Norwegian University
of Life Sciences

Master's Thesis 2016 30 Credits
Department of Animal and Aquacultural Sciences

Analysis of crosses between three strains of striped catfish *(Pangasianodon hypophthalmus*) in Viet Nam

Tran Huu Phuc
Master programme in Aquaculture

Analysis of crosses between three strains of striped catfish *(Pangasianodon hypophthalmus*) in Viet Nam

By

Tran Huu Phuc

Supervisor

HANS MAGNUS GJØEN

Department of Animal and Aquacultural Sciences
Norwegian University of Life Sciences (NMBU)

May 2016

Contents

List of Tables

List of Figures

Declaration

by

Student name
Tran Huu Phuc
Study programme and year of start
Master programme in Aquaculture _ 2014

Regarding submission of written assignments, term papers and exam papers at NMBU.

I hereby declare that I have read the description below regarding plagiarism and correct use of sources, understood the nuances and clarified any uncertainties with an academic adviser.

I have also studied all questions in the attached quiz, answered the questions correctly and understood the reasons for all answers.

If I submit plagiarised text as part of an assignment, term paper or exam paper I will not claim that I have received insufficient instruction.

Place and date
Ås, 15.05.2016
Student's signature


Acknowledgement

I am very grateful to my supervisor, Professor Hans Magnus Gjøen, for his professional support and effort to bring me into different aspects in this master thesis, I will keep it in my mind. Thanks Hans for your patience, nice discussion and detailed guiding in scientific writing. It was an honor to work with you.

I am deeply thankful to Dr. Nguyen Van Sang, Director of RIA2, for supporting my MSc programme, providing data and necessary information as well as valuable comments and guidance in my scientific writing.

I wish to express my gratitude to Trinh Quoc Trong for his encouragement and friendship.

I would like to thank all my colleagues and friends at department of Animal and Aquaculture Sciences. Special thanks to Mr. Pham Dinh Khoi for his encouragement, support and fun during my studying time in Norway.

Finally, to my family who have help me in many ways, I am deeply grateful.

Abstract

This study focused on harvest body weight of striped catfish (*Pangasianodon hypophthalmus)* in a selective breeding program in Vietnam. The first objective was to estimate additive, non-additive genetic effects and heritability two sets of data, namely (i) Whole population and (ii) Selection group. The second objective was to estimate selection responses by comparing estimated breeding values (EBVs) between Selection group and three other groups namely Control, Parent and Wild group. These four groups formed a dataset of a so-called 'G3 population'. The G3 population consisted of 6,826 records for Selection group; 1,116 for Control group; 1,035 for Parent group and 1,368 for Wild group. The Selection and Control group were established from a complete 3×3 diallel cross from three latest generation, namely G3_2001, G2_2002, and G2_2003. The Parent group were established from a complete 3×3 diallel cross from three earliest generations that still available, namely G2_2001, G1_2002, and G1_2003. The Wild group were established from 3 groups of wild fish that originated from Cambodia. A nested mating design (1 male mated to 2 females) was used to generate four groups (i.e., the G3 population), produced 206 full-sib families from 130 sires and 206 dams. Estimates of heritability (h^2), dominance genetic effect (d^2), and environment effects common to full-sibs (c^2) of 'Selection group' were 0.17 ± 0.17, 0.06 ± 0.03, and 0.27 ± 0.09 respectively. For 'Whole population' these estimates were 0.33 ± 0.16, 0.07 ± 0.02, and 0.24 ± 0.08 respectively. Actual selection response for Selection group in G3 population was 48% when compared with Parent group, 37% compared with Control group, and 15% compared with Wild group.

1. Introduction

Striped catfish (*Pangasianodon hypophthalmus* Sauvage 1878), also known as 'tra' catfish, is the most important freshwater farmed fish in Vietnam (Merican, 2011) that account for 52% of Vietnamese total aquaculture production. Production was 90,000 tonnes in 2000 and rapidly increased to 1,116,000 tonnes in 2014 and 740,000 tonnes in the first eight months of 2015 (Vietnamese Directorate of Fisheries, 2015). Currently, Vietnam produces approximately 80% world production of striped catfish. Most of the Vietnamese production (95%) are exported to 142 nations worldwide (http://www.seafood.vasep.com.vn). Main exported markets include Europe, the USA, Southeast Asian, Canada, the Middle East, and Japan. Total exported value was US$ 1.76 billion in 2014, accounting for 22.6% of Vietnamese total aquaculture export values (http://www.seafood.vasep.com.vn/). The current farming system is intensive in earthen ponds with yield ranges from 300 – 500 tonnes/ha. From 2000 to 2013, farming area increased fivefold, reaching 5,600 hectares. Production increases approximately 4.8 per cent yearly, and expected to reach 1.5 – 2.0 million tonnes in 2020 (http://www.seafood.vasep.com.vn/).

The first selective breeding programme for striped catfish has been carried out at the National Breeding Centre for Southern Freshwater Aquaculture (NABECSOFA), under the auspices of the Research Institute for Aquaculture No. 2 (RIA2). Research Institute for Aquaculture No. 2 is the government institution officially responsible for the enhancement of aquaculture production in the Mekong Delta region of southern Vietnam, which produces 70% of the Vietnam's aquaculture production. To the best of my knowledge, the breeding programme for striped catfish at RIA2 is the only one for striped catfish worldwide.

Selective breeding has been conducted in several aquaculture species for a number of traits of interest, resulting in encouraging improvement. Those included growth rate in Atlantic salmon (*Salmo salar*) (Gjedrem, 2012) and Nile tilapia (*Oreochromis niloticus*) (Bentsen *et al.*, 2012), Pacific white shrimp (*Litopenaeus vannamei*) (Argue *et al.*, 2002; Gitterle *et*

al., 2005a; Gitterle *et al.*, 2006), giant freshwater prawn (*Macrobrachium rosenbergii*) (Luan *et al.*, 2012; Hung *et al.*, 2013), abalone (*Haliotis diversicolor*) (Preston *et al.*, 2004), overall survival in Nile tilapia (Luân, 2010), disease resistant in Pacific white shrimp (Argue *et al.*, 2002), etc.

Genetic improvement becomes increasingly important in aquaculture because it will increase productivity of farmed aquatic species, especially through improvement of the additive genetic performance of farmed populations (Gjedrem, 2012). The benefit of utilising additive genetic effects is that genetics gain is accumulated via selection over time. On the other hand, several studies showed that non-additive effects such as environmental effects common to full-sibs and dominance genetic effects can be important components in the total phenotypic variance of quantitative traits in fish (Elvingson and Johansson, 1993; Gjerde *et al.*, 1994; Winkelman and Peterson, 1994a; Rye and Mao, 1998; Pante *et al.*, 2002; Wang *et al.*, 2006). However, Mrode (1996) suggested that non-additive genetic effects have little practical application in selection, and Varona and Misztal (1999) argued that estimation of these effects would involve large computational requirements. So non-additive genetic components such as dominance are usually ignored. However, accounting for non-additive genetic effects in genetic evaluation models is important for obtaining accurate predictions of breeding values of animals, estimation of heritability and precise prediction of response to selection (Josefa *et al.*, 2002). It is therefore important to estimate all genetic effects in order to adopt a suitable breeding strategy and selection method for the species of interest.

Environmental effects common to full-sibs caused by separately rearing of families in hapas (a type of net enclosure) or tanks until fish reach a sufficiently large size for individual physical tagging. Dominance effects can be understood as one parent contains genes that are missing in the other parent, and thus the offspring would contain more genes than either parent (Fu and Dooner, 2002). The term ‘dominance’ is frequently used when discussing models explaining heterosis, meaning the effect is not additively heritable, but

the unique positive combined effects of genes in a cross is decreasingly lost in subsequence generations if these cross-offspring are internally mated. Heterosis is the desirable effect of crossbreeding and the utilisation of differences between breeds to optimize genetic merit of different traits. Diallel cross experiments in breeding program have therefore been used as a tool to evaluate strains, establish synthetic base populations and estimate genetic parameters (Gjerde and Refstie, 1984; Gjerde, 1988; Bentsen *et al.*, 1998; Gjerde *et al.*, 2002). Diallel cross experiments can also be an efficient approach for improving productivity in aquatic animal by exploited heterosis in crossbred offspring. In common carp (*Cyprinus carpio*), Bakos *et al.* (2006) showed that crossbreeding combined with selective breeding in common carp in Hungary produced three hybrids that showed subtantial positive heterosis compared with pure lines. Similarly, in Nile tilapia Roberto *et al.* (2016) showed that four out of six crosses had better performance than the best pure line, demonstrating that improved heterosis is a relevant parameter for breeding strategies. The catfish industry in the USA produces over 300,000 tonnes/year, and 25–30% of the production is coming from a hybrid of channel and blue catfish (*Ictalurus punctatus* × *I. furcatus*) (Dunham, 2006). Similarly, more than 80% of catfish farmers in Thailand stock hybrid catfish (*Clarias macrocephalus* × *C. gariepinus*) due to their relatively fast growth and high disease resistance (Senanan *et al.*, 2004).

In this study, we tested genetic resources from three different geographical strains of striped catfish and three year-classes from a selective breeding program in a complete diallel cross. The aims of this study were to investigate the potential for a crossbreeding approach to improve the harvest weight in striped catfish, and to estimate genetic gain in the current selective breeding program. In this thesis, for body weight at harvest of striped catfish, I estimated (i) additive and non-additive genetic effects, (ii) heritability of the Selection group in G3 population, and (iii) selection responses by comparing the estimated breeding values (EBVs) between Selection group and the three other groups namely Control group, Parent group and Wild group.

2. Materials and methods

2.1. Experimental strains

The study was carried out at the National Breeding Centre for Southern Freshwater Aquaculture, Research Institute for Aquaculture No. 2, Vietnam. The program for striped catfish collected wild fish in 2001 and thereafter established a base population of the first year-class in 2001 (denoted as generation 1, G1) and two subsequent year-classes 2002 and 2003. The trait of interest has been growth, assessed by body weight at harvest. The third generation (G3) was to merge three year-classes into a single population, using the last generation in each year-class. In addition, wild fish were also incorporate into G3. Therefore, the newly formed G3 consisted of 4 groups, namely (i) Selection group, (ii) Control group, (iii) Parent group, and (iv) Wild group.

The parents of the Selection group were from three selected generations, namely G3_2001, G2_2002, and G2_2003. The parents were fish with highest individual EBVs (within their respective families) from best mean family EBVs for harvest body weight. Parents of Control group were also selected from three lines mentioned above (G3_2001, G2_2002 and G2_2003), but consisted of individuals with EBVs closed to the population mean of each line.

Fish from the earlies generation (that are still available) in each year-class, namely G2_2001, G1_2002 and G1_2003, were used to produce the so-called Parent group.

The Wild groups were all originated from wild fish in Cambodia. One group was collected in Cambodia by three Vietnamese local hatcheries, and thereafter recruited by RIA2 in 2013. In May 2014, researchers at RIA2 collected two more groups directly from Tonlé Sap and Kratie, Cambodia. They are referred as the Wild 1 (offspring from local hatcheries but originated in Cambodia), Wild 2 (offspring of Tonlé Sap strain) and Wild 3 (offspring of Kratie strain).

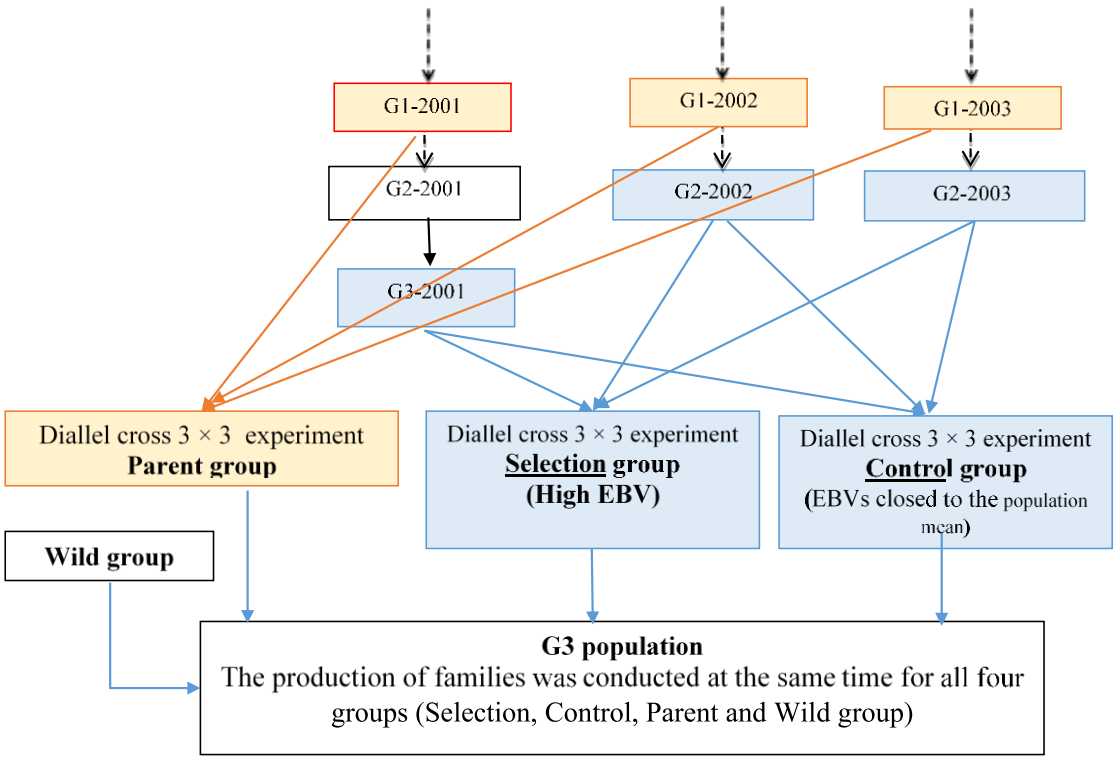

Figure 1. The structure of G3 population

2.2. Production of G3 population

The production of families was conducted at the same time for all four groups (Selection, Control, Parent and Wild group). A nested mating design, in which one male mated to two females, was used to partly facilitate estimation of environmental effects common to full-sibs. A partial factorial design, which would have been even better in this regard, was considered too labour- and time-consuming. In total 206 full-sibs families were produced from 130 sires and 206 dams over a total of 55 days from June 28 to August 22, 2014. The number of families produced was 139 for Selection group (6,826 individuals), 21 for Control group (1,116 individuals), 21 for Parent (1,035 individuals), and 25 for Wild group (1,368 individuals). The numbers of families that contributed to each cross are presented in Table 1.

The Selection, Control and Parent group, each consist of a complete 3 × 3 diallel cross of the three lines contributing in each group, i.e. six reciprocal crosses, along with the three types of purebred families, all done within each of the main groups that were to be compared (Table 1). The female parental strain is mentioned second in each cross. The three lines of wild group were only mated within each strain in order to create three new generations of Wild 1, Wild 2 and Wild 3 separately. The three new lines were associated together in one Wild-group.

Table 1.Diagram of the family mating design. Each completed cell represents the number of full-sibs families.

Sire		**Dam**											
		Selection			**Control**			**Parent**			**Wild**		
		G3_ 2001	**G2_ 2002**	**G2_ 2003**	**G3_ 2001**	**G2_ 2002**	**G2_ 2003**	**G2_ 2001**	**G1_ 2002**	**G1_ 2003**	**Wild 1**	**Wild 2**	**Wild 3**
Selection	**G3.2001**	30	11	15									
	G2.2002	9	15	10									
	G2.2003	15	10	24									
Control	**G3.2001**				2	1	2						
	G2.2002				3	3	2						
	G2.2003				2	1	5						
Parent	**G2.2001**							6	2	2			
	G1.2002							2	1	1			
	G1.2003							2	1	4			
Wild	**Wild1**										8		
	Wild2											13	
	Wild3												4

2.3. Nursing of families, tagging and growth-out environment

Approximately 3.000 fry, randomly sampled from each family, were start-fed 20 – 25 hours post-hatching, and reared separately in a 1 m^3 composite nursing tanks. The fry were fed with *Artemia* nauplii, *Moina* and powdered feed (40% crude protein). The water source and water exchange rate were the same for all nursing tanks. After 20 days, approximately 300 fry from each full-sib family were randomly sampled and moved into nursing hapas (1.5×2.0×1.0 m, mesh size 1 mm) suspended in a 2,000 m^2 earthen pond. The fry were fed with powdered feed and standard commercial pelleted feed (35% crude protein) given *ad libitum* twice per day. The hapas were thoroughly cleaned once a week to maintain good water circulation and to minimise the environmental variation among families. Due to differences in production dates and tagging dates, fingerlings were tagged at various size (7 – 100 g) and age (98 – 175 days). From each family, on average 75 fingerlings were randomly chosen and tagged with PIT (Passive Integrated Transponder) tags. All individuals in one family were tagged at the same time. Tagging was done over 39 days, from 21 November 2014 to 03 January 2015. In total, approximately 13.000 fish were tagged, representing 206 families (Table 2) from 130 sires and 206 dams. After tagging, fish from each family were kept in separate hapas for one week to monitor mortality. All tagged fish from four genetic groups were thereafter communally stocked in a 10,000 m^2 pond at the National Breeding Centre for Southern Freshwater Aquaculture, located in Cai Be district, Tien Giang province, Vietnam. Fish were fed *ad libitum* twice a day with commercial floating pelleted feed (28% crude protein).

2.4. Data analysis

2.4.1. Data collection

At harvest, body weight (HW) in grams and standard body length (L) in centimetres for all fish were recorded by the same person. Standard body length was measured at the maximum horizontal distance using a ruler, while weight was measured on an electronic scale with an accuracy of 0.1 g.

2.4.2. Data analysis

2.4.2.1. Estimation of variance components and heritability

Fixed, covariate, and random effects

Data were managed and checked in Microsoft Excel® 2013. The software package ASReml version 4.1 was used for all data analysis (Gilmour *et al.*, 2015), including test for significant levels of the fixed effects. Date of production, calculated as the number of days from 1st January to the date that a family was produced, was found significant ($P<0.05$), and therefore was fitted in the model as a fixed effect. Growing age, time from tagging until harvest, was found to be significant and therefore was fitted as covariate. Environmental effect common to full-sibs (*c*), random parental dominance genetic effect (*d*), and the random additive genetic effect (*a*) were fitted as random effects.

Statistical model

The following linear model was used in ASReml version 4.1 (Gilmour *et al.*, 2015) to estimate heritability and variance components for both (i) 'Selection group' and (ii) 'Whole population';

$$Y_{ijk} = \mu + P_i + \beta_1 G_{ijkl} + ANIMAL_j + DAM_k + DOMINANCE_l + e_{ijkl} \quad (1)$$

where,

- Y_{ijkl} is the phenotypic value of weight gain from tagging to harvest for the l^{th} fish:
    - For Selection group: l = 6,826 individuals
    - For Whole population: l = 10,345 individuals
- μ is overall mean of the body weight
- P_i is the fixed effect of the i^{th} date of production
    - For Selection: i = 1, 2, …., 8
    - For Whole population: i = 1, 2, …., 10

– β_1 is the regression coefficient of the co-variate growing age, G_{ijkl}

+ For Selection: *ijkl* = 1, 2, …, 70
+ For Whole population: *ijkl* = 1,2, …, 70

– $ANIMAL_j$ is the random additive genetic effect of the j^{th} fish with N (0, Aσ_a^2) where $\boldsymbol{A}$ is the additive genetic relationship matrix among the animals and σ_a^2 is the additive genetic variance;

+ For Selection:
  - j = 1, 2,…, 7702
  - A = [7702 : 7702]
+ For Whole population:
  - j = 1, 2, …, 11410
  - A = [11410 : 11410]

– DAM_k is the random environmental effect common to full-sibs with N(0, $\boldsymbol{I}\sigma_c^2$) where $\boldsymbol{I}$ is an identity matrix of dimension **N** and σ_c^2 is the environmental effects common to full-sibs variance;

+ For Selection:
  - k = 1, 2,…, 139
  - $\boldsymbol{I}$ = [6826 : 6826]
+ For Whole population:
  - k = 1, 2, …, 206
  - $\boldsymbol{I}$ = [10345 : 10345]

– $DOMINANCE_l$ is the random parental dominance genetic effect of the l^{th} fish with N(0, $D\sigma_c^2$) where $\boldsymbol{D}$ is the dominance genetic relationship matrix among the animals and σ_d^2 is the dominance genetic variance;

+ For Selection:
  - l = 1,2,…, 7702
  - $\boldsymbol{D}$ = [7702 : 7702]
+ For Whole population:
  - l = 1,2, …, 11410

- ***D*** = [11410 : 11410]

– e_{ijkl} is the random residual term with N(0, $\boldsymbol{I}\sigma_e^2$) where ***I*** is the identity matrix and σ_e^2 is the residual variance.

+ For Selection: ***I*** = [6826 : 6826]
+ For Whole population: ***I*** = [10345 : 10345]

Heritability (h^2), environmental effects common to full-sibs (c^2) and percentage of genetic dominance effect (d^2) were calculated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2+\sigma_c^2+\sigma_e^2};$$

$$c^2 = \frac{\sigma_c^2}{\sigma_a^2+\sigma_c^2+\sigma_e^2};$$

$$d^2 = \frac{\sigma_d^2}{\sigma_a^2+\sigma_c^2+\sigma_e^2};$$

where σ_a^2 is the additive genetic variance, σ_c^2 is the environmental variance common to full-sibs, σ_d^2 is the dominance genetic variance and σ_e^2 is the residual variance.

2.4.2.2. Estimation of the mean EBVs for the four genetic groups to assess genetic gain

Breeding values from G0 to G5 were estimated using Model 1 for 'Whole population' using ASReml version 4.1 (Gilmour *et al.*, 2015). Actual selection responses were estimated trough three different contrasts (i) difference in estimated breeding values (EBVs) between Selection group and the Control group, (ii) difference in EBVs between Selection and Parent group and (iii) difference in EBVs between Selection group and Wild group, all measured in the same year. Direct selection responses were expressed in grams and as a percentage of improvement, that is, how better the Selection group was compared to each of the other three groups.

3. Result

3.1. Descriptive statistics

Number of observations, families, mean value, minimum and maximum, standard deviation (Sang, #34) and coefficients of variation (CV) for body weight at harvest in each group are given in Table 2. Total number of fish recorded were 10,345, representing 206 families. Average growing age from tagging time to harvest time was 192 days. Overall survival rate was 80.7%, highest in the Wild group (83.7%) and lowest in Control group (77.8%). Mean harvest weight ranged from 852 g (Control group) to 993 g (Selection group). Coefficient of variance (CV) was not significant different among four groups, and was highest in Control group (0.44).

Table 2. Number of fish, mean of harvest weight and coefficient of variance (CV) of selection group

Group	N (ind.)	N (family)	Mean (g)	SD	CV	Min (g)	Max (g)
Selection	6,826	139	992.7*	305.4	0.31	250.8	2,598.0
Control	1,116	21	851.8*	240.1	0.44	278.0	1,924.6
Parent	1,035	21	881.6*	253.3	0.29	322.2	2,066.0
Wild	1,368	25	908.6*	280.0	0.31	114.8	2,327.2

* significantly different ($P < 0.001$).

3.2. Phenotypic and genetic parameters

Estimated variances for additive genetic (σ_A^2), environmental effects common to full-sibs (σ_c^2), dominance genetic (σ_d^2) and phenotypic (σ_P^2) of 'Selection group' and 'Whole population' are presented in Table 3.

Table 3. Estimated components variances for body weight at harvest for Selection and Whole population

Variance component	Selection group	Whole population
$\boldsymbol{\sigma_A^2}$ **± se**	10,961 ± 11,306	21,274 ± 10,737
$\boldsymbol{\sigma_d^2}$ **± se**	3,936 ± 1,587	4,360 ± 1,315
$\boldsymbol{\sigma_c^2}$ **± se**	17,547 ± 5,530	15,493 ± 4,853
$\boldsymbol{\sigma_P^2}$ **± se**	63,863 ± 3,218	64,061 ± 2,949

Heritability (h^2), environment effects common to full-sibs (c^2), and percentage of dominance genetic effect (d^2) of 'Selection group' and 'Whole population' are presented in Table 4.

Table 4. The estimated heritability (h^2), environment effects common to full-sibs (c^2) and % of dominance genetic effect (d^2) of body weight with their standard errors (± se)

	Selection group	Whole population
$\boldsymbol{h^2}$	0.17 ± 0.17	0.33 ± 0.16
$\boldsymbol{c^2}$	0.27 ± 0.09	0.24 ± 0.08
$\boldsymbol{d^2}$	0.06 ± 0.03	0.07 ± 0.02

3.3. Selection response

Mean EBVs for the four groups and actual selection responses for body weight are presented in Table 5.

Table 5. Direct selection response for body weight estimated by different methods and expressed as selection gain in grams and percentages

Contrast	Group	Mean EBV (± se)	Actual selection response	
			Grams	Percentage **
i	Selection Control	22 ± 118 -40 ± 118	62	37
ii	Selection Parent	22 ± 118 -52 ± 118	73	48
iii	Selection Wild	22 ± 118 -7.6 ± 119	29	15

* (i) difference in estimated breeding values (EBVs) between Selection and Control group, (ii) difference in EBVs between Selection and Parent group, and (iii) difference in EBVs between Selection and Wild group, all measured in the same year

** overall population mean for body weight (206 g) is used when fitting full model.

Table 6. Mean EBVs of 9 crosses in Selection group

Male × female	Mean EBVs	Standard deviation
G2_2002 × G2_2002	**27**	**118**
G2_2002 × G2_2003	39	118
G2_2002 × G3_2001	28	118
G2_2003 × G2_2003	**18**	**118**
G2_2003 × G2_2002	13	118
G2_2003 × G3_2001	0.3	117
G3_2001 × G3_2001	**27**	**117**
G3_2001 × G2_2002	58	118
G3_2001 × G2_2003	-24	118

In Selection group, mean EBVs (in grams) of crossbreed G3_2001 × G2_2002 (58 g) was highest among 6 crosses, followed by G2_2002 × G2_2003 (39 g), and G3_2001 ×

G2_2003 was the lowest (-24 g). With purebred, generation G2_2002 and G3_2001 had similar mean EBV (27 g) while G2_2003 was lower (18 g) (Table 6 and Figure 2).

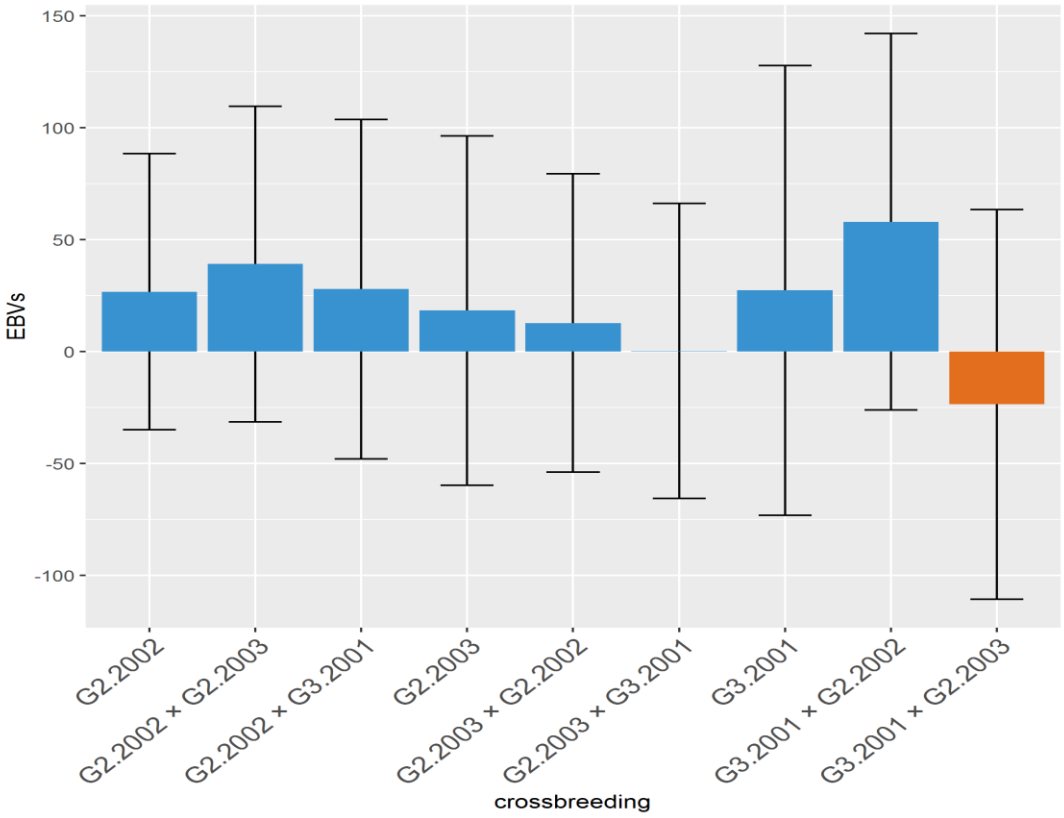

Figure 2. Mean EBVs for body weight of 9 crosses in Selection group, black lines indicate standard errors

Mean EBVs of two crossbreds G3_2001 × G2_2002 and G2_2002 × G2_2003 deviated positively from the mean of three purebreds, while mean EBVs of three others (G2_2003 × G2_2002, G2_2003 × G3_2001, G3_2001 × G2_2003) deviated negatively (Table 7).

Table 7. Deviation of EBVs mean of each cross-performance from the mean of the pure crosses.

Male × female	G2_2002 × G2_2002	G2_2003 × G2_2003	G3_2001 × G3_2001
G2_2002 × G2_2003	**12**	**21**	**12**
G2_2002 × G3_2001	1	10	1
G2_2003 × G2_2002	-14	-5	-14
G2_2003 × G3_2001	-26.7	-17.7	-26.7
G3_2001 × G2_2002	**31**	**40**	**31**
G3_2001 × G2_2003	-51	-45	-51

4. Discussion

4.1. Genetic parameters

In the current selective breeding program in striped catfish in Vietnam, estimates of heritability for body weight was 0.33 for all four genetic groups and was 0.17 for Selection group isolate alone. The results are similar to the results obtained for this species by Sang *et al.* (2012) (0.21 – 0.34, in different year-classes and generations). Similar heritability estimates have also been found in other species, for example, from 0.1 to 0.3 in salmonids (Gjedrem, 2000; Kause *et al.*, 2002; Quinton *et al.*, 2005; Powell *et al.*, 2008), 0.21 in white shrimp (Gitterle *et al.*, 2005b), and 0.23 (on average) in tilapia (Gjedrem, 2000; Bolivar and Newkirk, 2002; Gall and Bakar, 2002; Rutten *et al.*, 2005).

The difference between the estimated heritability found in whole population (0.33) and Selection group (0.17) was likely a result of the different genetic composition of the two nested groups (6,826 for Selection group and 10,345 individuals for whole population). Additive genetic variance for whole population (21,274) was almost two times larger than that of Selection group (10,961), while phenotypic variance was similar for both groups (63,863 and 64,061) (Table 3). It is also worth noting that estimate heritability of Selection group was not significant different from zero (0.17 ± 0.17). This can be explained by high

environmental effects common to full-sibs in the Selection group (0.27) caused by the hapa-rearing of full-sibs families. In addition, there are many random environmental effects that may influence the performance of individuals, such as nutrition, mortality, diseases, competition, temperature, stress, etc. Finally, it often exists limiting factors in these sub-optimal environments, such as dissolved oxygen, that make the best genotype unable to show their full genetic potential.

Estimates of environmental effects common to full-sibs (c^2) was relatively large and significant different from zero for both Selection group (0.27 ± 0.09) and Whole population (0.24 ± 0.08) (Table 4), which were higher than what Sang *et al.* (2012) found in the second generation of the year-class G_2001 (0.14 ± 0.06). This may be explained by the difference in nursing days in hapas, since Sang *et al.* (2012) reported shorter nursing time (150 – 170 days) than in the present study (98 – 175 days). Common environment effects of this size have also been found for both body weight in tilapia (0.23) (Maluwa and Gjerde, 2007; Luân, 2010), and rainbow trout (0.17) (Su *et al.*, 1996). The relatively large variation among full-sibs was likely a consequence of the unavoidable separately nursing isolation of full-sib groups in hapas for prolonged periods (98 – 175 days), which were approximately half of the grow-out period (192 – 261 days). In addition, high environmental covariance among full-sibs might be due to influences from the dams (Mrode, 2005). This maternal effect is mostly related to variation in egg size and egg quality, resulting in variation in hatching and survival during the first stages of growth and development (Gjedrem, 2005).

Estimate of dominance effects (d^2) were relatively low for both Selection (0.06 ± 0.03) and Whole population (0.07 ± 0.02) in this study (Table 4). Dominance effects of this size have also been found from in Atlantic salmon (0.02 – 0.18) (Rye and Mao, 1998), chinook salmon (0.08) (Winkelman and Peterson, 1994b), and coho salmon (*Oncorhynchus kisutch*) 0.06 to 0.19 (Gallardo *et al.*, 2010).

Additive and dominance genetic variances and environmental effects common to full-sibs variances are reported as a fraction of the total phenotypic variance. My results suggest that ignoring these effects could seriously reduce the accuracy of genetic evaluation if mating designs and statistical analyses do not include them, since that are likely to inflate the heritability estimates and estimated breeding values (Miglior *et al.*, 1995; Misztal, 1997; Rye and Mao, 1998; Josefa *et al.*, 2002).

4.2. Selection response

My results demonstrated that genetic selection and crossbreeding improved the performance in growth in striped catfish. Actual selection response was high when comparing the Selection with Parent, Control and Wild group. This could be explained by large additive genetic variance found, i.e. high h^2 and the effects of heterosis. Selection response when comparing with the Wild group was smaller than when comparing with Control and Parent groups. A higher additive genetic variance in Wild group compared to the Control and Parent group could be explained by selection; more specifically by the Bulmer effect that is known to cause reduction in the additive genetic variance (Falconer and Mackay, 1996). In addition, the Wild group was an association of three wild fish groups originated from Cambodia, indicating that they might had large effect on additive genetic variance compared with the Selection group.

The actual selection response for body weight in G3 population was higher than those of other fish species, for instant 10 – 15% response was reported in cold water fish (Gjedrem, 2000), 21% in Pacific white shrimp (Argue *et al.*, 2002); 12 – 20% (Dunham and Smitherman, 1983) and 20 – 30% (Rezk *et al.*, 2003) in channel catfish, 12 – 17% in Nile tilapia (Eknath *et al.*, 2007), 26.9% in *Fenneropenaeus chinensis* (Wang and Wang, 2005).

5. Conclusion

The present results indicate that there was high genetic variation for effective selection to improve body weight in the current population of striped catfish in Vietnam. The results also showed that environment effects common to full-sibs were high. I suggested using DNA-tagging method for identification of individual to reduce environmental effects common to full-sibs. When selecte candidate parents to produce a new generation, I suggested that beside three purebred strains, fish from three crossbreds G3_2001 × G2_2002, G2_2002 × G2_2003 and G2_2002 × G3_2001 should also be selected. In addition, three wild fish groups originated from Cambodia should wild be considered as a genetic source that contributes to the next generation.

References

Argue, B.J., Arce, S.M., Lotz, J.M., Moss, S.M., 2002. Selective breeding of Pacific white shrimp (Litopenaeus vannamei) for growth and resistance to Taura Syndrome Virus. Aquaculture Asia-Pacific, 447-460.

Bakos, J., Varadi, L., Gorda, S., Jeney, Z., 2006. Lessons from the breeding program on common carp in Hungary. In: Ponzoni, R.W., Acosta, B.O., Ponniah, A.G. (Eds.), Development of Aquatic Animal Genetic Improvement and Dissemination Programs: Current Status and Action Plans: WorldFish Center Conferences Proceedings, vol. 73, pp. 27-33.

Bentsen, H.B., Eknath, A.E., Palada-de Vera, M.S., Danting, J.C., Bolivar, H.L., Reyes, R.A., Dionisio, E.E., Longalong, F.M., Circa, A.V., Tayamen, M.M., Gjerde, B., 1998. Genetic improvement of farmed tilapias: growth performance in a complete diallel cross experiment with eight strains of *Oreochromis niloticus*. Aquaculture, 145-173.

Bentsen, H.B., Gjerde, B., Nguyen, N.H., Rye, M., Ponzoni, R.W., Paladade Vera, M.S., Bolivar, H.L., Velasco, R.R., Danting, J.C., Dionisio, E.E., Longalong, F.M., Reyes, R.A., Abella, T.A., Tayamen, M.M., Eknath, A.E., 2012. Genetic improvement of farmed tilapias: genetic parameters for body weight at harvest in Oreochromis niloticus during five generations of testing in multiple environments. Aquaculture, 56-65.

Bolivar, R.B., Newkirk, G.F., 2002. Response to within family selection for body weight in Nile tilapia (*Oreochromis niloticus*) using a single-trait animal model. *Aquaculture*, 204, 371-381.

Dunham, R.A., 2006. History of catfish breeding and its application in the United States: lessons to be learned? The Israeli Journal of Aquaculture-Bamidgeh 58, 251-256.

Dunham, R.A., Smitherman, R.O., 1983. {Tổng Cục Thủy Sản, 2015 #36}Response to selection and realized heritability for body weight in three strains of channel catfish, *Ictalurus punctatus*, grown in earthen ponds. *Aquaculture* 33, 89-96.

Eknath, A.E., Bentsen, H.B., Ponzoni, R.W., Rye, M., Nguyen, N.H., Thodesen, J., Gjerd, B., 2007. Genetic improvement of farmed tilapia: composition and genetic parameters of a synthetic base population of *Oreochromis niloticus* for selective breeding. *Aquaculture* 273, 1-14.

Elvingson, P., Johansson, K., 1993. Environmental components of variation in body traits of rainbow trout *Oncorhynchus mykiss* in relation to age. Aquaculture, 191-204.

Falconer, D.S., Mackay, T.F., 1996. Introduction to quantitative genetics (4th Ed).

Fu, H., Dooner, H.K., 2002. Intraspecific violation of genetic colinearity and its implications in maize. in: USA, P.N.A.S. (Ed.), pp. 9573-9578.

Gall, G.A.E., Bakar, Y., 2002. Application of mixed-model techniques to fish breed improvement: analysis of breeding-value selection to increase 98-day body weight in tilapia. *Aquaculture* 212, 93-113.

Gallardo, A.J., Lhorente, P.J., Neira, R., 2010. The consequences of including non-additive effects on the genetic evaluation of harvest body weight in Coho salmon (*Oncorhynchus kisutch*). Genetics Selection Evolution.

Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J., Thompson, R., 2015. ASReml User Guide Release 4.1 Structural Specification.

Gitterle, T., Ødegård, J., Gjerde, B., Rye, M., Salte, R., 2006. Genetic parameters and accuracy of selection for resistance to White Spot Syndrome Virus (WSSV) in *Penaeus (Litopenaeus) vannamei* using different statistical models. Aquaculture. 251, 210-218.

Gitterle, T., Salte, R., Gjerde, B., Cock, J., Johansen, H., Salazar, M., Lozano, C., Rye, M., 2005a. Genetic (co) variation in resistance to White Spot Syndrome Virus (WSSV) and harvest weight in *Penaeus (Litopenaeus) vannamei*. Aquaculture. 246, 139-149.

Gitterle, T., Rye, M., Salte, R., Cock, J., Johansen, H., Lozano, C., Suares, J.A., Gjerded, B., 2005b. Genetic (co)variance in harvest body weight and survical in Penaeus (Litopenaeus) vannamei under standard commercial conditions. Aquaculture, 83-92.

Gjedrem, T., 2000. Genetic improvement of cold-water species. *Aquac. Res.* 31, 25–33.

Gjedrem, T., 2012. Genetic improvement for the development of efficient global aquaculture: A personal opinion review. Aquaculture, 12-22.

Gjerde, B., 1988. Complete diallele cross between six inbred groups of rainbow trout, *Salmo gairdneri*. Aquaculture, 71-87.

Gjerde, B., Refstie, T., 1984. Complete diallel cross between five strains of Atlantic salmon. Livestock Production Science, 207-226.

Gjerde, B., Simianer, H., Refstie, T., 1994. Estimates of genetic and phenotypic parameters for bodyweight growth rate and sexual maturity in Atlantic salmon. Livest Prod Sci 133-143.

Gjerde, B., Reddy, P.V.G.K., Mahapatra, K.D., Saha, J.N., Jana, R.K., Meher, P.K., Sahoo, M., Lenka, S., Govindassamy, P., Rye, M., 2002. Growth and survival in two complete diallele crosses with five stocks of Rohu carp (*Labeo rohita*). Aquaculture. 209, 103-115.

Hung, D., Vu, N.T., Nguyen, N.H., Ponzoni, R.W., Hurwood, D.A., Mather, P.B., 2013. Genetic response to combined family selection for improved mean harvest weight in giant freshwater prawn (Macrobrachium rosenbergii) in Vietnam. Aquaculture. 412, 70-73.

Josefa, m., Pante, R., Gjerde, B., McMillan, I., Misztal, I., 2002. Estimation of additive and dominance genetic variances for body weight at harvest in rainbow trout, *Oncorhynchus mykiss*. Aquaculture, 383–392.

Kause, A., Ritola, O., Paananen, T., Mäntysaari, E., Eskelinen, U., 2002. Coupling body weight and its composition: a quantitative genetic analysis in rainbow trout. *Aquaculture* 211, 65-79.

Luan, S., Yang, G., Wang, J., Luo, K., Zhang, Y., Gao, Q., Hu, H., Kong, J., 2012. Genetic parameters and response to selection for harvest body weight of the giant freshwater prawn Macrobrachium rosenbergii. Aquaculture. 362, 88-96.

Luân, T.D., 2010. Genetic studies of Nile tilapia (*Oreochromis niloticus*) for farming in Northern Vietnam: growth, survival and cold tolerance in different farm environments. PhD thesis, Norwegian University of life Sciences.

Maluwa, A.O., Gjerde, B., 2007. Response to selection for harvest body weight of *Oreochromis shiranus*. *Aquaculture* 273 (1), 33-41.

Merican, Z., 2011. Tilapia is gaining popularity in Vietnam. AQUA CULTURE Asia Pacific, 40.

Miglior, F.A., Burnside, E.B., Kennedy, B.W., 1995. Production traits in Holstein cattle: estimation of non-additive genetic variance components and inbreeding depression. J. Dairy Sci. 78, 1174-1180.

Misztal, I., 1997. Estimation of variance components with large-scale dominance models. J. Dairy Sci. 80, 965-974.

Mrode, R.A., 1996. Linear Models for the Prediction of Animal Breeding Values. in: CAB International, W., Oxon, UK (Ed.).

Mrode, R.A., 2005. Linear Models for the Prediction of Animal Breeding Values, 2nd Edition; chapter 4 - Best Linear Unbiased Prediction of Breeding Value: Models with Random Environmental Effects. P. 71-82.

Pante, M., Gjerde, B., McMillan, I., Misztal, I., 2002. Estimation of additive and dominance genetic variances for body weight at harvest in rainbou trout Oncorhynchus mykiss Oncorhynchus mykiss. Aquaculture, 383-392.

Powell, J., White, I., Guy, D., Brotherstone, S., 2008. Genetic parameters of production traits in Atlantic salmon (*Salmo salar*). *Aquaculture* 274, 225-231.

Preston, N.P., Crocos, P.J., Keys, S.J., Coman, G.J., Koenig, R., 2004. omparative growth of selected and non-selected Kuruma shrim Penaeus (Marsupenaeus) japonicus in commercial farmponds; implications for broodstock production. Aquaculture, 73-82.

Quinton, C.D., McMillan, I., Glebe, B.D., 2005. Development of an Atlantic salmon (*Salmo salar*) genetic improvement program: genetic parameters of harvest body weight and carcass quality traits estimated with animal models. *Aquaculture* 247, 211-217.

Rezk, M.A., Smitherman, R.O., Williams, J.C., Nichols, A., Kucuktas, H., Dunhama, R.A., 2003. Response to three generations of selection for increased body weight in channel catfish, *Ictalurus punctatus*, grown in earthen ponds. *Aquaculture* 228. 69-79.

Roberto, N., Garcíaa, X., Lhorenteb, J.P., Filpb, M., José Manuel Yáñezb, c., Cascanted, A.M., 2016. Evaluation of the growth and carcass quality of diallel crosses of four strains of Nile tilapia *(Oerochromis niloticus)*. Aquaculture. 451.

Rutten, M.J.M., Bovenhuis, H., Komen, H., 2005. Genetic parameters for fillet traits and body measurements in Nile tilapia (Oreochromis niloticus L.). Aquaculture, 125-132.

Rye, M., Mao, I., 1998. Nonadditive genetic effects of inbreeding depression for body weight in Atlantic salmon (Salmo salar L.). Livest Prod Sci, 15-22.

Sang, N.V., Klemetsdal, G., Ødegård, J., Gjøen, H.M., 2012. Genetic parameters of economically important traits recorded at a given age in striped catfish (*Pangasianodon hypophthalmus*). Aquaculture, 82-89.

Senanan, W., Kapuscinski, A.R., Na-Nakorn, U., Miller, L.M., 2004. Genetic impacts of hybrid catfish farming (*Clarias macrocephalus x C. gariepinus*) on native catfish populations in central Thailand. *Aquaculture* 235, 167-184.

Su, G.-S., Liljedahl, L.-E., Gall, G.A.E., 1996. Genetic and environmental variation of body weight in rainbow trout (*Oncorhynchus mykis)*. *Aquaculture* 144 (1-3), 71-80.

Varona, L., Misztal, I., 1999. Prediction of parental dominance combinations for planned matings, methodology and simulation results. J. Dairy Sci, 2186-2191.

Vietnamese Directorate of Fisheries, 2015. Hội nghị bàn giải pháp nâng cao chất lượng giống cá Tra (10/02/2015). http://www.fistenet.gov.vn/e-nuoi-trong-thuy-san/a-san-xuat-giong/hoi-nghi-ban-giai-phap-nang-cao-chat-luong-giong-ca-tra.

Wang, C., Li, S., Xiang, S., Wang, J., Liu, Z., Pang, Z., Duan, J., Xu, Z., 2006. Additive dominance genetic effects for growth-related traits in common carp Cyprinus carpio L. Cyprinus carpio. Aquac Res, 1481-1486.

Wang, Q.Y., Wang, Q., 2005. Recent trends in China's aquaculture industry. Aquac. Asia Pacific 1, 18-20.

Winkelman, A., Peterson, R., 1994a. Heritabilities dominance variation common environmental effects and genotype by environment interactions for weight and length in chinook salmon. Aquaculture Asia-Pacific, 17-30.

Winkelman, A.M., Peterson, R.G., 1994b. Heritabilities, dominance variation, common environmental effects and genotype by environment interactions for weight and length in chinook salmon. *Aquaculture* 125,17-30.

Appendix

Appendix 1. Model used to estimate genetic variance components for Whole population

```
!WORKSPACE 1600
Model
 animal       !A !P
 sire         !A
 dam          !A
 farm         !A
 produceday   !I
 hapaday      !I
 PITday       !I
 harvestday   !I
 productiondate  !I
 nurseage
 hapaage
 growage
 totalage
 tagw
 harw
 Net_w
 harwlengt
 sire_strain  !A
 dam_strain   !A
 crossbreeding !A
 population   !A
 H_G_01
 H_G_02
 H_G_03
 H_W1
 H_W2
 H_W3
 R_G_01
 R_G_02
 R_G_03
 R_W1
 R_W2
 R_W3
 no_tag_per_farm
 no_harvest_per_farm
 survival_rate

ped.total.csv !SKIP 1 !ALPHA !MAKE
Dinv_new.giv !SKIP 1
data2015.total.csv  !SKIP 1
Net_w ~ mu productiondate growage !r animal dam giv(animal,1)
```

```
residual units
VPREDICT !DEFINE
F domvar giv(animal,1)
F FSeffect dam
F phenvar units + animal + domvar+ FSeffect
F genvar  animal
H c2 FSeffect  phenvar
H d2 domvar phenvar
H herit genvar phenvar
```

Appendix 2. Fixed and random effects for estimate the genetic variance components of Whole population

- - - Results from analysis of Net_w - - -
Akaike Information Criterion 119841.46 (assuming 4 parameters).
Bayesian Information Criterion 119870.43

Model_Term		Gamma	Sigma	Sigma/SE	% C
dam	IDV_V 206	0.675515	15492.7	3.19	0 P
animal	NRM_V 11410	0.927598	21274.1	1.98	0 P
giv(animal,1)	GRM_V 11410	0.190097	4359.80	3.32	0 P
units	10345 effects				
Residual	SCA_V 10345	1.00000	22934.6	4.18	0 P

Wald F statistics

Source of Variation	NumDF	F-inc
37 mu	1	3742.94
9 productiondate	9	14.54
12 growage	1	696.47
3 dam	206 effects fitted	
1 animal	11410 effects fitted	
38 giv(animal,1)	11410 effects fitted (1014 are zero)	

Appendix 3. Model used to estimate the genetic variance components of Selection Group

```
!WORKSPACE 1600
Model with d2 and sire and dam strain
 animal       !A !P
 sire         !A
 dam          !A
 farm         !A
 produceday   !I
 hapaday      !I
 pitday       !I
 harday       !I
 productiondate   !I
 nurseage
 hapaage
 growage
 totalage
 tagw
 harw
 Net_w
 harwlengt
 groupsire   !A
 groupdam    !A
 crossbreeding !A
 heterosis1
 heterosis2
 heterosis3
 reciprocal1
 reciprocal2
 reciprocal3
 notagging
 nohar
 survival

ped.selected.selected.csv !SKIP 1 !ALPHA !MAKE
Dinv_new.giv !SKIP 1
data2015.selected.selected.csv  !SKIP 1
Net_w ~ mu productiondate growage !r animal dam giv(animal,1)
residual units
VPREDICT !DEFINE
F domvar giv(animal,1)
F FSeffect dam
F phenvar units + animal + domvar+ FSeffect
F genvar  animal
H c2 FSeffect  phenvar
H d2 domvar phenvar
H herit genvar phenvar
```

Appendix 4. fixed and random effects for estimate the genetic variance components of Selection Group

- - - Results from analysis of Net_w - - -

Akaike Information Criterion 79576.73 (assuming 4 parameters).

Bayesian Information Criterion 79604.04

Model_Term		Gamma	Sigma	Sigma/SE	% C
dam	IDV_V 139	0.558502	17547.4	3.17	0 P
animal	NRM_V 7702	0.348864	10960.8	0.97	0 P
giv(animal,1)	GRM_V 11410	0.125267	3935.71	2.48	0 P
units	6826 effects				
Residual	SCA_V 6826	1.00000	31418.6	5.39	0 P

Wald F statistics

Source of Variation	NumDF	F-inc
30 mu	1	3540.22
9 productiondate	7	19.34
12 growage	1	331.94
3 dam	139 effects fitted	
1 animal	7702 effects fitted	
31 giv(animal,1)	11410 effects fitted (2875 are zero)	