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GENETIC PARAMETERS OF FIELD SURVIVAL IN STRIPED CATFISH (*Pangasianodon hypophthalmus*)

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ABSTRACT

Grow-out or field survival (GS) is one of the most important traits of striped catfish. Genetic parameters of GS in generation 4 of the growth selected population of this species were estimated based on the data of 8,004 tagged and stocked and 6,410 harvested fish representing 152 full-sib and half-sib families. The heritability and estimated and realized correlated responses for GS, its phenotypic or genetic correlations with harvest weight (HW) and other growth traits, and direct realized response for HW were calculated. The low and significantly different from zero heritability for GS (0.12±0.05) was estimated. The medium positive and no significant difference from zero genetic correlation between GS and HW was found, 0.41±0.24. The estimated selection responses with the proposed selection proportion of 13.0% for GS was 8.5% in trait unit. Current and accumulated correlated selection responses for GS were -7.8% and -1.6%, and 25.5% and 47.6%, respectively, by Estimated Breeding Value and Least Square Means estimation methods. In addition to these results, the high heritability and direct estimated and realized responses for HW pose a great potential for applying multi-trait selection, including both GS and HW in G4 and in the long run.

KEYWORDS: field survival; genetic parameters; growth rate; striped catfish

INTRODUCTION

Large-scale family-based genetic improvement programs, now established as the standard for genetic improvement of aquaculture species, were first developed for some high-value salmonid species and Nile tilapia reviewed by Gjedrem & AKVAFORSK (2005) and recently expanded in some other species worldwide such as white leg shrimp, black tiger shrimp, carps, catfish, mollusk and marine fish. There were many important traits estimated and selected, such as growth, survival, disease resistance, environmental tolerance, fillet yield, early maturation and so on. Both main desirable traits, growth rate and grow-out survival, determined as production yield, profit and economic return of the industry were considered, estimated and included in the selection program of several species worldwide, such as black tiger shrimp

(Krishna *et al.*, 2011; Nguyen, 2010), white leg shrimp (Zhang *et al.*, 2017), freshwater prawn (Vu *et al.*, 2017), rainbow trout (Vehviläinen *et al.*, 2008), common carp (Dong *et al.*, 2015), tilapia (Thodesen *et al.*, 2013; Ninh *et al.*, 2014) and abalone (Liu *et al.*, 2015).

Striped catfish (*Pangasianodon hypophthalmus*) is one of the most widely traded fish commodities in the world that originates from pond farming in a single locality of the Mekong Delta which is in the southern part of Vietnam (De Silva & Phuong, 2011). Striped catfish was the highest in Vietnam aquaculture production and reached 1.56 million tonnes, and the second biggest in export value and reached 1.5 billion USD in 2020, according to a report from the Vietnam Association of Seafood Exporters and Producers (VASEP, 2020).

Selective breeding of striped catfish was started in 2001, and economically important traits were selected, such as growth rate and recently disease resistance to Bacillary Necrosis of *Pangasius* (BNP) caused by bacteria *Edwardsiella ictaluri*, and estimated

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such as survival, fillet yield and fillet quality (color and fat) at Research Institute for Aquaculture No. 2 (RIA2) (Nguyen, 2010; Van Sang *et al.*, 2012; Vu *et al.*, 2019a; Vu *et al.*, 2019b; Pham *et al.*, 2021). In striped catfish, both growth rate and survival at harvest are also the main desirable traits as that in other species. It is more challenging that the survival at harvest in pond (grow-out survival) has been reduced recently, from 75,0-80,0% in 2010 (Belton *et al.*, 2011) down to 71.4-76.1% in 2018 (Hien *et al.*, 2020). Moreover, survival is also the trait contributing to the increase in animal welfare (Knol *et al.*, 2002; Goyache *et al.*, 2003) which is currently aware of by consumers and aquatic animal breeders. The moderate to high heritability of grow-out survival and its low to moderate positive genetic correlations with both growth and resistance to BNP on the 3rd and merged all three generations of striped catfish were estimated. Additionally, genetic gain for a single trait selection of harvest body weight of this species was from 5.4% to 18.2% per generation (Nguyen, 2010; Sang *et al.*, 2017; Vu *et al.*, 2019a) and 13.4% for accumulated one for three generations (Vu *et al.*, 2019a). However, grow-out survival is not selected for yet. Moreover, genetic variation of survival at harvest is often changed by testing environments due to different pathogens and water quality in different selection generation (Vehviläinen *et al.*, 2008).

The objectives of this study were to examine 1) the genetic variation of grow-out survival; 2) the genetic correlation between grow-out survival and growth traits; 3) direct and correlated selection responses for grow-out survival and growth traits on the fourth generation of selection in striped catfish. In addition, the use of these results for actual selection work in the future for grow-out survival in the context of the current single trait selection of harvest body weight of the program in Vietnam were also discussed.

MATERIALS AND METHODS

Parental Fish, Mating, Hatching, Nursing and Individual Tagging

The base population was made of stocks from three to four hatcheries in the Mekong Delta, Vietnam. Each stock was collected from 1999-2001 from grow-out farms that reared wild fingerlings caught at several seasons and locations from the Mekong River. From 2001 to 2003, the three-year classes named G0-2001, G0-2002 and G0-2003 were produced and selected. Subsequently, the first, second, and third generations (G1-3) were selected in three-year classes, each from 2005-2016. In 2016, three latest-year classes were merged and selected to establish G3-merged growth line generation (G3), which was kept at the Southern National Breeding Centre for Freshwater Aquaculture, NBCEFAS (Sang *et al.*, 2017).

The G3 matured candidates composing 400 high-growth selected parents and 100 average-growth control parents were conditioned for four months, from late February to early July 2019, in an earthen pond with a density of 0.33 fish.m^{-2}. The fish were fed twice a day with a commercial floating pelleted feed produced by RIA2 with approximately 32% of crude protein and 10% fat at a feeding rate of 3-5% of body weight daily. In July 2019, G4 families were produced, which is the main spawning season for this species. A nested mating design was used, one male mated to two females. Full-sib families were produced in four batches. By stripping, 105 males mated with 152 females to produce 152 families (105 full-sib and 47 half-sib families), composing 112 G4 selected, 20 G4 control and 20 wild control group families (Table 1). Fertilized eggs were washed to remove sticky layers and then incubated in separate net jars in one cement tank. Fertilized eggs usually hatch 22-24 hours after fertilization.

Around 20-25 hours post-hatching, three thousand start-fed fries were randomly sampled from each family and reared separately in one-m^3 fiberglass tanks. At this stage, fry was fed with newly-hatched artemia, moina, and, lately, commercial powder and pellet feed. The water source and water exchange were the same for all rearing tanks. To reduce the tank effect on full-sib family performance, on average, 350 fries from each full-sib family were randomly sampled at 20 days from first feeding and reared separately in net hapas $(1.5 \times 2.0 \times 1.0)$ m^3 of mesh size 1 mm suspended in a 2,000-m^2 earthen pond. Fries were then fed with a standard commercial pellet feed. The net hapas were cleaned frequently to maintain good water circulation and thus even out the environmental effects among the families.

At the average size of 21.6 grams at an average of 150 days from spawning till tagging (*Nurseage*), an average of 60 fingerlings from each full-sib family were randomly sampled and marked by Passive Integrated Transponder tags (PIT-tags, Sokymat, Switzerland) (Table 1) within 20 days. Tagged fish were kept for one week in family hapas to monitor mortality before they were communally stocked in a 2,000 m^2 pond at the NBCEFAS - RIA2. In total, 8,004 fish were tagged, representing 152 families (Table 1).

Growth Testing and Data Recording

Fish were individually weighed at tagging (TW, about 0.1g). The fish were fed *ad libitum* with commercial pelleted feed, containing 22-28% protein and

Table 1. Description of family production of G4 offspring of striped catfish in 2019

Parameters	Selected group	Control group[2]	Wild control[3]	Overall
No. of families produced and nursed till tagging	112	20	20	152
No. of sires	74	15	16	105
No. of dams	112	20	20	152
No. of days from spawning till tagging (*Nurseage*)	93-200 (146.4±33.3)	101-195 (156.5±26.4)	103-192 (165.7±18.2)	93-200 (150.1±31.6)
No. of tagged fish in total	6,009	1,012	983	8,004
No. of days from tagging till harvest (*Growage*)	161-204 (184.3±10.8)	162-202 (184.2±11.2)	162-202 (190.2±6.7)	161-204 (184.9±10.7)
Traits recorded in the previous generation[1]	HW, HL, fillet weight, fillet yield, intestinal fat, fillet fat, fillet color, BNP, GS			
Traits selected for in previous generation	HW			
Selection method in previous generation	Combined selection			

Description: [1] GS= growth survival, HW= body weight at harvest, HL= standard length at harvest

[2] Control group established in G4, the same generation with selected group to calculate one generation response

[3] Control group collected from the wild used as control for calculating accumulated response

twice per day (7:00 am and 5:00 pm). Water parameters were monitored every other day for pH, dissolved oxygen and temperature and weekly for ammonia and controlled by exchanging water regularly and necessarily. In July 2020, after an average culture period of 185 days, 6,410 surviving fish (i.e. on average 42 individuals per family, representing 152 families, Table 2) were randomly recorded HW and HL within 15 days. Growth traits such as Body weight (HW, about 0.1g), standard length (SL, about 0.1cm), specific growth rate (SGR, g.day^{-1}) and daily weight gain (DWG, g.day^{-1}), and grow-out survival (GS, coded as '1' for alive and '0' dead or missing) at harvest were recorded and calculated. SGR refers to the estimate of the growth of fish over a specified period and is calculated as $100*(Ln\ HW – Ln\ TW)/t$, where t is the number of days from tagging till harvest (*Growage*). DWG is calculated as $(HW-TW)/t$. Each trait was recorded by the same person for all fish.

Data Analysis

For variance component estimation in the G4 data, each trait was analyzed univariately with the following linear model:

$$Y_{ijkl} = u + b_1X_i + B_2X_j + b_3X_{3l} + b_4X_{4l} + f_k + a_l + e_{ijkl} ...(1)$$

where Y_{ijkl} = one observation for one trait for fish *1*, in batch *i (1-7)*, in group *j* (1: selected G4 group, 2: control G4 group, 3: wild control group), in full-sib family *k*, at *nurseage* and *growage l*; μ= overall mean for the trait; b_3= the regression coefficient of the phenotypic value of the trait on *nurseage* (X_3), b_4=

the regression coefficient of the phenotypic value of the trait on *growage* (X_4), f_k = the random environmental effect common to full-sib family $k \sim N(0, I\sigma_f^2)$; a_l is a random additive genetic effect of fish*l* with $\mathbf{a} = \begin{bmatrix} a_1 & .... & a_p \end{bmatrix} \sim N(0, \mathbf{A}\sigma_a^2)$, *p* is the number of animals in pedigree, A is the additive relationship matrix and e_{ijkl} is a random, residual for fish *l*, $\mathbf{e} = \begin{bmatrix} e_1 & .... & e_N \end{bmatrix}' \sim N(0, I\sigma_e^2)$, where *N* is number of records for the relevant trait (N = 6,410 for growth trait such as HW, HL, SGR, DWG, and N=8,004 for GS), and I is an identity matrix of dimension *N*, while σ_f^2, σ_a^2 and σ_e^2 are corresponding variance components. Pedigree is traced back to G0. Heritability (h^2) and environmental effects common to full-sibs (c^2) were calculated based on the following equations (accordingly, Eq.2 and Eq.3) based on the above variance components from model (1).

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2} = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_c^2 + \sigma_e^2} .....(2)$$

$$c^2 = \frac{\sigma_c^2}{\sigma_a^2 + \sigma_c^2 + \sigma_e^2} .....(3)$$

Phenotypic (r_p) and genetic (r_a) correlations were estimated using a bivariate setup of (1) and calculated using equation (4) (Falconer & Mackay, 1996). The models for both univariate and bivariate analysis

were solved using restricted maximum likelihood, as implemented in the ASReml software release 4.1 (Gilmour, Gogel, Cullis, Welham, & Thompson, 2015).

$$r_{12} = \frac{\sigma_{12}}{\sqrt{\sigma_1^2} \, x \sqrt{\sigma_2^2}} ...(4)$$

where r_{12} is phenotypic or genetic correlation between two traits, σ_{12} is the covariance of phenotypic or additive genetic or effect of traits studied, σ_2 and σ_2 are variances of phenotypic or additive genetic effects of trait 1 and 2, respectively.

The estimated selection response (R-estimate) for HW and GS is calculated according to equation (5). The proposed selection proportion (*p*) is 13%. The corresponding selection intensity (*i*) accordingly with *p* is in appendix A, page 379 (Falconer & Mackay, 1996), σ_p is the square root of the phenotypic variance (σ_p^2), h^2 is the heritability of the trait.

$$R = i \times h^2 \times \sigma_p ...(5)$$

Direct and correlated realize selection responses accordingly for HW and GS in G4 were measured as the difference: 1) in the least squares means between the G4 selected (LSM$_{selected}$) and G4 control groups (LSM$_{control}$) in trait unit (R, Eq.6) and in percentage (R%, Eq.7) and 2) in estimated breeding value (EBV) between two groups (Eq. 8 and Eq. 9). Similarly, accumulated direct and correlated realize selection responses for HW and GS were measured as the difference of LSM and EBV between the G4 selected and wild control group (similar as Eq.6-9 below, but replacing "control" group by "wild" group). A similar model as Eq. (1) was used except for the exclusion of the random effect of a full-sib family (f_k) and additive genetic effect (a_i). For GS, the response is the correlated one since GS has not been selected yet in the parental generation. The LSM of the G4 selected group, G4 control and wild control groups were estimated using the MIXED Procedure in SAS (SAS, 2004).

$$R\,(trait\,unit) = LSM_{selected} - LSM_{control/wild} ...(6)$$

$$R\,(\%) = (LSM_{selected} - LSM_{control/wild}) * \frac{100}{LSM_{control/wild}} ...(7)$$

$$R\,(trait\,unit) = (EBV_{selected} - EBV_{control/wild}) ...(8)$$

$$R\,(\%) = (EBV_{selected} - EBV_{control/wild}) * \frac{100}{LSM_{control/wild}} ...(9)$$

RESULTS AND DISCUSSION

Basic Statistics of Traits Studied

Mean, standard deviation (SD) and coefficient of variation CV (%) of the recorded traits in generation 4 are given in Table 2. Note that the mean TW of wild control group (22.8 g) was significantly heavier than those of the other two groups, while the CV of TW in G4 control group (47.4%) was higher than those of the other two groups. Fish were harvested at approximately 1 kg (average of 1,078 g) and the average survival rate was high (80.1%). There was no significant difference in mean for GS, HW and DWG between G4 selected and G4 control groups, while there was a significant difference for HL and SGR among the three fish groups. The CV was high, approximate 25-47.3% for TW, HW and DWG, while it was low to nearly half that (<20%) for GS, HL and SGR, except that for GS of wild control group (30.9%). The CV of HW and HL was similar and in the range of that in the previous generations (G1-G3) of the same selective population of this species (Van Sang *et al.*, 2012; Vu *et al.*, 2019a) while it was lower for SGR than that in the previous generations, G1-G2 (Van Sang *et al.*, 2012).

Heritable Grow-Out Survival and Growth Traits

Grow-out survival and harvest weight are the two main traits to determine production yield, profit and economic return of the industry of this species. The estimated additive genetic and common environmental variances, heritabilities and common environmental effects for these traits in G4 are presented in Table 3. The heritability of GS in G4 was low but significantly different from zero (0.12±0.05), which gives an opportunity to include this trait in the selection objectives for this species. Moreover, the low to medium heritability of GS in G3 (0.19±0.09 ÷ 0.28±0.06; (Pham *et al.*, 2021) and in all three generations, G1-G3 in one analysis (0.27±0.03; (Vu et al., 2019a) in the same selective population of this species give a strong confirmation the feasibility of selection for this trait in the current population. This magnitude of heritability for GS in G4 was also in the range of that estimated and reported in several aquaculture species worldwide, from low to high heritable, 0.21-0.50, such as in black tiger shrimp (Krishna *et al.*, 2011; Sang *et al.*, 2020), 0.01-0.06 in white leg shrimp (Zhang *et al.*, 2017), 0.14 in freshwater prawn (Vu *et al.*, 2017), 0.08-0.17 in rainbow trout (Vehviläinen *et al.*, 2008), 0.05-0.17 in common carp (Dong *et al.*, 2015), 0.21-0.54 in tilapia (Thodesen *et al.*, 2013; Ninh *et al.*, 2014) and 0.07 abalone (Liu *et al.*, 2015).

Table 2. Means, standard deviation, coefficient of variation of tagged weight (TW) and recorded traits at harvest on G4 offspring

Trait[1]	N	No. of families	Mean[2]	SD	CV (%)
TW (g)					
Selected group	6,009	112	20.1[a]	4.8	23.9
Control group	1,012	20	22.0[a]	10.4	47.4
Wild control	983	20	22.8[b]	8.0	35.0
Sum/average	8,004	152	21.6	7.7	35.4
GS (%)					
Selected group	4,945	112	82.3[a]	12.7	15.4
Control group	820	20	81.1[a]	8.4	10.3
Wild control	645	20	75.5[b]	23.4	30.9
Sum/average	6,41	152	80.1	15.3	19.1
HW (g)					
Selected group	4,945	112	1,111.5[a]	310.2	31.0
Control group	820	20	1,011.0[a]	294.4	30.6
Wild control	645	20	852.0[b]	212.4	25.0
Sum/average	6,41	152	1,078.0	272.4	28.9
HL (cm)					
Selected group	4,945	112	39.1[a]	3.7	9.5
Control group	820	20	38.4[b]	3.4	8.8
Wild control	645	20	37.7[c]	2.8	7.4
Sum/average	6,41	152	38.4	3.3	8.6
SGR (g.day^{-1})					
Selected group	4,945	112	2.2[a]	0.3	12.4
Control group	820	20	2.1[b]	0.2	8.6
Wild control	645	20	1.9[c]	0.2	8.9
Sum/average	6,41	152	2.1	0.2	10.0
DWG (g.day^{-1})					
Selected group	4,945	112	5.3[a]	1.5	28.2
Control group	820	20	5.1[a]	1.4	26.4
Wild control	645	20	4.3[b]	1.1	24.4
Sum/average	6,41	152	4.9	1.3	26.3

[1] TW= Tagged weight, SGR= specific growth rate, DWG=daily weight gain

[2] Different letters by column indicate a significant difference between groups at $p < 0.05$ for each trait

Heritabilities larger than 0.40 were estimated for HW, HL, SGR and DWG and significantly different from zero except that of SGR (0.46±0.25). Due to its importance in striped catfish, growth has been selected since the start of the breeding program in 2001. The high heritability for growth traits (HW, HL, SGR and DWG, 0.43-0.53), especially that for HW ($h^2 = 0.46$) in G4 in this study correspond well with the estimates in G1 and G2 ($h^2 = 0.21–0.34$) from Sang *et al.* (2012), those in G3 ($h^2 = 0.27$-0.50) from Pham *et al.* (2021) and those in all three generations G1-G3 in one analysis ($h^2 = 0.34$-0.39) from (Vu *et al.*, 2019a; Vu *et al.*, 2019b). This magnitude of heritability for HW in G4 (0.11-0.53) was also in the range of that in several aquaculture species worldwide, such as in black tiger shrimp, white leg shrimp, freshwater prawn, common carp, tilapia and abalone documented by authors mentioned for GS as above and in salmon (Gjedrem & AKVAFORSK, 2005). With this high heritability for HW in G4 in this study and in combination with those

Table 3. Estimated variance components, heritability and common environmental effects with their standard errors ($\pm$se) for recorded traits in G4 offspring at harvest

Trait	σ_A^2	σ_C^2	σ_E^2	σ_P^2	$h^2 \pm se$	$c^2 \pm se$
GS	0.021	0.008	0.152	0.181	0.12$\pm$0.05	0.04$\pm$0.02
HW	26,828.7	16,752.1	14,527.1	58,107.9	0.46$\pm$0.14	0.29$\pm$0.07
HL	3.31	1.94	2.42	7.67	0.43$\pm$0.13	0.25$\pm$0.06
SGR	0.08235	0.05582	0.03903	0.1772	0.46$\pm$0.25	0.32$\pm$0.11
DWG	1.0	0.5	0.4	1.9	0.53$\pm$0.15	0.26$\pm$0.07

reported in G1-G3 previously help us to conclude that the potential for long-term selection for improving HW exists.

The common environmental effect for growth traits (HW, HL, SGR, and DWG) was large and significantly different from zero (0.25-0.32). The common environmental effect for GS was low, but significantly different from zero (0.04$\pm$0.02). The magnitude of common environmental effect in this study in G4 was quite similar or in the range of that in the previous generations of the same selective population of this species, for GS (Vu *et al.*, 2019a; Pham *et al.*, 2021), for HW and HL (Van Sang *et al.*, 2012; Vu *et al.*, 2019a; Vu *et al.*, 2019b; Pham *et al.*, 2021) and for SGR (Van Sang *et al.*, 2012).

Favorable Genetic Correlation Between Grow-Out Survival and Growth Traits

Estimated phenotypic and genetic correlations for all traits based on the data from G4 are presented in Table 4. Generally, genetic correlations were larger than phenotypic correlations, except those between HW and DWG were equal and unity. Very high positive genetic correlations were estimated between BW and SL (0.94) and DWG (0.93). In contrast, low and non-significant differences from zero genetic correlations were found between SGR with HW, HL and DWG, 0.06$\pm$0.17, -0.17$\pm$0.17 and -0.12$\pm$0.16, respectively. The high to unity genetic correlations among HW, HL and DWG (0.93-1.0) means that they are similar traits and are improved simultaneously through the selection applied for one of these traits. Internally, low to medium positive genetic correlations were found between GS and growth traits, but they were not significantly different from zero (0.16$\pm$0.24 $\div$ 0.41$\pm$0.24), except that between GS and DWG (0.52$\pm$0.23). These results illustrate that if selection applies for one trait, e.g., GS, the expectations of low to medium positive responses are obtained for HW, HL, SGR and DWG. This result is inconsistent with the genetic correlations between GS and HW in previous generations of the same selective population of striped catfish reported for G3 (0.09-0.45; Pham *et al.*, 2021) and all three generations G1-G3 in one analysis (0.27; Vu *et al.*, 2019a). The result of this study is in line with the weak negative to medium positive genetic correlation between GS and HW or HL (-0.15$\pm$0.47) that reported for black tiger shrimp, white leg shrimp, freshwater prawn, rainbow trout, common carp, tilapia and abalone (Krishna *et al.*, 2011; Sae-Lim *et al.*, 2013; Thodesen *et al.*, 2013; Ninh *et al.*, 2014; Dong *et al.*, 2015; Liu *et al.*, 2015; Hamzah *et al.*, 2017; Vu *et al.*, 2017; Zhang *et al.*, 2017; Van Sang *et al.*, 2020).

Moderate Responses for Both Grow-Out Survival and Harvest Weight in The Current Generation and Long-Term Expectation

The estimated selection responses for GS and HW on the data of G4 are presented in Table 5. Supposed that the selection proportion (*p*) is 13.0% and equivalent to the selection intensity (*i*) of 1.667, the estimated selection response for GS and HW was 10.4% and 16.6%, respectively.

Direct realized selection response for HW and correlated one for GS on the data of G4 and wild control group are presented in Table 6 & Table 7. The current direct response for HW in G4 was medium, 9.9% and 11.2% by EBV and LSM estimation methods, respectively, while the accumulated direct response for HW in G4 was also medium, 29.3% and 31.2% by EBV and LSM estimation methods for the total of 4 generations respectively, equivalent to approximate 7.5% per generation (Table 6). However, these direct realized selection responses for HW were lower than the estimated selection response for HW (16.6%) on the data of G4 (Table 5). The direct realized response corresponds well with the high heritability estimates reported in G3 by (Vu *et al.*, 2019a) and is comparable with those reported in G1-G2 (5.4-18.2% per generation; Sang *et al.*, 2015) and G3 (9.3% per generation; Vu *et al.*, 2019a) of the same selective popu-

Table 4. Estimated phenotypic (above diagonal) and genetic (below diagonal) correlations, with their standard errors ($\pm$SE) between the different traits recorded in G4 offspring at harvest

Trait	GS	HW	HL	SGR	DWG
GS	-	0.03$\pm$0.03	0.03$\pm$0.03	-0.14$\pm$0.03	0.05$\pm$0.03
HW	0.41$\pm$0.24	-	0.92$\pm$0.01	-0.06$\pm$0.05	1.00$\pm$0.001
HL	0.40$\pm$0.25	0.94$\pm$0.03	-	-0.04$\pm$0.05	0.09$\pm$0.01
SGR	0.16$\pm$0.24	0.06$\pm$0.17	-0.17$\pm$0.17	-	-0.07$\pm$0.05
DWG	0.52$\pm$0.23	1.00$\pm$0.001	0.93$\pm$0.03	-0.12$\pm$0.16	-

Table 5. Estimated responses in the case of single trait selection for each HW and GS

Trait	Selection proportion (%)	Selection intensity (i)[1]	Estimated heritability (h^2)	σ_P[2]	R (trait unit)[3]	R (%)[4]
GS	13.0	1.667	0.12	0.43	8.5	10.4
HW	13.0	1.667	0.46	241.1	184.9	16,6

[1] i is the selection intensity in appendix A, page 379 (Falconer & Mackay, 1996), [2] σ_P is the square root of σ_p^2 from Table 3; [3] $R = i \; x \; h^2 \; x \; \sigma_p$; [4]R (%) based on the LSM of HW of selected G4 off spring in Table 5.

lation. This realized selection response for HW in the range of reviewed reports for many species (8.7-17.8% per generation; Gjedrem & Rye, 2018).

The grow-out survival was not directly selected yet in previous generations, but based on its positive correlation with HW, the realized correlated response was negative for comparing direct control in G3 (-1,6% by LSM and -7.8% by EBV), but positive high for comparing with the wild population (47.6% by LSM and 25.5%% by EBV) (Table 7). The accumulated direct realized selection response for HW (29.3% by LSM and 31.2% by EBV, equivalent to approximately 7.5% per generation) and correlated realized one for GS on the data of G4 (47.6% by LSM and 25.5% by EBV) in this study pointed out that the selection in G3 on only HW improved GS simultaneously. The positive accumulated correlated response for GS also proved clearly in G3 of the same selective population, 7.4% per generation (Vu *et al.*, 2019a). The negative direct

correlated response for GS in G4 is probably due to the difference in pathogens caused by disease and mortality in this generation from other generations in the field test. Overall, the results from this and previous studies confirm that GS can be improved by direct selection or indirect selection through HW. The feasibility of selection for GS to achieve positive direct or correlated responses was published in several aquaculture species, such as direct response on average of five estimates (4.9% per generation; Gjedrem & Rye, 2018), direct one in abalone (4,1%; Liu *et al.*, 2015), accumulated one from index selection in red tilapia (5,0% after four generations; Thodesen*et al.*, 2013) and correlated one through HW selection in freshwater prawn (2.5-10.4%; Vu *et al.*, 2017). However, there was one case that the long term-selection program for high growth in the Genetically Improved Farmed Tilapia (GIFT) strain over ten generations did not acquire any changes in grow-out survival in pond (Hamzah *et al.*, 2017).

Table 6. Direct (selected vs. control) and accumulated (selected vs. wild) realized response to selection for HW

Group	Mean EBV (g)	R by EBV		LSM (g)	R by LSM	
		Trait unit	%		Trait unit	%
Selected	81.4			1,114.5		
Direct control	-17.3	98.7*	9.9	1,001.5	112.1*	11.3
Wild	-167.5	232.1*	29.3	849.5	264.2*	31.2

* Significant difference at p<0.05

Table 7.   Correlated (selected vs. control) and accumulated (selected vs. wild) realized response to selection for GS.

Group	Mean EBV (g)	R by EBV		LSM (g)	R by LSM	
		Trait unit	%		Trait unit	%
Selected	1.9			78.3		
Direct control	6.8	-4.9	-7.8	79.3	-1.0	-1.6
Wild	-7.3	9.2	25.5	60.1	17.2	47.6

Vehviläinen *et al.* (2008) argued that treating growth survival as one trait over time may not reveal its true genetic architecture because individuals from different year classes or generations might not be exposed to the same factors causing the mortality. Therefore, the grow-out survival of one year class or generation may not be the same trait as in another year class that might be exposed to a different environment. In our case, the significantly different from zero heritability of GS (0.12 ± 0.05), its medium positive genetic correlation with HW (0.41 ± 0.24), its medium estimated direct response (25.5% by EBV and 47.6% by LSM when comparing to the wild group), its medium correlated response in G4 and especially the similar results found in previous generations, G1-G3 (Van Sang *et al.*, 2012; Sang *et al.*, 2015; Vu *et al.*, 2019a; Vu *et al.*, 2019b; Pham *et al.*, 2021) confirm that GS can be improved by direct or indirect selection through HW or growth traits. Do aquaculture breeders consider survival as a measure of general resistance as animal breeders do? In animal breeding, a common goal is to select animals that have general resistance or robustness against multiple environmental disturbances, stressors, and mortality factors. This topic is currently becoming a major target of research because it strongly contributes to increased animal welfare and ability to manage animals across a wide range of environments (Mulder & Bijma, 2005).

In Vietnam, the current single trait selection of harvest body weight of the program has been applied and the other traits of interest such as disease resistance to BNP and grow-out survival were recently estimated but not yet included into selection application. Besides, both harvest weight and grow-out survival is the two main desirable traits, determined as production yield, profit and economic return of the industry. Generally, in the long run, grow-out survival must be estimated and selected. We then have to conduct an entire research to establish economic weights for these traits, HW, GS and possibly resistance to BNP disease in order to apply index selection for this species. The higher beneficial way for applying index selection with the inclusion of re-

sistance to BNP disease is due to its positive genetic correlations between BNP disease resistance and HW (0.09-0.45) and BNP disease resistance and GS (-0.01 ± 0.58) in generation 3 of the same selective population as this study (Vu *et al.*, 2019b; Pham *et al.*, 2021).

CONCLUSION

Grow-out survival and harvest weight in striped catfish are heritable with their moderate positive genetic correlation and correspondingly their direct and correlated significant realized responses to selection in G4. There is great potential for applying multi-trait selection, including both harvest weight and grow-out survival in the long run. Necessarily, entire research on establishing economic weights for these traits is conducted in advance for use in the selective breeding of this striped catfish population.

Availability of data and materials

The datasets of this study are confidential required by owners.

Ethics approval and consent to participate

This manuscript does not require ethics approval because there are no human and animal participants.

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