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Population genetic structure of *Catla catla* (Hamilton) revealed by microsatellite DNA markers

Md. Samsul Alam[a,*], Md. Shahidul Islam[b]

[a]*Department of Fisheries Biology and Genetics, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh*
[b]*Department of Biotechnology, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh*

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Abstract

Information on the genetic structure of cultured fish species is essential for optimising fisheries management and stock improvement programs. Eight microsatellite loci (*Cc6*, *Cc7*, *Cc8*, *Cc9*, *Ccat C3*, *Ccat A12*, *Ccat G1*, and *Ccat G2*) were analysed to study the genetic variation in three river populations, (the Halda, Jamuna, and Padma rivers) and one hatchery population of *Catla catla*. Seven of the eight loci analysed were polymorphic in all the populations. Locus *Ccat G2* had the highest numbers of alleles (8), while the locus *Cc9* had the lowest (2). Differences were observed in heterozygosities and average numbers of alleles among the four populations; however, no difference was observed in proportion of polymorphic loci (P_{95}) among the populations. All the studied populations deviated from Hardy–Weinberg equilibrium proportions at a number of loci, mostly due to the deficiency of heterozygosities. A low level of population differentiation (F_{ST}) was observed among populations; however, significant differentiation was evident only between the Halda and hatchery populations. The genetic distance computed by Nei [M. Nei, Genetic distance between populations. Am. Nat. 106, 1972, 283–292.] between the Halda and the other three populations was higher than the genetic distances between all other population pairs. The study revealed a relatively low level of genetic variation at microsatellite loci within and between catla populations, with genetic variation in the hatchery population lower than the river populations. Knowledge of genetic structure of the major river populations and a typical hatchery population is helpful for management of the populations in order to maintain their genetic quality.

Keywords: Microsatellites; Genetic variation; Polymorphism; *Catla catla*

1. Introduction

Catla (*Catla catla* Hamilton), an Indian major carp species, is widely distributed in India, Bangladesh, Pakistan and Myanmar (Jhingran, 1968). As a principal species, it contributed 469,070 tonnes to total aquaculture production of the world in 2002

* Corresponding author. Tel.: +880 91 52236; fax: +880 91 55810.
E-mail address: samsul@royalten.net (M.S. Alam).

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(FAO, 2004). In Bangladesh, it is the second most popular indigenous aquacultured species, because of its fast growth rate and good taste. It is mostly found in the Padma–Brahmaputra (i.e., Padma, Jamuna, Arial Khan, Kumar and Old Brahmaputra rivers) and Halda river systems. As the natural breeding of the major carp has become constrained by degradation of habitats resulting from environmental modification and human interventions (overfishing, dam construction, pollution, etc.), the contribution of the rivers as natural sources of fry for major carp species for aquaculture has been reduced to almost nil (1%) in 2003, as against 80% in the early 1980s (DoF, 2003). In recent years, 99% of seed are produced through induced breeding in over 800 government/private hatcheries (DoF, 2003) to meet the demand for expanding aquaculture practices in Bangladesh. The operation of hatcheries is driven primarily by profit, and as such, hatchery owners set their target on quantity of spawn rather than quality. They usually maintain a small number of relatively small-sized broodfish to keep the production cost at minimum. They also hybridize among different carp species when broodstock of one sex of a species are not available at the time of need. Hence, farmers always incur a risk of having to use poor quality fry. The deterioration in quality of hatchery-produced fry is a much-discussed topic in the fisheries sector of Bangladesh (Rajts et al., 2002). In recent comparative studies, river-derived fry have shown much better growth than hatchery-derived fry (Alam and Alam, 2003; Shah and Biswas, 2004). The poor performance of the hatchery strain could be explained by genetic erosion through inbreeding, negative selection, hybridization among major carp species (catla, rohu, mrigal, and calbasu), insufficient effective breeding number in the hatcheries, or a combination of these factors. Regular monitoring of genetic variation in hatchery stocks is necessary to determine whether breeding programs are causing genetic erosion by reducing genetic variability and improper hybridization and gene introgression. Molecular markers offer the most realistic method to assess the genetic status of the hatcheries against known levels of variation in wild populations. Recently, Barman et al. (2003) used Random Amplified Polymorphic DNA (RAPD) markers to analyse the genetic structure of the Indian major carps. These authors detected low levels of intraspecific genetic variation and some species-specific RAPD markers for the Indian major carps. In a previous study involving isozyme electrophoresis, we observed a low level of intra- and inter-population variation in river and hatchery populations of catla and a high incidence of hybridization in the hatchery samples among the Indian major carp species, *Labeo rohita, Catla catla* and *Cirrhinus mrigala* (Simonsen et al., 2004). The low variability at isozyme loci in the Indian major carp species, involving primarily diallelic polymorphism, reduces their sensitivity. In contrast, microsatellite DNA markers (one-to-eight-nucleotide tandem repeats, randomly distributed in the genome) have been found useful for detecting high levels of polymorphism and rare alleles. These markers are now widely used for the determination of genetic variation in wild and cultured fish populations (Brooker et al., 1994; Norris et al., 1999; DeWoody and Avise, 2000; Was and Wenne, 2002). Naish and Skibinski (1998) developed five tetranucleotide microsatellite markers for *Catla catla* and screened in five river and five hatchery samples from India, Bangladesh and Nepal. They did not, however, mention the names of the populations and describe the population-specific variation. McConnell et al. (2001) also developed five pairs of microsatellite markers for catla and reported the numbers of alleles and heterozygosity observed in a single sample comprising 26 fish from the Halda River. The aim of the present study was to assess the intra- and inter-population genetic variation in three major river and one hatchery populations of catla in Bangladesh using the microsatellite DNA markers developed by Naish and Skibinski (1998) and McConnell et al. (2001).

2. Materials and methods

2.1. Experimental fish

Fry of *C. catla* were collected from the nursery operators from Sirajgonj (the Jamuna River source) and Sreepur, Magura (the Padma River source) on 15 July 2002. Fry of hatchery source were collected on the same date from the local fish seed market, Jessore (the ancestry of the hatchery fish could not be obtained). The fry were stocked in a pond at the