

## Research Article

## Analysis of parentage assignment and parental contribution of silver carp (*Hypophthalmichthys molitrix*) in a semi-natural system of propagation using microsatellites

E. Jorfi<sup>1\*</sup>, M. R. Kalbassi MasjedShahi<sup>2</sup>

<sup>1</sup> Iranian Fisheries Science Research Institute, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran

<sup>2</sup> Dept. of Fisheries, Faculty of Marine Sciences, Tarbiat Modares University, Noor, I.R. of Iran

Received: August 2022

Accepted: November 2022

### Abstract

Study on pedigree information and genetic diversity is essential for effective management of hatcheries. In this study we used six microsatellite loci for analysis of offspring parentage from two sets of brooders, to evaluate the genetic diversity and parental contribution in the production of progeny of *Hypophthalmichthys molitrix*. The effective number of alleles and the heterozygosity for parents and offspring was (3.63 and 4.38) and (0.943 and 0.960) for two groups, respectively. The contribution of the females and males to the offspring for the two groups was 61% and 91%, respectively. Females mated with 2–6 males, and males fertilized 2–5 females, revealing multiple paternity in this species. Our results revealed that the ratio of males to females plays an important role in parental contribution to offspring production.

Despite a decrease in the heterozygosity among larvae towards their parents, the values obtained were still acceptable, which supports the hypothesis of genetic factors involves in mating patterns selected by parents to maintain the proper levels of heterozygosity in their progenies.

**Keyword:** Molecular marker, Medigree, Heterozygosity, Parentage analysis

### Introduction

One of the main strategies for sustainable aquaculture is the planning of basic breeding of hatcheries. Several studies have been focused on breeding programs in recent decades due to the occurrence of various problems (Hulak *et al.*, 2010, Wedekind *et al.*, 2007, Fessehayee *et al.*, 2006).

Keeping genetic diversity safe and monitoring its changes in hatcheries is one of the main plans of genetic management involved

\*Corresponding author's email:  
ejorfi@gmail.com

in aquatic breeding programs (Hedrick, 2004). Genetic diversity, particularly in mammals, birds, and fish is related to the effective population size (Horreo *et al.*, 2008). A sharp decline in genetic diversity would impair population, and even lead to the extinction of species (Machado-Schiaffino *et al.*, 2007).

There are many determinative factors which can influence the actual participation of broodstocks during mating in generations. These factors include the size of the broodstock in the hatcheries, contribution of males and females to reproduction (due to unequal sex ratios or differences in reproductive success between them), the criteria of broodstock selection, and gamete collection and the way of encountering them (Tiou, 2010; Gall, 1988). Executive protocols in hatcheries play an effective role in reducing effective reproduction size of aquatic organisms and the genetic diversity of their offspring.

Genetic diversity in a population is dependent on the diversity of alleles at different genetic loci. Genetic diversity can be assessed through the evaluation of the number and the distribution pattern of alleles among individuals and populations (Abdul-Muneer, 2014). So far, several molecular techniques have been used to examine genetic changes in natural populations, in breeding stocks and in their interactions (Subasinghe *et al.*, 2003; Yudha *et al.*, 2012; Ruzzante *et al.*, 2016).

Microsatellites are noncoding, highly polymorphic, codominant DNA markers with short nucleotide repetitions (1–6 bp) that are powerful tools to evaluate genetic diversion

(Kantartzis, 2013). Microsatellites have several advantages, such as good frequency and distribution at the genomic level (O'Connell & Wright 1997), high diversity and polymorphism, codominant inheritance, compliance with Mendelian laws (DeWoody & Avise 2000), lack of functional features in the genome (in most cases), need for small amounts of DNA samples, and the applicability of microsatellite primers for closely-related species (Briñez *et al.*, 2011).

Simple sequence repeats (SSRs) have been used in various population genetics studies, for instance; study on the effects of domestication on the genetic structure of populations of Atlantic salmon (*Salmo salar*) (Koljonen *et al.*, 2005), turbot (*Scophthalmus maximus*) (Coughlan *et al.*, 1998), brown trout (*Salmo trutta*) (Hansen, 2002, Was & Wenne 2002), common carp (*Cyprinus carpio*) (Bartfai *et al.*, 2003) and black tiger Shrimp (*Penaeus monodon*) (Xu *et al.*, 2001). Majority of them revealed weak genetic diversity of hatchery stocks.

The application of SSRs for determining the relationship between brooders and progenies for parentage assignment has emerged simultaneously with a software revolution in the life sciences and the development of statistical approaches (Liu and Cordes 2004). Application of microsatellites includes assessment genetic parameters for desirable traits during breeding (Herbinger *et al.*, 1995; Vandeputte *et al.*, 2004), evaluation of inbreeding in hatcheries (Letcher & King, 2001), determining the exact number of parents

(Frost *et al.*, 2006), and estimating differences in individuals (Norris *et al.*, 2000.; Jerry *et al.*, 2004.; Liu *et al.*, 2012).

Silver carp (*Hypophthalmichthys molitrix* from Cyprinidae family), is one of the most important species in aquaculture from China. Because of the achievement in captive reproduction through hormone injections, Silver carp introduced to many parts of the world (Kolar *et al.*, 2005) and its Commercially reproduction and farming spread rapidly. Production of silver carp has been reached over 85–170 thousand tons recently, the first place of production of freshwater fish in Iran (FIGIS 2016).

Almost 80% of fingerlings are supplied by private hatcheries, while the rest comes from governmental hatcheries that belong to Iran's Fishery Organization.

Reduction in genetic variability as a consequence of inbreeding in the populations of *H. molitrix* led to a low production of fish, to an increase in offspring mortality and deformity, as well as to imbalanced ratio of males and females in hatcheries. Despite the overall growth of cyprinid farming in Iran, there is still a relatively low production rate of fish, in comparison to other Asian countries (Motallebi & Sharif-rohani, 2011). Possibly due to genetic variability reduction, in Iran death and deformities of juveniles of silver carp (Mortezaei, 2006), and imbalanced ratio of males and females in hatcheries (five females per male), have become a major concern in cyprinid production in captivity. Evaluating the reproductive success rate of each parent provides a good picture of the distribution of genetic diversity between two generations.

Thus, in this study we examined genetic diversity indicators between silver carp progeny and their parents to evaluate the effectiveness of semi-natural breeding method as a common type of reproduction of this species in Iran. We used a number of pre-introduced microsatellites for parentage assignment, and then calculated the success rate of each parent to contribute to the breeding process.

## Materials and methods

### Breeding and sampling

The experiments were performed in a private hatchery, named Abzigostaran, in Khouzestan (32° 01' 03" N, 48° 51' 16" E) province of Iran. Two independent groups with different sex ratios were set. In the first group (named Semi1), 8 females and seven males with an average weight of  $5320 \pm 438.16$  g, and  $4 \pm 192.72$  g, respectively, were used. In the second group (Semi2) 8 females and 10 males with an average weight of  $5313.75 \pm 250.81$  g and  $6220 \pm 496.3$  g, respectively, were used. Parents were prepared for spawning using the standard method in warm-water fishes, which involves two rounds of hormone injections of pituitary gland extract (Horvath *et al.*, 2015). Females were injected intramuscularly with 2 mg/kg PG, 10% of which (0.2 mg/kg) was injected 12 h before the second injection (1.8 mg/kg). Simultaneously males were injected with 0.5 mg/kg PG. Then, they were transferred to 50–60 m<sup>3</sup> circular tanks. Running water (0.2–0.3m/s) toward the center of the pool where an outlet pipe leading to the egg collection chamber, was regularly checked and transferred

in to the incubators. Spawning started ~8 h after the second injection, and lasted for 6–7 h. Fin clips of all brooders were taken and preserved in 95% alcohol. Fertilized eggs were incubated at 25–26 °C. Approximately 24–36 h later, the larvae were hatched and manual feeding was performed from the third day after fertilization. At days 5–6 of the incubation period, larvae (about 100 larvae/incubator) were sampled; they were preserved in 95% alcohol and kept in a fridge until DNA.

#### Analysis of the sperm quality

Male brooders were sampled for evaluating sperm motility and concentration according to Rahman, Rahman & Hasan (2011), using a hemocytometer (Depth 0.1 mm). Sperm was diluted 1000 times in a 0.3% NaCl solution. After 10 min (to allow for sperm sedimentation), the number of spermatozoa were counted in 16 cells and calculated as follows:

Sperm density (ml) =  $1000 \times \text{number of counted sperm} / [\text{area (mm}^2) \times \text{chamber depth (mm)} \times \text{dilution ratio}]$

To evaluate sperm motility, the total period of sperm motility was measured, until 95% of the spermatozoa were immotile. For this purpose a light microscope (Nikon Eclipse 50i) was used at 400 × magnification. Sperm was diluted 1:10 in 0.3% NaCl. Measurements were performed twice for each sample.

#### DNA extraction

DNA was extracted from 160 larvae (80 larvae from each group, Semi1 and Semi2), and from fin clips of 33 males and females using Chelex (Chelex® 100, Sigma-Aldrich) (Estoup *et al.*, 1996) and the phenol-chloroform method (Hillis, 1996). The concentration of total DNA was estimated from absorbance readings at 260 nm (Nanodrop2000). DNA quality was verified by measuring the A260 nm/A280 nm ratio (> 1.8) and the A230 nm/A260 nm ratio (> 2), and by gel electrophoresis. DNA samples were stored at –20 °C until analysis.

#### Microsatellite analysis

Ten primers were selected for this study from a set of microsatellite markers previously introduced for silver carp (Gheyas *et al.*, 2006) (Table 1). All PCRs were performed using a Bio-Rad (T100) thermal cycler. PCR amplification was performed in 10 µl with 1× PCR Buffer (MasterMix, Ampliqon) containing 1.5 mM MgCl<sub>2</sub>, 0.4 mM dNTP, 1 unit Taq DNA polymerase, 0.2 µM of each primer and 20 ng of extracted DNA template. The following program was used: 95 °C for 3 min, followed by 30 cycles of denaturation at 94 °C for 50 s, annealing at 60–64 °C (depending on the primer) for 50 s, and extension at 72 °C for 50 s, followed by a final step of 72 °C for 10 min. PCR products were electrophoresed using 6% polyacrylamide gels for 4 h at 180–200 V, followed by silver staining (Benbouza *et al.*, 2006).

**Table 1-** Microsatellite primers for the 10 loci used in parentage assignment. The first two columns indicate the loci name and their accession numbers, respectively. Sequences correspond to forward (F) and reverse (R) primers used for microsatellite genotyping of *H. molitrix*. Tm, annealing temperature (°C)

Locus name	Accession no.	Sequence (5'-3')	Tm (°C)
Hmo11	AM086451	F: CTG CTT GAT CAC AGG GTT TG R:CCT TAC AGA TAG ACA GAT ATT CAG	60
Hmo13	AM086452	F:AAA CCT GGA AGA TGT TCA CTG AAT R:GCG CGA GTG TTT GAA GTC TG	60
Hmo25	AM086454	F:TGT GCT GCA TTT TCA CTT CA R:TTC TTA CTA TCC ACA TTT GTT GTA TG	60
Hmo26	AM086455	F:GAT TTC AGG CAC ATT GCT TAT CT R:GAG CGT TTC TCA TTT GTA CTT ATT TT	60
Hmo33	AM086458	F:GTG CAG CAG TAT GTG AAT CAG GAC AC R:GTG CTT CGG GAT ACC ACA CTC TTG	60
Hmo34	AM086459	F:GTT CCC TGA GGC TTT ACA A R:GGG TCA TTA TCC TCT CAC TTT	60
Hmo36	AM086460	F:ATC GGA GGA GTG CTG TTC AGT CTG GA R:ACG ATT GTT GCC GAA CGG GTT GAT	64
Hmo37	AM086461	F:CAC AGC GGA GGG GCA AAG GTC R:GGA CGC CGT GTG ACT GGA GAT TTT	64
Hmo39	AM086462	F:ACA GTT ATG AGC TAG CAG CAG TTT CT R:TAC GTC GTA ATA CCA GTG TAA TAC CC	60
Hmo40	AM086463	F:CAG GCA GGC ATC CAC ATA GAG AAT C R:AGA AGA AAT CTG ATC GTC ACC TAT GA	64

### Data analysis

The size of the alleles obtained for each sample was calculated using Gel Scanner program (ver. 1.3). The allele number, allele frequency, observed heterozygosity (Ho) and expected heterozygosity (He), were calculated using GenAlEx (Peakall & Smouse, 2006, 2012). The Cervus Ver. 3.0.7 program (Marshall, 2014) was used to estimate polymorphic information content, null alleles frequency, and exclusionary power indicators, including Excl-1P (mean power assignment for a parent), Excl-2P (mean power assignment for one parent and the other parent of the opposite sex with a given genotype), and Excl-PP (mean power assignment for a pair parent), which are required to determine the assignment power of

parents. According to relations A and B, the calculated values for the power exclusion (PE) of loci were used to determine the combined exclusion power (CPE) of parents (Vandeputte, Kocour, Mauger *et al.*, 2004): relation A, PE = 1-Excl; relation B; CPE = 1-Multiplication of PEs for all loci.

Parentage assignment analysis was performed in Cervus Ver. 3.0.7 (Marshall, 2014), using the maximum likelihood method with the most potential exclusion power. The natural logarithm likelihood ratio is called LOD. Through 10,000 simulations in the Cervus program, the distinctive limit was generated in the form of a LOD score between the first and second possible parents with confidence levels greater than 95% and lower than 90%. From

this analysis the number of larvae produced by both male and female parents, and consequently the contribution rate of each parent to the process of reproduction, was determined. Chi-square analysis was used to determine significant differences in contribution between brooders ( $p < 0.05$ ).

The effective genetic size of the population ( $N_e$ ) was calculated to examine the effects of family sizes according to this formula (Chevassus 1989):  $N_e = [4(n - 2)] / [(K_s + V_s / K_s) + (K_d + V_d / K_d)] - 2$ ; where  $n$  is the sample size of the larvae,  $K_s$ , and  $K_d$  are the mean number of larvae produced per sire and dam, respectively, and  $V_s$  and  $V_d$  are the variances of family sizes produced by sire and dam (Falconer, 1989). Assuming random family samples within equally sized families, the effective population size of brooders is calculated by the following formula (Falconer 1989):  $N_e = 4(N_m \times N_f) / (N_m + N_f)$ ; where  $N_e$  is the effective population size of parents, and  $N_m$ , and  $N_f$  are the number of male and female parents participating in a mating group, respectively.

## Results

### Genetic diversity

Analysis of genetic diversity in parents using eight microsatellite loci showed the lowest number of alleles in loci Hmo11, Hmo39 and Hmo40 (4 alleles), and the highest number of alleles in loci Hmo37 locus (10 alleles) (Table 2). The mean number of alleles per locus was 6.25. The highest rates of expected heterozygosity were obtained at loci Hmo37 (0.860) and Hmo34 (0.796), while the lowest rate was seen at Hmo40 locus (0.414). The maximum and minimum rates of polymorphism information content were obtained at loci Hmo37 (0.845) and Hmo40 (0.378), respectively. The null allele frequency was negative in all loci except in the Hmo40 locus (0.418) (Table 2). After computing the loci exclusion power, six loci were selected to assign the parents (Hmo13, Hmo25, Hmo25, Hmo26, Hmo37, and Hmo39). The CPE of parents for all studied loci were  $\text{Excl-1P} = 0.959$ ,  $\text{Excl-2P} = -0.996$ , and  $\text{Excl-PP} = 0.999$ . For selected loci in this study, the factors estimated as 0.943, 0.992 and 0.999, respectively.

**Table 2.** N.A., Number and size of alleles;  $H_o$ , observed heterozygosity;  $H_e$ , expected heterozygosity; PIC, polymorphic information content; N.U., null alleles;  $\text{Excl-1P}$ ,  $\text{Excl-2P}$ , and  $\text{Excl-PP}$ , average exclusion probabilities

Locus	N.A.	$H_o$	$H_e$	PIC	N.U.	$\text{Excl-1P}$	$\text{Excl-2P}$	$\text{Excl-PP}$	Size of alleles (bp)
Hmo11	4	1	0.631	0.567	-0.268	0.533	0.366	0.213	142-148
*Hmo13	6	0.805	0.696	0.653	-0.068	0.652	0.463	0.287	136-162
*Hmo25	6	1	0.686	0.643	-0.230	0.643	0.454	0.279	134-144
*Hmo26	9	1	0.767	0.739	-0.154	0.767	0.573	0.391	146-220
*Hmo34	7	1	0.796	0.768	-0.122	0.791	0.606	0.428	114-128
*Hmo37	10	0.976	0.860	0.845	-0.068	0.887	0.723	0.564	148-194
*Hmo39	4	1	0.707	0.653	-0.174	0.621	0.449	0.28	128-140
Hmo40	4	0.366	0.414	0.378	0.041	0.359	0.22	0.087	208-238
Means (all studied loci)	6.25	0.893	0.695	0.655	-0.131	0.999	0.996	0.959	-
Means (Selected - loci)	7	0.963	0.752	0.716	-0.137	0.999	0.992	0.943	-

### Comparison of genetic diversity of parents and offspring

Genetic diversity indices obtained for the larvae in groups Semi1 and Semi2, and for the contributing parents in each group, are presented in Table 3. The numbers of alleles were identical in all loci of parents and larvae, except for Hmo25, where one allele less is observed in the larvae (Semi2).

The mean values for He, Ho, and polymorphic information content in the parents of group Semi1 were 0.714, 0.962, and 0.673, respectively, while the equivalent values in their larvae were  $0.693 \pm 0.034$ ,

$0.925 \pm 0.039$ , and  $0.646 \pm 0.096$ , respectively. Also, in parents of larvae in the group Semi2, the mentioned indicators were 0.755, 0.969, and 0.718, respectively, while the estimation in the offspring of this group was  $0.745 \pm 0.036$ ,  $0.925 \pm 0.032$ , and  $0.705 \pm 0.107$ , respectively. Chi-square test showed no significant differences between parents and their larvae for both of the groups. The mean number of effective alleles in the parents and larvae of group Semi1 was 3.70, and 3.56, respectively. The mean number of effective alleles in the parents and larvae of group Semi2 was 4.40 and 4.37, respectively.

**Table 3.** Genetic diversity in parents and offspring in two group semi-natural propagation of *Hypophthalmichthys molitrix*. N.A., Number and size of alleles; Ho, observed heterozygosity; He, expected heterozygosity; Ne, Number of effective alleles

Loci	Groups	N.A.		He		Ho		Ne	
	Sample	Semi1	Semi2	Semi1	Semi2	Semi1	Semi2	Semi1	Semi2
Hmo13	Parents	4	4	0.618	0.689	0.769	0.813	2.62	3.22
	Larvae	4	4	0.651	0.656	0.825	0.8	2.86	2.9
Hmo25	Parents	6	6	0.686	0.699	1	1	3.18	3.32
	Larvae	6	5	0.665	0.714	1	0.988	2.98	3.5
Hmo26	Parents	7	7	0.738	0.811	1	1	3.44	5.270
	Larvae	7	7	0.617	0.799	0.788	0.938	2.61	4.960
Hmo34	Parents	7	7	0.809	0.752	1	1	4.5	4.030
	Larvae	7	7	0.728	0.8	0.938	1	3.67	5.000
Hmo37	Parents	8	10	0.843	0.857	1	1	5.28	7.010
	Larvae	8	10	0.843	0.859	1	0.988	6.38	7.080
Hmo39	Parents	4	4	0.711	0.719	1	1	3.15	3.550
	Larvae	4	4	0.648	0.64	1	1	2.88	2.770
Mean	Parents	6	6.33	0.714	0.755	0.962	0.969	3.7	4.400
	SE	0.683	0.843	0.028	0.027	0.038	0.031	0.993	1.480
Mean	Larvae	6	6.167	0.693	0.745	0.925	0.952	3.56	4.370
	SE	0.683	0.946	0.034	0.036	0.039	0.032	1.42	1.640

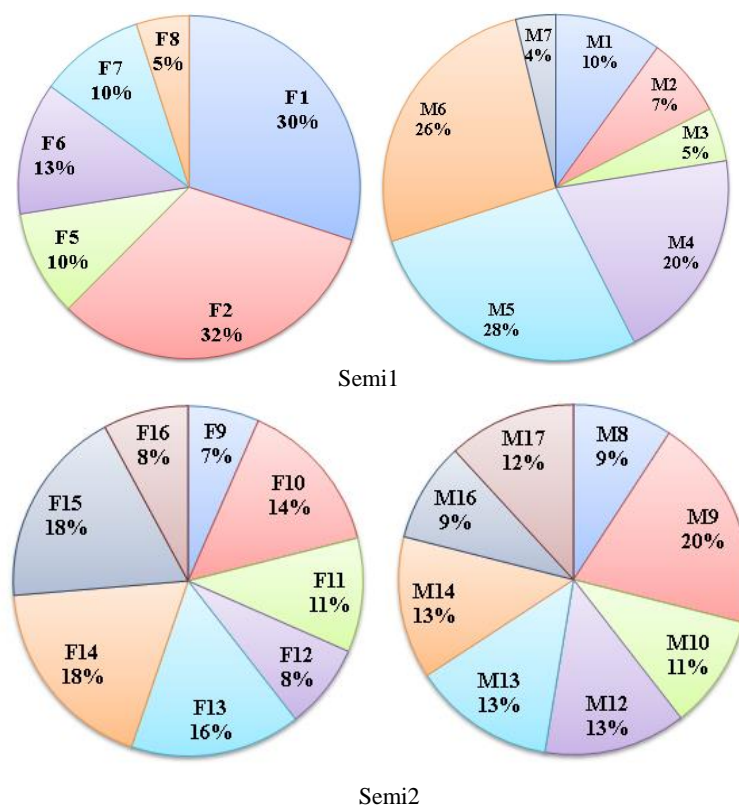
### Parent's contribution to offspring

The parentage analysis, using six selected loci, in two groups of Semi1 and Semi2 assigned 100%

and 95% of offspring to their parents, respectively. Individual parents, and the number

of larvae produced by each parent, are presented in Table 4, according to parentage assignment in Semi1 and 2. Assuming a balanced participation, Chi-square tests in the Semi1 group showed significant differences on the number of larvae produced by the sires (and dams), regardless of type of crossing with dams (and sires) ( $p < 0.05$ ). In Semi1, 30% and 32% of the progeny (more than half of the larvae) belonged to females F1 and F2, respectively. The female F8 had the lowest percentage of the progeny (5%). Among

males, M4, M5 and M6 produced more than 60% of larvae (Figure 1), revealing a disproportionate contribution to the progeny. None of the larvae in Semi1 group were attributed to females F3 or F4. Therefore, females F3 or F4 were eliminated from the participating brooders of the group. The mean larvae production in Semi1 by males and females was 16.32 and 18.7, respectively (Table 5). The variance of larvae production in this group by males and females was 44.34 and 69.78, respectively (Table 5).



**Figure 1.** Parental contribution to offspring production of *Hypophthalmichthys molitrix* in two groups of semi-natural reproduction system (Semi1 and Semi2).

In the group Semi2, the Chi-square test showed no significant differences between contributing males and females to produce larvae ( $p > 0.05$ ), except for the male M9, there was a roughly balanced male participation. although among the females (Figure 1). Most of the larvae (>50%) were produced by females F13, F14,

and F15. In Semi2 group no progeny was attributed to males M11 and M15. Thus, they were eliminated from the participating males of the group. The mean and variance of larvae reproduction in this group by males and females were calculated respectively as (10.10–0.71) and (7.21–9.96) (Table 4).

Comparing the numbers presented in Table 5 in relation to the effective population size of parents in the both groups, a significant reduction of  $N_e$  can be clearly seen in the group Semi1. Assuming full participation of all males and females in Semi1, the expected effective population size would be 12.9, however this number was actually 7.9, which is equivalent to a 39% reduction compared to equally sized families. The decline in the population of Semi2 group was 9.5% (Table 5).

The females were in participant with 2–6 males, while the males fertilized 2–5 females, which can be indicative of multiple paternity in this species (Table 4). Qualitative sperm analysis in males of Semi1 and Semi2 showed that the mean concentrations were  $421.66 \pm 6.37$ , and  $398.5 \pm 12.74$ , respectively. Average sperm motility in Semi1 and Semi2 was  $65.23 \pm 0.45$ , and  $63.16 \pm 0.35$ , respectively (Table 6). Comparing to previous results in other studies of this species, all of the males were able to fertilize the females.

**Table 4.** Parentage assignment for two groups of *Hypophthalmichthys molitrix*

Semi1	M1	M2	M3	M4	M5	M6	M7	Total			
F1	1	0	0	2	18	3	0	24			
F2	1	5	1	7	1	9	2	26			
F3	0	0	0	0	0	0	0	0			
F4	0	0	0	0	0	0	0	0			
F5	5	0	1	0	0	2	0	8			
F6	0	0	0	5	2	3	0	10			
F7	1	1	2	0	0	4	0	8			
F8	0	0	0	2	1	0	1	4			
Total	8	6	4	16	22	21	3	80			
Semi2	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	Total
F9	4	0	0	0	0	0	1	0	0	0	5
F10	1	1	2	0	3	4	1	0	0	0	12
F11	1	1	0	0	2	0	0	0	3	1	8
F12	0	0	1	0	0	0	4	0	0	1	6
F13	0	0	2	0	0	4	3	0	0	3	12
F14	1	1	0	0	5	2	0	0	2	2	13
F15	0	10	3	0	0	0	0	0	1	0	14
F16	0	2	0	0	0	0	1	0	1	2	6
Total	7	15	8	0	10	10	10	0	7	9	

**Table 5.** Number of broodstock in each group

Group	Number of broodstock	Mean contribution of parents		Variance of produced larvae		$N_e(1)$	$N_e(2)$	$N_e(2)/N_e(1)$
		$K_s$ (Male)	$K_d$ (Females)	$V_s$ (Male)	$V_d$ (Females)			
Semi1	15	16.32	18.7	44.34	69.78	12.9	7.9	0.61
Semi2	18	10.10	10.71	7.21	9.96	16	14.48	0.91

$K_d$ , mean contribution of males parents to produced larvae;  $K_s$ , mean contribution of female parents to produced larvae;  $V_d$ , variance of produced larvae for males;  $V_s$ , variance of produced larvae for females; effective population sizes using  $4(N_m \times N_f)/(N_m + N_f)$ , ( $N_e(1)$ ), effective population sizes using  $N_e(2) = 4(N/2)/[(K_s + V_s/K_s) + (K_d + V_d/K_d) - 2]$  (Chevassus, 1989) ( $N_e(2)$ ) and the ratio of  $N_e(1)/N_e(2)$ .

**Table 6.** Sperm characteristics of *Hypophthalmichthys molitrix*. Compared to other studies in the same species

Species	Mean concentration of sperm( $10^7$ /ml)	Mean motility of sperm (s)	Reference
<i>H. molitrix</i>	315 $\pm$ 2	96.1 $\pm$ 1(early season)	Khara, Baradaran, Dadras, Rahbar, Ahmadnejad & Khodadoost (2012)
<i>H. molitrix</i>	-	36 $\pm$ 9	Rahman, Rahman & Hasan (2011 (2011))
<i>H. molitrix</i>	421.66 $\pm$ 6.37	65.23 $\pm$ 0.45	This study, group Semi1
<i>H. molitrix</i>	398.5 $\pm$ 12.74	63.16 $\pm$ 0.35	This study, group Semi2

## Discussion

In this study the parentage assignment was successful for about 97% of all larvae studied. It seems that factors such as the absence of null alleles and using loci with appropriate diversity (proper amount of effective allele size) have led to the efficient performance of the technique on the larvae analyzed. In numerous reports, an appropriate success rate in detecting parents and their contribution to offspring production have been reported using SSRs: Weinman *et al.* 2014, 95% success; Gheyas *et al.* 2009, 96.3%; and Liu *et al.* 2012 99.6%. In a microsatellite study on Caspian Salmon (*Salmo trutta caspius*) discrimination of more than 98% of brooders was successfully performed (Sourinejad *et al.*, 2011).

The use of a minimum number of microsatellite loci to achieve a high level of parentage assignment power in parental groups is one of the main goals of this technique (Castro *et al.*, 2007). However different factors, such as null alleles, mutations, and genetic linkage between the examined loci, can affect the exclusionary power and consequently the success rate of parentage assignment (Vandeputte *et al.*, 2011). In previous studies, 6–8 microsatellite loci were considered a

reliable number for parentage assignment (Fessehay *et al.*, 2006). In this study, we tried to minimize the number of loci required for analysis on silver carp (Gheyas *et al.*, 2006), using SSRs markers and preliminary evaluation and selection of the most appropriate loci (in terms of discrimination power; CPE calculation).

In the animal kingdom, fish have the most complex mating systems (Neff 2001). Multiple paternity has also been observed in other species, such as Perches, Gastropods and Paco fish (*Piaractus mesopotamicus*) (Xue, 2014; Fessehay *et al.*, 2006; Povh *et al.*, 2010). Mating with a greater number of females increases the chance for male reproductive success, which highlights the role of males as the determinant of the fertilization event. However, the ongoing effort of females for mating with a greater number of males should not be ignored. Besides fish, polyandrous events associated with adaptive behaviors have been reported in a variety of animals (Gowaty, 1994). Females try to maximize adaptation, survival, and fitness through mating with multiple males. which include successful fertilization despite poor reproductive success

in males (poor quality sperm), achieving better genes for their larvae, reproducing offspring with greater genetic diversity (and as a result higher adaptability), and preventing inbreeding (Avise *et al.*, 2002). This event is possible through multiple spawning of females at different intervals (DeWoody & Avise, 2001). In this study, evaluation of the mating patterns between parents of Semi1 and Semi2 groups revealed that females mated with two or more males, which supports the polyandrous participation hypothesis in silver carp, and this could have occurred in several stages.

According to the results of parent contribution, two males of the second group (M13 and M15) did not participate in reproduction. Comparing the sperm quality in this study with previous studies (Khara *et al.*, 2012, Rahman *et al.*, 2011), the sperm of fish in our study had appropriate motility and concentration values (Table 6). So it does not seem to be related to sperm quality factors, since other parents with similar sperm features participated in reproduction and produced larvae. On the other hand, all of the females produced larvae so it seems no problem with them. However, the incidence of some differences in the values obtained may be attributed to various reasons such as differences in the maturity of parents, in the hormonal stimulation methods, contamination during sperm collecting, differences in concentration estimation methods, different time periods during a reproductive season, and the conditions of parents in terms of nutrition, age, etc. (Khara *et al.*, 2012, Alavi *et al.*, 2010).

In this study, the difference in the participation rate of parents in reproduction (especially for males) and a high variance in family size in Semi1 limited  $N_e$  (7.9), when compared to the expected  $N_e$  value (12.9) (Table 5). However, in the group Semi2, which had an equal contribution of parents to reproduction, the estimated  $N_e$  (14.4) was closer to the expected value (16). Evaluating the genetic diversity in parents and their progeny showed that despite the decrease in the effective size of broodstock in both groups, the heterozygosity in offspring was maintained at acceptable levels that were similar to the parents' (0.962–0.952 in group Semi1, and 0.969–0.952 in group Semi2). This issue, would strengthen the hypothesis of reproductive behaviors, such as dissimilar mating to profit the progenies from its effects as an increase in the amount of heterozygosity (Tregenza & Wedell, 2000), when considering the negative  $F$  values reveals the selection in favor of heterozygous individuals. According to heterozygosity-fitness correlations at noncoding genetic markers, heterozygosity is a sign of fitness effects, which is the result of genes distributed through the genome (Hansson *et al.*, 2004).

In general, the microsatellite markers used in this study were useful for assigning parentage with a high degree, and made it possible to estimate  $N_e$  during a semi-natural process of propagation. The analysis of parentage assignment suggested an unequal contribution of parents in an unbalanced sex ratio. However, in the group with a balanced sex ratio, a balanced participation of parents in

reproduction was observed, which highlights the importance of sex ratio among males. The use of equal sex ratios of males and females in silver carp, and ensuring the sexual maturity of the brooders and their health status, can benefit the proportional distribution of genetic diversity from parents to the offspring.

### Conflict of interest

The authors have no conflict of interest in this work.

### References

Abdul-Muneer, P.M., 2014. Application of microsatellite markers in conservation genetics and fisheries management: recent advances in population structure analysis and conservation strategies. *Genetics research international*, 2014. Article ID 691759. 11pp. <https://doi.org/10.1155/2014/691759>

Adiputra, Y.T., Chuang, J.L. and Gwo, J.C., 2012. Genetic diversity of Indonesia milkfish (*Chanos chanos*) using amplified fragment length polymorphism (AFLP) analysis. *African Journal of Biotechnology*, 11(13), 3055-3060. <https://doi.org/10.5897/AJB10.1985>

Aho, T., Rönn, J., Piironen, J. and Björklund, M., 2006. Impacts of effective population size on genetic diversity in hatchery reared Brown trout (*Salmo trutta* L.) populations. *Aquaculture*, 253(1-4), 244-248. <https://doi.org/10.1016/j.aquaculture.2005.09.013>

Avise, J.C., Jones, A.G., Walker, D., DeWoody, J.A. and collaborators, 2002.

Genetic mating systems and reproductive natural histories of fishes: lessons for ecology and evolution. *Annual review of genetics*, 36(1), 19-45.

<https://doi.org/10.1146/annurev.genet.36.030602.090831>

Bártfai, R., Egedi, S., Yue, G.H., Kovács, B., Urbányi, B., Tamás, G., Horváth, L. and Orbán, L., 2003. Genetic analysis of two common carp broodstocks by RAPD and microsatellite markers. *Aquaculture*, 219(1-4), 157-167. [https://doi.org/10.1016/S0044-8486\(02\)00571-9](https://doi.org/10.1016/S0044-8486(02)00571-9)

Benbouza, H., Jacquemin, J.M., Baudoin, J.P. and Mergeai, G., 2006. Optimization of a reliable, fast, cheap and sensitive silver staining method to detect SSR markers in polyacrylamide gels. *Biotechnologie, agronomie, société et environnement*, 10(2), 77-81.

Briñez R, B., Caraballo O, X. and Salazar V, M., 2011. Genetic diversity of six populations of red hybrid tilapia, using microsatellites genetic markers. *Revista MVZ Córdoba*, 16(2), 2491-2498. <https://doi.org/10.21897/rmvz.1010>

Castro, J., Pino, A., Hermida, M., Bouza, C., Chavarriás, D., Merino, P., Sánchez, L. and Martínez, P., 2007. A microsatellite marker tool for parentage assessment in gilthead seabream (*Sparus aurata*). *Aquaculture*, 272, 210-216. <https://doi.org/10.1016/j.aquaculture.2007.08.020>

Chevassus, B., 1989. Aspects génétiques de la constitution de populations d'élevage destinées

au repeuplement. *Bulletin Français de la Pêche et de la Pisciculture*, (314), 146-168. <https://doi.org/10.1051/kmae:1989010>

Coughlan, J.P., Imsland, A.K., Galvin, P.T., Fitzgerald, R.D., Naevdal, G. and Cross, T.F., 1998. Microsatellite DNA variation in wild populations and farmed strains of turbot from Ireland and Norway: a preliminary study. *Journal of Fish Biology*, 52(5), 916-922. <https://doi.org/10.1111/j.1095-8649.1998.tb00592.x>

DeWoody, J.A. and Avise, J.C., 2000. Microsatellite variation in marine, freshwater and anadromous fishes compared with other animals. *Journal of fish biology*, 56(3), 461-473. <https://doi.org/10.1111/j.1095-8649.2000.tb00748.x>

DeWoody, J.A. and Avise, J.C., 2001. Genetic perspectives on the natural history of fish mating systems. *Journal of Heredity*, 92(2), 167-172. <https://doi.org/10.1093/jhered/92.2.167>

Estoup, A., Largi Estoup, A.C.R.L., 1996. Rapid one-tube extraction for reliable PCR detection of fish polymorphic markers and transgenes. *Mol Mar Biol Biotechnol*, 5(4), 295-298.

Falconer, D.S., 1989. Introduction to quantitative genetics 3rd ed. *Harlow Longman Scientific & Technical*.

Fessehay, Y., El-bialy, Z., Rezk, M.A., Crooijmans, R., Bovenhuis, H. and Komen, H., 2006. Mating systems and male reproductive

success in Nile tilapia (*Oreochromis niloticus*) in breeding hapas: a microsatellite analysis. *Aquaculture*, 256(1-4), 148-158. <https://doi.org/10.1016/j.aquaculture.2006.02.024>

Frost, L.A., Evans, B.S. and Jerry, D.R., 2006. Loss of genetic diversity due to hatchery culture practices in barramundi (*Lates calcarifer*). *Aquaculture*, 261(3), 1056-1064. <https://doi.org/10.1016/j.aquaculture.2006.09.004>

Gheyas, A.A., Cairney, M., Gilmour, A.E., Sattar, M.A., Das, T.K., McAndrew, B.J., Penman, D.J. and Taggart, J.B., 2006. Characterization of microsatellite loci in silver carp (*Hypophthalmichthys molitrix*), and cross-amplification in other cyprinid species. *Molecular Ecology Notes*, 6(3), 656-659. <https://doi.org/10.1111/j.1471-8286.2006.01288.x>

Gheyas, A.A., Woolliams, J.A., Taggart, J.B., Sattar, M.A., Das, T.K., McAndrew, B.J. and Penman, D.J., 2009. Heritability estimation of silver carp (*Hypophthalmichthys molitrix*) harvest traits using microsatellite based parentage assignment. *Aquaculture*, 294(3-4), 187-193. <https://doi.org/10.1016/j.aquaculture.2009.06.013>

Gowaty, P.A., 1994. Architects of sperm competition. *Trends in Ecology & Evolution*, 9(5), 160-162. [https://doi.org/10.1016/0169-5347\(94\)90076-0](https://doi.org/10.1016/0169-5347(94)90076-0)

Hadi Alavi, S.M., Jorfi, E., Hatef, A. and Saheb Mortezaei, S.A., 2010. Sperm motility and

seminal plasma characteristics in *Barbus sharpeyi* (Günther, 1874). *Aquaculture research*, 41(10), e688-e694.

Hansen, M.M., 2002. Estimating the long-term effects of stocking domesticated trout into wild brown trout (*Salmo trutta*) populations: An approach using microsatellite DNA analysis of historical and contemporary samples. *Molecular Ecology*, 11(6), 1003-1015. <https://doi.org/10.1046/j.1365-294X.2002.01495.x>

Hansson, B., Westerdahl, H., Hasselquist, D., Akesson, M. and Bensch, S., 2004. Does linkage disequilibrium generate heterozygosity-fitness correlations in great reed warblers? *Evolution*, 58(4), 870-879. <https://doi.org/10.1111/j.0014-3820.2004.tb00418.x>

Hedrick, P.W., 2004. Recent developments in conservation genetics. *Journal of Forest Ecology and Management*, 197(1-3), 3-19. <https://doi.org/10.1016/j.foreco.2004.05.002>

Herbinger, C.M., Doyle, R.W., Pitman, E.R., Paquet, D., Mesa, K.A., Morris, D.B., Wright, J.M. and Cook, D., 1995. DNA fingerprint based analysis of paternal and maternal effects on offspring growth and survival in communally reared rainbow trout. *Aquaculture*, 137(1-4), 245-256. [https://doi.org/10.1016/0044-8486\(95\)01109-9](https://doi.org/10.1016/0044-8486(95)01109-9)

Hillis, D.M., Moritz, C. and Mable, B.K., 1996. *Molecular Systematics* 2nd Edition Sinauer

Associates. Sunderland, MA. <https://doi.org/10.2307/1447682>

Horreo, J.L., Machado-Schiaffino, G., Griffiths, A., Bright, D., Stevens, J. and Garcia-Vazquez, E., 2008. Identification of differential broodstock contribution affecting genetic variability in hatchery stocks of Atlantic salmon (*Salmo salar*). *Aquaculture*, 280(1-4), 89-93. <https://doi.org/10.1016/j.aquaculture.2008.05.004>

Horváth, L., Tamás, G., Coche, A.G., Kovács, E., Moth-Poulsen, T. and Woynarovich, A., 2015. Training manual on the artificial propagation of carps. A handout for on-farm training workshops on artificial propagation of common carp and Chinese major carps in Central and Eastern Europe, the Caucasus and Central Asia. FAO, Second Edition, 31p.

Hulak, M., Kaspar, V., Kohlmann, K., Coward, K., Tešitel, J., Rodina, M., Gela, D., Kocour, M. and Linhart, O., 2010. Microsatellite-based genetic diversity and differentiation of foreign common carp (*Cyprinus carpio*) strains farmed in the Czech Republic. *Aquaculture*, 298(3-4), 194-201. <https://doi.org/10.1016/j.aquaculture.2009.10.021>

Jerry, D.R., Preston, N.P., Crocos, P.J., Keys, S., Meadows, J.R. and Li, Y., 2004. Parentage determination of Kuruma shrimp *Penaeus (Marsupenaeus) japonicus* using microsatellite markers (Bate). *Aquaculture*, 235(1-4), 237-247.

<https://doi.org/10.1016/j.aquaculture.2004.01.019>

Kantartzi, S. K. (2013). Microsatellites: methods and protocols. Springer, New York, 475 p. <https://doi.org/10.1007/978-1-62703-389-3>

Khara, H., Shahrooz, B.N., Hadiseh, D., Rahbar, M., Ahmadnejad, M. and Khodadoost, A., 2012. The effect of cations on sperm motility performance and fertilizing ability of silver carp *Hypophthalmichthys molitrix*. *Acta veterinaria*, 62(5-6), 599-609. <https://doi.org/10.2298/AVB1206599K>

Kolar, C.S., Chapman, D.C., Courtenay Jr, W.R., Housel, C.M., Williams, J.D. and Jennings, D.P., 2005. Asian carps of the genus *Hypophthalmichthys* (Pisces, Cyprinidae) a biological synopsis and environmental risk assessment, Report to U.S. Fish and Wildlife Service per Interagency Agreement 94400-3-0128, 173p.

Koljonen, M.L., Pella, J.J. and Masuda, M., 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. *Canadian Journal of Fisheries and Aquatic Sciences*, 62(9), 2143-2158. <https://doi.org/10.1139/f05-128>

Letcher, B.H. and King, T.L., 2001. Parentage and grandparentage assignment with known and unknown matings: application to Connecticut River Atlantic salmon restoration. *Canadian Journal of Fisheries and Aquatic*

*Sciences*, 58(9), 1812-1821. <https://doi.org/10.1139/f01-125>

Liu, P., Xia, J.H., Lin, G., Sun, F., Liu, F., Lim, H.S., Pang, H.Y. and Yue, G.H., 2012. Molecular parentage analysis is essential in breeding Asian seabass. *PloS one*, 7(12), p.e51142. <https://doi.org/10.1371/journal.pone.0051142>

Liu, X., Zhao, G., Wang, Z., Cai, M., Ye, H. and Wang, Q., 2012. Parentage assignment and parental contribution analysis in large yellow croaker *Larimichthys crocea* using microsatellite markers. *Current Zoology*, 58(2), 244-249. <https://doi.org/10.1093/czoolo/58.2.244>

Liu, Z.J. and Cordes, J.F., 2004. DNA marker technologies and their applications in aquaculture genetics. *Aquaculture*, 238(1-4), 1-37. <https://doi.org/10.1016/j.aquaculture.2004.05.027>

Machado-Schiaffino, G., Dopico, E. and Garcia-Vazquez, E., 2007. Genetic variation losses in Atlantic salmon stocks created for supportive breeding. *Aquaculture*, 264(1-4), 59-65. <https://doi.org/10.1016/j.aquaculture.2006.12.026>

Marshall, T.C., Slate, J.B.K.E., Kruuk, L.E.B. and Pemberton, J.M., 1998. Statistical confidence for likelihood-based paternity inference in natural populations. *Molecular ecology*, 7(5), 639-655.

<https://doi.org/10.1046/j.1365-294x.1998.00374.x>

Moretzaei, S.R.S., Hooshmand, H., Ahangarzadeh, M., Jorfi E., Dehghan, S.M., Kianersi, F., Tavasoli, M., Soleimani, J., Mohseninejad, L. and Sanjari M., 2011. Investigate warm water fish ponds in order to identify causes of mortalities in Silver carp. General administration of Fisheries in Khouzestan province, 162 p.

Motllebi, A., Sharifrohani, M. 2010. Developmental Map for warm water fishes of Iran, Coordination of science and Aquaculture society, First edition, 115 p. (In Persian)

Neff, B.D., 2001. Genetic paternity analysis and breeding success in bluegill sunfish (*Lepomis macrochirus*). *Journal of Heredity*, 92(2), 111-119. <https://doi.org/10.1093/jhered/92.2.111>

Norris, A.T., Bradley, D.G. and Cunningham, E.P., 2000. Parentage and relatedness determination in farmed Atlantic salmon (*Salmo salar*) using microsatellite markers. *Aquaculture*, 182(1-2), 73-83. [https://doi.org/10.1016/S0044-8486\(99\)00247-1](https://doi.org/10.1016/S0044-8486(99)00247-1)

O'connell, M. and Wright, J.M., 1997. Microsatellite DNA in fishes. *Reviews in fish biology and fisheries*, 7, 331-363. <https://doi.org/10.1023/A:1018443912945>

Peakall, R.O.D. and Smouse, P.E., 2006. GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Molecular ecology notes*, 6(1), 288-92

295. <https://doi.org/10.1111/j.1471-8286.2005.01155.x>

Peakall, R.O.D. and Smouse, P.E., 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics*, 28(19), 2537-2539. <https://doi.org/10.1093/bioinformatics/bts460>

Povh, J.A., Ribeiro, R.P., Sirol, R.N., Streit Jr, D.P., Moreira, H.L.M., Siewerdt, F., Lopera-Barrero, N.M., Mangolin, C.A. and Vargas, L., 2010. Microsatellite analysis of the parental contribution of *Piaractus mesopotamicus* to the production of offspring in the semi-natural system of reproduction. *Brazilian Archives of Biology and Technology*, 53, 389-396. <https://doi.org/10.1590/S1516-89132010000200018>

Rahman, M.M., Rahman, M.S. and Hasan, M., 2011. Changes in sperm quality of silver (*Hypophthalmichthys molitrix*) and bighead carps (*Hypophthalmichthys nobilis*) during the spawning season. *Asian Fisher Sci*, 24, 413-425. <https://doi.org/10.33997/j.afs.2011.24.4.006>

Ruzzante, D.E., McCracken, G.R., Parmelee, S., Hill, K., Corrigan, A., MacMillan, J. and Walde, S.J., 2016. Effective number of breeders, effective population size and their relationship with census size in an iteroparous species, *Salvelinus fontinalis*. *Proceedings of the Royal Society B: Biological Sciences*, 283(1823), 20152601. <https://doi.org/10.1098/rspb.2015.2601>

- Sourinejad, I., Kalbassi, M.R., Pino-Querido, A., Vera, M., Bouza, C. and Martinez, P., 2011. Parentage assignment of progeny in mixed milt fertilization of Caspian brown trout *Salmo trutta caspius* using microsatellite DNA markers: Implications for conservation. *African Journal of Biotechnology*, 10(26), 5084-5090.
- Subasinghe, R.P., Curry, D., McGladdery, S.E. and Bartley, D., 2003. Recent Technological Innovations in Aquaculture. In: Review of the State of World Aquaculture. *FAO Fisheries Circular No.886, Rev. 2*, 59-74.
- Tregenza, T. and Wedell, N., 2000. Genetic compatibility, mate choice and patterns of parentage: invited review. *Molecular ecology*, 9(8), 1013-1027. <https://doi.org/10.1046/j.1365-294x.2000.00964.x>
- Vandeputte, M., Kocour, M., Mauger, S., Dupont-Nivet, M., De Guerry, D., Gela, D., Vallod, D., Linhart, O. and Chevassus, B., 2005. Heritability estimates for growth-related traits using microsatellite parentage assignment in juvenile common carp (*Cyprinus carpio* L.). *Aquaculture*, 247, 31-32. <https://doi.org/10.1016/j.aquaculture.2003.12.019>
- Vandeputte, M., Rossignol, M.N. and Pincet, C., 2011. From theory to practice: empirical evaluation of the assignment power of marker sets for pedigree analysis in fish breeding. *Aquaculture*, 314(1-4), 80-86. <https://doi.org/10.1016/j.aquaculture.2011.01.043>
- Was, A. and Wenne, R., 2002. Genetic differentiation in hatchery and wild sea trout (*Salmo trutta*) in the Southern Baltic at microsatellite loci. *Aquaculture*, 204(3-4), pp.493-506. [https://doi.org/10.1016/S0044-8486\(01\)00835-3](https://doi.org/10.1016/S0044-8486(01)00835-3)
- Wedekind, C., Rudolfsen, G., Jacob, A., Urbach, D. and Müller, R., 2007. The genetic consequences of hatchery-induced sperm competition in a salmonid. *Biological conservation*, 137(2), 180-188. <https://doi.org/10.1016/j.biocon.2007.01.025>
- Weinman, L.R., Solomon, J.W. and Rubenstein, D.R., 2015. A comparison of single nucleotide polymorphism and microsatellite markers for analysis of parentage and kinship in a cooperatively breeding bird. *Molecular ecology resources*, 15(3), 502-511. <https://doi.org/10.1111/1755-0998.12330>
- Xu, Z., Primavera, J.H., de la Pena, L.D., Pettit, P., Belak, J. and Alcivar-Warren, A., 2001. Genetic diversity of wild and cultured black tiger shrimp (*Penaeus monodon*) in the Philippines using microsatellites. *Aquaculture*, 199(1-2), 13-40. [https://doi.org/10.1016/S0044-8486\(00\)00535-4](https://doi.org/10.1016/S0044-8486(00)00535-4)
- Xue, D., Zhang, T. and Liu, J.X., 2014. Microsatellite evidence for high frequency of multiple paternity in the marine gastropod *Rapana venosa*. *PLoS One*, 9(1), p.e86508. <https://doi.org/10.1371/journal.pone.0086508>