai	Hatchery
Bang Giang River	BGR	Cao Bang town, Cao Bang	Wild
Lo River	LOR	Yen Son, Tuyen Quang	Wild
Red River	RER	Van Giang, Hi Hung	Wild
Lam River	LAR	Nam Dan, Nghe An	Wild
Son River	SOR	Bo Trach, Quang Binh	Wild
Dak Lak	DAL	Ea Kao, Dak Lak	Wild

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and the dissemination of introduced stocks and genetic improved lines, mitochondrial DNA (mtDNA) only represents a single locus and the maternal gene pool.

Microsatellites are highly variable nuclear genetic markers, which are inherited co-dominantly in a Mendelian fashion and, as such, offer an alternative perspective to mtDNA data (Liu and Cordes, 2004). Microsatellites have been found suitable for a variety of applications in fisheries and aquaculture research, particularly where genetic differentiation within and between populations may be limited. Potential applications in aquaculture include monitoring changes in genetic variation as a consequence of different breeding strategies, the investigation of interactions between wild and cultured populations, parentage assignment and estimation of relatedness between potential breeding pairs (Cross, 2000; Cross et al., 2005; Davis and Hetzel, 2000; Liu and Cordes, 2004; Norris et al., 1999).

In this study, genetic diversity of wild and cultured common carp in Vietnam is investigated using four microsatellite loci, and the same samples as a previous study that utilized mtDNA data (Thai et al., 2006). The results of this study, together with the mtDNA data, provide important new insights into the management of

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