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Evaluation of 1-stage and 2-stage selection in yellow perch I: Genetic and phenotypic parameters for body weight of F_1 fish reared in ponds using microsatellite parentage assignment[1]

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ABSTRACT: Two selection methods, 1-stage selection (OSS) and 2-stage selection (TSS), for improving efficiency and profitability of selective breeding of yellow perch were evaluated, through examining the genetic and phenotypic parameters for BW of F_1 fish using microsatellite parentage assignment in this study. Approximately 94% of the sampled yellow perch progeny were assigned to single parental pairs using 8 microsatellite markers, which confirmed the applicability of the communal rearing technique in yellow perch breeding. Within OSS, the genetic correlation between 1-yr-BW and 2-yr-BW was high (0.98), indicating that the growth of yellow perch recorded at yr 1 could predict their growth for yr 2. Also mean family BW and family EBV for BW between yr 1 and 2 were found to be significantly correlated, suggesting yr 1 fast-growing yellow perch families continued to be the fast growing families in yr 2. Two-year random fish undergoing TSS were significantly heavier ($P < 0.01$) than those undergoing OSS. In addition, top males and females with TSS were heavier ($P < 0.01$) than those with OSS. Based on these results we concluded that the TSS was more desirable and effective for yellow perch breeding compared with OSS in terms of improving selection efficiency and reducing costs.

Key words: genetic and phenotypic parameter, growth trait, microsatellite, one-stage selection, parentage assignment, two-stage selection

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INTRODUCTION

The yellow perch, *Perca flavescens*, has a native distribution throughout the Nearctic ecozone from South Carolina to Nova Scotia, westward throughout the Great Lakes region and the Mississippi Valley, and northward to the Red River Basin (Nelson, 1976). The mild taste and firm flesh with low fat and phospholipid content make this species a traditional regional favorite with consumers (Malison, 1999, 2000). In addition, this species is a popular recreational angling resource (Leclerc et al., 2008). However, dramatic reductions in population sizes of yellow perch have been underway in the Great Lakes area since approximately 1950 (Eshenroder, 1977; McComish, 1986; Marsden and Robillard, 2004). At present, commercial fishing of yellow perch has diminished or ceased altogether in some states surrounding the Great Lakes (Kelly, 2000), whereas yellow perch still have a high market demand and value in their native regions (Malison, 2000). No doubt, this species holds tremendous potential for aquaculture in its native region. Despite of the recent technical advancements in yellow perch aquaculture methods (Manci, 2001), this species is still considered as an alternate aquaculture species. A major constraint to the expansion of the yellow perch aquaculture industry is the slow growth rate

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of currently cultured populations of this species (Malison et al., 2003).

The increased productivity of modern breeds of terrestrial livestock species is primarily due to genetic improvement programs utilizing selective breeding. In recent years, selective breeding has become an increasingly important component in aquaculture production and genetic gains have been made for some aquaculture species (Robert, 2004; Gjedrem and Thodesen, 2005). As part of the effort to enhance yellow perch aquaculture production, our laboratory (Aquaculture Genetics and Breeding Laboratory, Ohio State University South Centers, Piketon) has initiated a selective breeding program aimed at solving the "slow growth" problem in this species.

Choosing a suitable selection method is a prerequisite for implementing a sound breeding program. Individual selection and family selection have been often applied in breeding programs for many aquaculture species (Moav and Wohlfarth, 1976; Gjedrem, 1983; Gjerde, 1986; Huang and Liao, 1990). Compared with family selection, individual selection generally seems to be less effective (Hershberger et al., 1990; O'Flynn et al., 1999). Moreover, in some breeding programs of aquaculture animals where the individual selection method is applied, the positive response obtained from the first generation does not continue in successive generations (Chevassus et al., 2004). However, because individual selection is much cheaper, it is still of special interest to aquaculture animal breeders. Funds play an important role in the development of selective breeding of aquaculture animals and have a strong impact on the choice of selection methods. To reduce the costs of breeding programs for aquaculture animals, many methods and techniques are introduced and applied.

One method is to practice selection in stages (Cochran, 1951; Mueller, 1984; Wade and James, 1996; Martinez et al., 2006). The selection procedure can be carried out based on traits measured in early life, which correlate positively with the same traits measured in later life (in general, at maturity; Martinez and Neira, 1998). The savings for breeding programs can be achieved by reducing considerably the number of individuals needed to be reared up to reproduction (namely, culling inferior individuals in early life).

Under traditional family selection, the fingerlings from different families need to be reared separately until they are large enough to be physically tagged. Therefore, large numbers of culture facilities (e.g., ponds or tanks), which are expensive, are needed for selective breeding. Thanks to the advent of molecular markers (e.g., RFLP, amplified fragment-length polymorphism, microsatellites, SNP) that can be used to determine the parentage of each communally reared individual (Vandeputte et al., 2004; Couch, 2006; Saillant et al., 2006; Castro et al., 2008; Dupont-Nivet et al., 2008; Gray et al., 2008), a communal rearing technique (i.e., rearing all families in the same environment) can be applied to selective breeding in aquaculture. The communal rearing technique can reduce the costs of culture facilities and increase the number of families or groups used for breeding programs (McGinty, 1987; Macbeth, 2005). Additionally, the environmental component of phenotypic variation among families can be largely minimized, unmasking additive genetic contributions to commercially important performance traits (Couch, 2006). Therefore, due to the application of molecular markers in aquaculture animal breeding, molecular marker-aided family selection seems to be an effective and money-saving selection method, which is becoming widely used in breeding programs of aquaculture animals (O'Reilly et al., 1998; Dupont-Nivet et al., 2008; Gheyas et al., 2009).

To improve efficiency and reduce costs of selective breeding of yellow perch, 2 selection methods, designated as 1-stage selection (**OSS**) and 2-stage selection (**TSS**), were tested by analyzing genotypic and phenotypic parameters for BW of F_1 yellow perch reared in ponds using microsatellite parentage assignment in this study. In TSS, young of the year (**YOY**) fish were selectively graded according to their length and width, and the top 50% were selected to be continuously reared to the end of yr 2. No culling-selection procedure was used in OSS. For each selection method (i.e., OSS and TSS), the largest and unrelated fish by family were selected as candidate broodfish of next generation at the end of yr 2.

MATERIALS AND METHODS

All experimental procedures involving animals were approved by the Ohio State University Institutional Animal Care and Use Committee.

Mating and Fry Production

Yellow perch broodfish used in the study were selected from the base generation of the genetic improvement program at the Ohio State University South Centers. Thirteen dams and 21 sires were used to produce the experimental fish in March 2006. Each dam was put into a 55-L round tank with 1 or 2 sires for spawning (1 dam × 2 sires for 12 mating sets and 1 dam × 1 sire for 1 mating set). Four sires were used twice during mating. Dams spawned naturally in the tanks, resulting in eggs of each dam fertilized by either 1 or both sires (for 1 dam × 2 sires). Fertilized eggs obtained from different mating sets were separately incubated in 25-L round tanks with flow-through well water for 11 to 12 d at 11 to 12°C. Thirteen mating sets were successfully hatched, and the same numbers of fry from each set were combined and stocked into earthen ponds for a 6-wk nursery phase. Subsequently, feed training was conducted in 400-L round tanks for 3 wk.

Communal Rearing and Culling Selection

A total of 6,100 feed-trained fingerlings were stocked into each of four 0.1-ha earthen ponds (labeled pond 4, 6, 7, and 8) in June 2006 and communally reared for 21 mo. Commercial floating feed (Silver Cup, 45% protein, 16% fat, Nelson and Sons Inc., Murray, UT) was used during the period of communal rearing. Fish were fed daily at 2% of their BW over the summer, 3% BW in the spring and fall, and 1% BW during the winter when water temperature (**WT**) was above 10°C, based on an assumed survival of 75% and estimated or calculated biomass. Daily ration was distributed over the entire surface of each pond twice daily at 0900 and 1600 h. Dissolved oxygen (**DO**) and WT measurements were taken twice daily, morning and afternoon, with a YSI 51B DO meter (Yellow Spring Instruments, Yellow Spring, OH). Any pond with DO concentrations at or below 5.0 mg/L received aeration with electrical aerators until the DO concentrations stabilized above 7.0 mg/L. No significant differences ($P > 0.05$) in these 2 variables were found among the 4 ponds for the entire period of the experiment.

At the end of yr 1, fish from 2 ponds (pond 4 and pond 7) were graded based on the following procedure: 100 fish were randomly collected from each of the 2 ponds and their lengths measured and ordered to determine the size-cut-off points for the top 50% fish. Based on these cut-off points, 10 to 20 fish were selected from each pond group for testing to properly set the grader bar gap. Then the top 50% of fish were selected from the remaining fish from each of the 2 ponds. The top 50% fish from pond 4 and pond 7 were restocked into pond 6 and pond 8, respectively, for yr-2 grow-out (TSS). Fish from the other 2 ponds (pond 6 and pond 8) were harvested for sampling and restocked into pond 4 and pond 7, respectively, without culling the bottom 50% fish (OSS). In this study, the total length was chosen as a culling criterion because it is highly correlated with BW and easy to measure on large numbers of fish. It was agreed that correlations among body measurements (such as BW, length, depth, and width) in fish were usually highly significant (Rutten et al., 2005; Nguyen et al., 2007).

Samples and Measurements

In April 2007 at the end of yr-1 rearing, all 4 ponds were drained and harvested. All fish from each pond were counted and group-weighed (drained BW) to the nearest 1 g to determine total biomass. A total of 150 fish were randomly sampled from each of the 4 ponds at the end of yr 1 before grading selection for BW and total length measurements and fin-clipped. At the end of yr-2 rearing in March 2008, the same sampling procedures were conducted as at the end of yr 1. A total of 148 and 146 fish were randomly sampled from pond 4 and pond 7, respectively, with OSS, and 122 and 147 fish were similarly collected from pond 6 and pond 8, respectively, with TSS. In addition, a total of 137, 127, 111, and 105 fish were obtained as the top 10% largest fish from pond 4, 7, 6, and 8, respectively. A nonlethal biopsy (fin clip) obtained from each specimen (including broodfish and progeny) was preserved immediately in 95% ethanol for DNA analyses and subsequent parentage analysis.

Genotyping

A total of 1,677 fish including 34 broodfish and 1,643 progeny were genotyped with 8 highly polymorphic microsatellite markers (YP30, YP41, YP49, YP60, YP73, YP78, YP96, and YP109; Li et al., 2007). Amplification of microsatellite loci was performed with the 3-primer system where a universal primer had a 5′ label of NED, FAM, or HEX. Polymerase chain reactions of 6 μL contained 2.6 μL of JumpStart RedMix (Sigma, St. Louis, MO), 0.75 pmol of nontailed primer, 0.375 pmol of labeled primer, 0.05 pmol of the tailed primer, 25 ng of DNA, and 267 μM spermidine. Amplification was performed in PTC-200 thermal cyclers (MJ Research, Waltham, MA) using an initial denaturation at 94°C for 2 min, followed by 35 cycles of 30 s denaturation at 94°C, 30 s annealing at 55°C, 30 s extension at 72°C, and a final 5-min extension at 72°C. Amplification products were separated using an ABI 3130 Prism DNA genetic analyzer (Foster City, CA), and the results were analyzed using GeneMapper software (Foster City, CA).

Genotypic Data Analyses

Cervus 3.0 (Field Genetics, London, UK) was used to estimate allele frequencies [number of alleles (***A***)], heterozygosities [observed heterozygosity (***H*****$_o$**) and expected heterozygosity (***H*****$_e$**)], and polymorphism information content (**PIC**) for yellow perch from each pond in different years (yr 1 and 2) according the genotypic data. In addition, A and H_e for yellow perch from the 2 selection methods were examined. The DNA pedigrees for each fish group (randomly selected fish in yr 1, and randomly selected fish and the top 10% largest fish in yr 2) from each pond were constructed based on the genotypic data using Cervus 3.0. To assess the correctness of allocation, simulations were run with the same parameters, with the set of parents and the same number of progeny as those used in the allocation procedure. No pedigree information was available on the broodfish.

Statistical Analyses

Differences in mean A and H_e for yellow perch between any 2 ponds in yr 1, between 2 ponds within each selection method, between the 2 selection methods, between 1- and 2-yr-old fish from the OSS method,

and between 1- and 2-yr-old fish from the TSS method were analyzed using paired-samples *t*-test. Significant differences for DO, WT, 1-yr BW (**OYW**), and 1-yr length (**OYL**) for yellow perch among the 4 ponds were evaluated using 1-way ANOVA. Differences in 2-yr BW (**TYW**) and 2-yr lengths (**TYL**) for random fish and the top 10% of the largest fish between the 2 different selection methods were examined using the independent-samples *t*-test. Within each selection method, differences in TYW and TYL for random fish and the top 10% of the largest fish between 2 ponds were also estimated using the independent-samples *t*-test. The differences among the numbers of progeny assigned to each maternal family (i.e., maternal family size) in each pond from different years were examined using χ^2 tests. Correlation coefficients of family size, mean family BW, and family length for yellow perch between any 2 ponds in yr 1 were estimated using the Bivariate correlations program with Pearson's linear correlation coefficient (SPSS Inc., Chicago, IL). For yr 2, estimations for correlation coefficients of family size, mean family BW, and family length for random fish and the top 10% of the largest fish between 2 ponds within each selection method were also performed using the Bivariate correlations program with Pearson's linear correlation coefficient. Significant differences were accepted at $P < 0.05$.

Variance and covariance components were estimated using the average information algorithm REML as implemented in ASReml (VSN International Ltd., Hemel Hempstead, UK) and using the following multi-trait animal model:

$$\mathbf{Y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e},$$

where **Y** is a vector of phenotypic observations for the studied traits (BW and total lengths) of random fish; **b** is a vector of fixed effects (pond and sex); **a** is a vector of random breeding values (sires, dams, and progeny); **e** is a vector of random errors; and **X** and **Z** are design matrices relating phenotypic observations to elements of **b** and **a**, respectively.

The heritability was calculated as the ratio $h^2 = \sigma^2_a/(\sigma^2_a + \sigma^2_e)$, where σ^2_a and σ^2_e denoted additive genetic variance and residual variance, respectively. In this study, estimates of h^2 were generated for OYW, OYL, and TYW and TYL recorded from OSS.

Genetic correlation ($r_{a(i,j)}$) between the 2 traits was determined from the genetic covariance ($\sigma_{a(i,j)}$) and genetic SD ($\sigma_{a(i)}$ and $\sigma_{a(j)}$, square roots of the genetic variances), calculated as $r_{a(i,j)} = \sigma_{a(i,j)}/\sigma_{a(i)}\sigma_{a(j)}$. The phenotypic correlation between the 2 traits was estimated as the ratio of phenotypic covariance ($\sigma_{p(i,j)}$) to the product of the square roots of the phenotypic variances of trait i and trait j (i.e., $r_{p(i,j)} = \sigma_{p(i,j)}/\sigma_{p(i)}\sigma_{p(j)}$). Genetic and phenotypic correlations were estimated between OYW and OYL, between TYW and TYL recorded from OSS, and between OYW and TYW of yellow perch within OSS.

Best linear unbiased prediction analyses in ASReml were used to estimate breeding values for broodfish and progeny. In OSS, the correlation of mean family EBV for BW of random yellow perch between yr 1 and 2 was estimated using the Bivariate correlations program with Pearson's linear correlation coefficient.

RESULTS

Genotype Diversity and Parentage Assignment

Near-complete genotyping was obtained for all the broodfish and progeny in this study. The average total number of alleles observed per locus for progeny in yr 1, and progeny from OSS and TSS in yr 2 were 9.8, 10.8, and 11, respectively. The observed heterozygosity obtained from 4 ponds at yr 1 ranged from 0.40 to 0.96. At yr 2, the values for this variable ranged from 0.45 to 0.96. The average expected heterozygosity observed per locus for progeny at yr 1, and progeny from OSS and TSS at yr 2 were 0.68, 0.68, and 0.67, respectively. Allelic diversity in the broodfish provided good resolving power for assigning parentage to progeny because the mean polymorphic information content for yellow perch reared in each pond from different years ranged from 0.61 to 0.66. For yr 1, there were no significant differences in mean A and H_e for yellow perch between any 2 ponds. At yr 2, no significant differences were found in mean A and H_e for yellow perch between the 2 ponds with TSS, whereas significant differences ($P = 0.006$ for A and $P = 0.22$ for H_e) were detected in these 2 variables between the 2 ponds with OSS. There were no significant differences detected in mean A and H_e for yellow perch between 2 selection methods. In addition,

Table 1. Success ratio of parental assignment for yellow perch progeny according to genetic pedigree analyses[1]

	Yr 1 (random fish)				Yr 2 (random fish)				Yr 2 (top 10% largest fish)				
Item	P4[2]	P7[2]	P6	P8	P6[2]	P8[2]	P4	P7	P6[2]	P8[2]	P4	P7	Total
NOSP	150	150	150	150	122	147	148	146	111	105	137	127	1,643
NOPAP	142	139	145	140	117	137	138	137	101	98	126	123	1,543
SROPA, %	95	93	97	93	96	93	93	94	91	93	92	97	94

[1]P4 = pond 4; P7 = pond 7; P6 = pond 6; P8 = pond 8; NOSP = number of sampled progeny; NOPAP = number of progeny assigned to single parental pairs; SROPA = success ratio of parental assignment.

[2]Two-stage selection.

Table 2. Correlation coefficients (CC) and their *P*-values of family size for yellow perch of yr 1 rearing between any 2 ponds and for yellow perch (random fish and the top 10% largest fish) between the 2 ponds within each selection method at yr 2

	Yr 1			Yr 2 (random fish)		Yr 2 (10% largest fish)	
CC	Pond 7	Pond 6	Pond 8	Pond 7	Pond 8[1]	Pond 7	Pond 8[1]
Pond 4	0.8*	0.85*	0.88*	0.82*	—	0.78*	—
Pond 7	—	0.82*	0.77*	—	—	—	—
Pond 6[1]	—	—	0.82*	—	0.93*	—	0.65*

[1]Two-stage selection.

*Significant correlation ($P < 0.01$).

no significant differences were presented in mean A and H_e for yellow perch between 1 and 2 yr of age with OSS, and between 1 and 2 yr of age with TSS.

High success ratios of parental assignment (each progeny was assigned to a single parental pair) for yellow perch were obtained using 8 polymorphic microsatellite markers in this study (Table 1). The ratio was from 91 to 97%. In this study, 1,543 progeny were successfully assigned to single parental pairs; that is, approximately 94% of all the sampled yellow perch progeny were assigned to single parental pairs.

A total of 25 full-sib families were represented in the sampled progeny. Significant differences in the maternal family size (the number of progeny assigned to a single pair parent) was observed in each pond from yr 1 and 2 (χ^2 test, $P = 0.00$), indicating the presence of parental genetic variations in survival of yellow perch. Moreover, in each mating set with 1 dam × 2 sires, contributions of 2 sires for the maternal family differed greatly, which together with the situation described above resulted in significant differences in family size. About 50% of the progeny were from 5 families in each pond, and some families had no progeny or a few progeny found. High similarities were found ($P < 0.01$; Table 2) in the ranking of family size between any 2 ponds at yr 1 and between 2 ponds within each selection method at yr 2 for random fish and the top 10% largest fish, suggesting there were no pond effects on family survival.

Growth Performances and Pond by Family Effects

Yr-1 Fish. The mean BW and total length of yellow perch at the end of yr 1 in 4 replicated ponds ranged from 16.91 to 27.46 g, and 11.05 to 13.03 cm, respectively (Figure 1). There were significant differences ($P < 0.05$) in the BW and total length among most of ponds at yr 1 (Figure 1). With the exception of the correlation in mean family BW between pond 4 and 7, there were no significant correlations in mean family BW and family length between any other 2 ponds (Table 3). This indicated the families demonstrating superior mean growth performances (BW and total length) in 1 pond did not exhibit superior growth performances in other ponds, reflecting significant environment effects.

Yr-2 Fish. Measurements of BW and total lengths of yellow perch for yr 2 (random fish and top 10% largest fish) with OSS and TSS selection are shown in Table 4. There were significant differences ($P < 0.01$) in BW and total lengths for random fish and the top 10% largest fish recorded at yr 2 between the OSS and TSS. Year-2 yellow perch from TSS were significantly heavier and longer than yr-2 yellow perch from OSS. Significant differences ($P < 0.05$) in BW and length for random fish and the top 10% largest fish were found between 2 ponds within a selection method in some cases.

There were no significant correlations in mean family BW and family length for random fish between 2 ponds within each selection method at the end of yr-2 culture (Table 5). In addition, no significant correlations in mean family BW and length for top 10% largest fish were detected between 2 ponds with TSS, whereas opposite results were observed in OSS. These results indicated there were significant pond effects at yr 2 as detected for yr-1 fish.

Heritabilities, and Genetic and Phenotypic Correlations

Heritability estimates for growth traits (i.e., OYW and OYL, and TYW and TYL recorded from OSS), and genetic and phenotypic correlations between BW

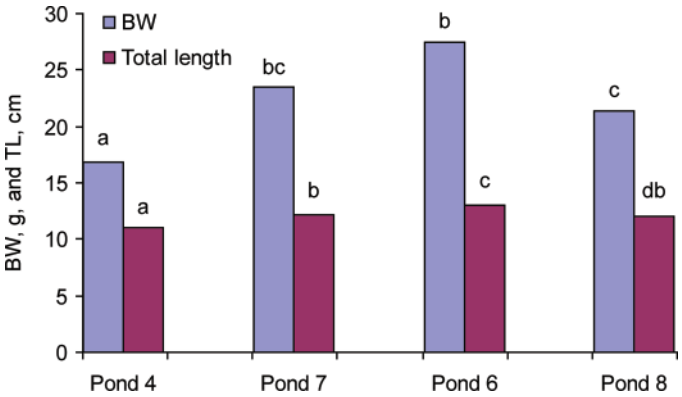

Figure 1. Mean BW and total length (TL) of 1-yr-old yellow perch stocked into 4 ponds and their significance levels. Groups with the same letter (a–d) were not significantly different ($P > 0.05$) for BW or length. Color version available in the online PDF.

Table 3. Correlation coefficients (CC) of mean family BW and family length for yellow perch between any 2 ponds at yr 1 and their significance levels

	Mean family BW			Mean family length		
CC (P-value)	Pond 7	Pond 6	Pond 8	Pond 7	Pond 6	Pond 8
Pond 4	0.51* ($P = 0.043$)	0.085 ($P = 0.75$)	0.20 ($P = 0.46$)	0.48 ($P = 0.063$)	−0.007 ($P = 0.98$)	0.15 ($P = 0.58$)
Pond 7	—	−0.05 ($P = 0.85$)	0.17 ($P = 0.53$)	—	−0.084 ($P = 0.76$)	0.18 ($P = 0.51$)
Pond 6	—	—	−0.16 ($P = 0.56$)	—	—	−0.17 ($P = 0.53$)

*Significant correlation ($P < 0.05$).

and total length are shown in Table 6. Heritabilities estimated for OYW, OYL, TYW, and TYL were very low. The genetic and phenotypic correlations between BW and total length were high and close to 1 at 1 yr of age and at 2 yr of age for fish within OSS. Because of the high correlations between BW and total length, we estimated the correlations for BW recorded in yr 1 and 2. Correlations between OYW and TYW of yellow perch with OSS were high, resulting in 0.98 for genetic correlation and 0.71 for phenotypic correlation (Table 7). Significant correlation ($P = 0.004$) in mean family BW between yr 1 and 2 was found (Table 7, Figure 2). Correlation in mean family EBV for BW between yr 1 and 2 was significant ($P = 0.035$) also (Table 7, Figure 2).

DISCUSSION

A relatively low average total number of alleles per locus for yellow perch progeny was observed in this study (mean number of alleles: 9.8 for 1-yr yellow perch, 10.8 for 2-yr yellow perch with OSS, and 11 for 2-yr yellow perch with TSS), which could be the result of low genetic variation. These results further contribute to the hypothesis that yellow perch exhibit only moderate levels of genetic variation, as inferred by Brown et al. (2007), and evidence that inbreeding could potentially become an issue of importance in the breeding program for yellow perch. There were no significant differences in mean A and H_e for yellow perch between any 2 replicated ponds, suggesting the pond effect on genetic structures of pond populations was not significant. No significant differences were found in mean A and H_e for yellow perch between OSS and TSS, indicating that removing the bottom 50% fish from the population at end of yr 1 (i.e., TSS) did not significantly affect the genetic variation of the cultured population.

The establishment of pedigrees is necessary for estimates of genetic parameters and breeding values for traits with high economic values for a marker-aided breeding program. Greater success rates of parental assignments using microsatellite markers have been observed in many commercial fish species reared communally. Fishback et al. (2002) used microsatellite multiplex genotyping systems to resolve pedigrees for groups of rainbow trout progeny and obtained a success rate of 91 to 95%. In gilthead seabream, Castro et al. (2008) and Navarro et al. (2009) successfully assigned 100% of the progeny to a single parental pair using microsatellite markers through single and multiplex reaction, respectively. Up to 88.0% of the parental assignment ratio in yellow perch has been documented by Wang et al. (2009) using 7 microsatellite markers. In the current study, a greater assignment ratio (approximately 94%) was obtained using 8 microsatellite markers. Five of the markers used in this study were identical to the microsatellite markers used by Wang et al. (2009).

Table 4. Body weight and total length (TL; mean ± SE) for yellow perch (random fish and top 10% largest fish) with 1-stage (OSS) and 2-stage selection (TSS) in yr 2

	Random fish		Top 10% largest fish	
Item	BW, g	TL, cm	BW, g	TL, cm
TSS				
Pond 6	123.06 ± 3.50[a]	22.42 ± 0.21[a]	193.62 ± 6.64[a]	24.04 ± 0.24[a]
Pond 8	128.29 ± 3.87[a]	21.55 ± 0.19[b]	178.05 ± 6.14[a]	23.42 ± 0.24[a]
OSS				
Pond 4	102.40 ± 2.78[a]	21.08 ± 0.20[a]	146.79 ± 5.08[a]	22.29 ± 0.21[a]
Pond 7	119.11 ± 4.25[b]	20.98 ± 0.20[a]	183.71 ± 5.29[b]	23.77 ± 0.20[b]
TSS	125.91 ± 2.64[a]	21.95 ± 0.14[a]	186.05 ± 4.55[a]	23.74 ± 0.17[a]
OSS	110.70 ± 2.58[b]	21.03 ± 0.14[b]	164.55 ± 3.83[b]	23.00 ± 0.15[b]

[a,b]Within a column, means followed by different superscript letters within each selection method or between the 2 selection methods were significantly different ($P < 0.05$).

Table 5. Correlation coefficients (CC) and their *P*-values of mean family BW (MFW) and mean family length (MFL) for yellow perch (random fish and top 10% largest fish) between the 2 ponds within each selection method at yr 2

	Random fish		Top 10% largest fish	
CC (*P*-value)	Pond 6[1] × Pond 8[1]	Pond 4 × Pond 7	Pond 6[1] × Pond 8[1]	Pond 4 × Pond 7
MFW	0.027 ($P = 0.92$)	−0.039 ($P = 0.88$)	0.19 ($P = 0.47$)	0.58* ($P = 0.011$)
MFL	−0.07 ($P = 0.78$)	−0.045 ($P = 0.86$)	0.17 ($P = 0.55$)	0.53* ($P = 0.024$)

[1]Two-stage selection.
*Significant correlation ($P < 0.05$).

Using molecular markers to establish pedigrees allows for the use of communal rearing in selective breeding programs. This technique can reduce the number of rearing units necessary for production of families and increase the number of families or groups that can be compared (McGinty, 1987; Macbeth, 2005). Communal rearing has the additional importance of largely minimizing the environmental component of phenotypic variation among families and unmasking additive genetic contributions to commercially important performance traits (Couch, 2006). In recent years, this technique has been successfully applied in selective breeding for several aquaculture species (O'Reilly et al., 1998; Dupont-Nivet et al., 2008; Gheyas et al., 2009). The increased success ratio of parental assignment obtained in this study further confirmed the feasibility and applicability of the communal rearing technique in the yellow perch selective breeding program.

Significant differences in the number of yellow perch progeny assigned to each family were observed. Similarities were reported in many other fish species (Fishback et al., 2002; Navarro et al., 2009). The unequal family sizes could result in some bias in the estimates of the genetic parameters. A strategy of dividing the eggs from each dam into equal aliquots according to the number of males used before fertilization was recommended by many authors (Vandeputte et al., 2004; Saillant et al., 2006) to reduce the differences in family sizes.

In pond culture situations, environmental factors such as DO, WT, fish density, and feeding are the most important factors relative to fish growth. Some studies in yellow perch have demonstrated that WT and fish density have a profound influence on growth (Tidwell et al., 1999; Headley and Lauer, 2008). During the entire period of the experiment, we strove to maintain the environmental factors (DO, water temperature, fish density, and feeding) of the 4 ponds as similar as possible. However, significant differences in BW and total length were found among replicated ponds at yr 1 and 2, indicating there were strong pond effects on growth in communal rearing systems for yellow perch. Many studies of genotype × environment interactions on phenotype have been widely reported in various aquatic animals (Fishback et al., 2002; Saillant et al., 2006; Wang and Li, 2007). One of our previous studies (Wang et al., 2009) suggested that there was no significant difference in family rankings of the top 10% heaviest yellow perch between replicated ponds. This similar result was obtained with the OSS method in the current experiment. However, no significant correlations in mean family BW and length for random yr-1 fish, random yr-2 fish, and the top 10% largest fish with TSS between 2 replicated ponds were found in this study. These results indicate that there were strong pond and social interactions on fish growth in the communal pond rearing system. In some cases, they were not so great as to override the greater genetic growth capacity of certain yellow perch families communally reared in ponds, but in other cases they were. Therefore, other than the very top fish, a second level of the largest fish should be included into breeding candidates for the selective breeding program. We must point out that egg quality, bias in survival in ponds, and ability to go "on

Table 6. Estimates of heritability ($h^2 \pm$ SE, on the diagonal) for 1-yr BW and 1-yr length, and 2-yr BW and 2-yr length recorded from 1-stage selection (OSS), and genetic correlations [$r_a \pm$ SE, with (G)] and phenotypic correlations [$r_p \pm$ SE, with (P)] between the BW and total length of yellow perch

Item	1-yr BW	1-yr length
1-yr BW	0.082 ± 0.056	0.96 ± 0.0038 (P)
1-yr length	0.97 ± 0.031 (G)	0.075 ± 0.053
OSS	2-yr BW	2-yr length
2-yr BW	0.14 ± 0.09	0.92 ± 0.01 (P)
2-yr length	0.93 ± 0.13 (G)	0.049 ± 0.057

Table 7. Correlation coefficients (CC) of mean family BW and family EBV for BW between yr 1 and 2, and genetic correlations ($r_a \pm$ SE) and phenotypic correlations ($r_p \pm$ SE) between the 1-yr BW and 2-yr BW of yellow perch with 1-stage selection (OSS)

OSS	Yr 1 × yr 2
CC of mean family BW	0.67**
CC of mean family EBV for BW	0.44*
Genetic correlation between BW	0.98 ± 0.29
Phenotypic correlation between BW	0.71 ± 0.076

*$P < 0.05$; **$P < 0.01$.

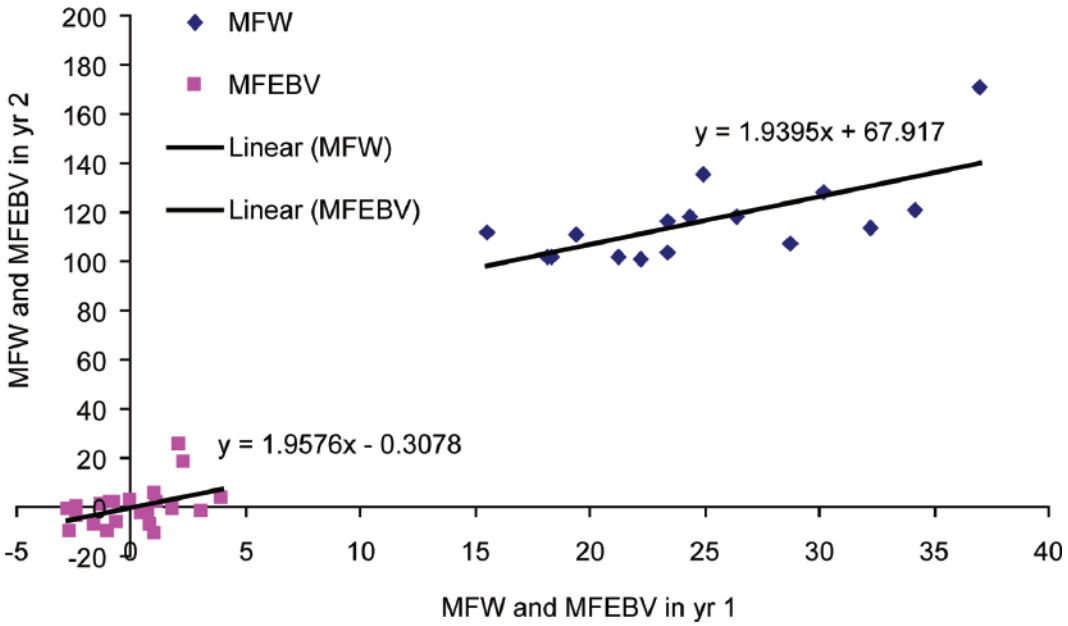

Figure 2. Correlation diagram for mean family BW (MFW) and family EBV (MFEBV) for BW between yr 1 and 2, within 1-stage selection. Color version available in the online PDF.

feed" might affect family survival and family rankings observed in the experiment.

Heritability estimates in this study constituted the first report of this for growth traits in yellow perch. Heritabilities for BW and length have been described as medium-high values in many fish species, such as rainbow trout (0.546 to 0.719 for BW and 0.517 to 0.664 for length) by Fishback et al. (2002), sea bass (0.62 for BW and 0.54 for length) by Dupont-Nivet et al. (2008), and gilthead seabream (0.28 to 0.34 for BW and 0.27 to 0.35 for length) by Navarro et al. (2009). The heritabilities obtained here were less than many other species and of lesser magnitude according to the classification of Cardellino and Rovira (1987). However, our estimates were based on 25 full-sib families and thus should be taken with caution because they might largely reflect the genetic variance in this specific population. More families and a larger sample size would be useful to further improve the accuracy of heritability estimates for yellow perch.

The genetic and phenotypic correlations between BW and total length of yellow perch were increased and close to 1 at each age. Similar results have been found in many other species (Vandeputte et al., 2004; Rutten et al., 2005; Nguyen et al., 2007; Navarro et al., 2009). In fish species, BW and length are generally considered genetically and phenotypically correlated. The high correlation between length and BW in this study suggested that selective breeding for increased BW could be achieved using an indirect selection method based on length, because female BW during breeding season is increased by their larger volume of gonads.

The estimate of genetic correlations among ages is of high significance because it is prerequisite for making a decision about preselection at early life stages. Genetic correlation estimates for BW among ages have been performed in many species (Su et al., 2002; Saillant et al., 2006). Navarro et al. (2009) indicated the genetic correlation for BW in gilthead seabream between 130 and 509 d (i.e., slaughter age) was 0.11, which was consistent with the inference that genetic correlations between BW for distant ages were low (Kolstad et al., 2006; Vandeputte et al., 2008). Navarro et al. (2009) also found that the genetic correlations for BW between 130 and 330 d was reduced (0.36) and between 330 and 509 d was greater (0.93). Saillant et al. (2006) pointed out that genetic correlations among log BW recorded from 341 to 818 d in sea bass were greater (ranging from 0.61 to 0.85), indicating the growth recorded at 341 d could be used as a predictor of later progeny growth (until 818 d). Fishback et al. (2002) showed that the genetic correlations for BW in rainbow trout between 9 and 12 mo were high. These instances above, together with other studies (Elvingson and Johansson, 1993; Winkelman and Peterson, 1994), might hint that genetic correlations for BW between ages near slaughter were generally increased and BW recorded at younger stage usually could predict the later BW. In the present study, within OSS the genetic correlation between 1- and 2-yr BW was greater (0.98), indicating that the growth of yellow perch recorded at yr 1 could predict their growth for yr 2. In addition, mean family BW and family EBV for BW between yr 1 and 2 were found to be significantly correlated in OSS, which demonstrated that the fastest growing yellow perch families in yr 1 would continue to be the fastest growing families in yr 2. Significant differences ($P < 0.01$) in BW and total lengths for random fish and the top 10% largest fish recorded at yr 2 between the OSS and TSS were found here, suggesting yr-2 yellow perch selected using

the TSS method were significantly heavier and longer than yr-2 yellow perch undergoing the OSS method. Therefore, based on the results described above, we concluded that the TSS method was desirable and more effective for yellow perch breeding compared with OSS in terms of improving selection efficiency and reducing costs (e.g., feed, pond/tank, and labor).

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