

Short communication

Optimizing the gain of social genetic effect under the control of inbreeding using genetic algorithm

Pingxian Wu, Yanzhi Jiang, Li Zhu, Xuewei Li, Guoqing Tang*

Farm Animal Genetic Resources Exploration and Innovation Key Laboratory of Sichuan Province, Sichuan Agricultural University, Chengdu 611130, China

ARTICLE INFO

Article history:

Received 16 October 2015

Received in revised form

9 March 2016

Accepted 6 June 2016

Keywords:

Blup

Genetic algorithm

Inbreeding

Optimization

Social genetic effect

ABSTRACT

Social interactions among animals are widely existed in livestock population. However, some studies showed that the selection of social genetic effect led to extra increase of inbreeding. In this study, two optimization methods (SBLUP+GA1, SBLUP+GA2) based on genetic algorithm were used to obtain the optimal genetic contributions of seedstocks and maximize the average genetic gains of direct and social genetic component while minimizing the inbreeding. In SBLUP+GA1, only the contributions of sires were optimized. In SBLUP+GA2, the contributions of sires and dams were optimized together. The results showed SBLUP+GA1 and SBLUP+GA2 resulted in 18.52% and 25.93% lower inbreeding rate than common social genetic effect selection based on BLUP method (SBLUP) under base parameters, respectively. Under that situation, the average gains for direct, social and total genetic effect component in SBLUP+GA1 were actually improved 3.59%, 10.02% and 4.32% relative to SBLUP, respectively. In SBLUP+GA2, they were 1.28%, 10.00% and 2.02%, respectively. SBLUP+GA2 resulted in lower inbreeding rate, but, obtained slightly less genetic gain than SBLUP+GA1.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

The interactions between animals are very common in a highly social population. In livestock production, animals are usually penned or caged together into a contemporary group. Competition and cooperation among individuals in this group are widespread, some animals would benefit due to their advantages in body shape or temperament, and moreover, these effects are heritable (Muir, 2005; Bijma et al., 2007; Bergsma et al., 2008; Chen et al., 2009).

When interactions take place, the phenotypic value of each animal can be modeled as the sum of a direct effect itself and the summed social effects due its group members because each individual is also affected by its group members. The heritable component of social effect is defined as social genetic effect, which is the genetic impact of an animal on the trait value of another animal. Some studies showed that genetic gain of socially affected traits could be improved further by applying a selection strategy that considers both direct and social genetic effects (Muir, 1996; 2005; Bijma et al., 2007; Ellen et al., 2007; Bergsma et al., 2008; Gómez et al., 2011).

The heritability estimations of social effects usually are very low in practical breeding programs (Cassady and Van Vleck, 2004;

Arango et al., 2005; Chen et al., 2009). However, the contribution of social genetic effect to selection response of interesting trait is significant. Recently, this group showed that a social effect with 0.3% direct phenotypic variance (very small social genetic effect) resulted in 15.27% extra selection response. Unfortunately, some studies also showed that the selection of social genetic effect caused an extra increase of inbreeding in a long term breeding program (Khaw et al., 2014). The objective of this study is to use genetic algorithm to optimize the genetic contributions of selected animals and maximize the selection response of social genetic effect under the control of inbreeding.

2. Material and methods

2.1. The data simulated

A FORTRAN package developed was used to simulate a dataset with 10 generations, in which, founder animals were assumed unrelated. In base population, 10 sires and 100 dams were simulated. A socially affected trait with different positive social effect was simulated. Bivariate normal distribution was used to simulate both the genetic and non-genetic direct and social effects of base animals (Khaw et al., 2014). The detailed parameters are listed in Table 1.

In subsequent generations, 10 sires and 100 dams were selected and mated. The progeny number of each dam was fixed as 10.

* Corresponding author.

E-mail address: tyq003@163.com (G. Tang).

Table 1
The parameters used in dataset simulated.

Parameters	Scenarios		
	Base	1	2
Number of replicates	50		
Trait parameters			
Heritability of direct effect	0.5		
Heritability of social effect	0.3		
Correlation between direct and social genetic effect	0.3		
Correlation between direct and social non-genetic effect	0.3		
Direct phenotypic variance (DPV)	5.5	5.5	5.5
Percentage of social phenotypic variance relative to DPV	0.3%	1%	10%
Population parameters			
Sire number	20		
Dam number	100		
Group member number	10	15	5
Generation number	10		
Ratio assigned to EBV and mean relationship (w1/w2)			
SBLUP+GA1	1/10	1/1	1/100
SBLUP+GA2	1/100	1/10	1/200

Direct and social genetic effects of a progeny were calculated as the sum of parents' mean breeding value and a Mendelian sampling deviation (Falconer and Mackay, 1996). The latter sampled from a bivariate normal distribution with mean zero and variance $0.5\sigma^2(1 - 0.5(F_s + F_d))$, where σ^2 is genetic variance; F_s and F_d are the inbreeding coefficients of the sire and dam, respectively. The

genetic and non-genetic correlations between direct and social effect are listed in Table 1. For convenience, all members of a full sib family was assigned to a group if its size was smaller than the group size, and the remainder of this group came from another full sib family. The phenotypes of individuals were calculated according to the following equation:

$$y_{ijk} = sex_i + l_j + a_{dk} + \sum_{m \neq k} a_{sm} + \sum_{m \neq k} e_{sm} + e_{ijk},$$

where sex_i is sex effect; l_j is litter effect, which samples from a normal distribution; a_{dk} is direct additive genetic effect; a_{sm} is social genetic effect; e_{sm} is social permanent environmental effect; e_{ijk} is residual effect. For each scenario, 10 generations of selection were simulated. All these cases were replicated 50 times. The end results were the mean values of all these replicates.

2.2. Statistical models

A full model with direct and social genetic effect was designed to evaluate the breeding values of animals using DMU software (Madsen and Jensen, 2006). Both the heritable and non-heritable direct and social effects were included in this model. Non-genetic social permanent environmental effect was considered as random group effect. The estimated breeding value (EBV) was calculated using the following model:

$$y_{ijkm} = \mu + sex_i + l_j + g_k + a_{dm} + \sum_{n \neq m} a_{sn} + e_{ijkm},$$

where y_{ijkm} is the phenotypic observation; μ is the overall mean;

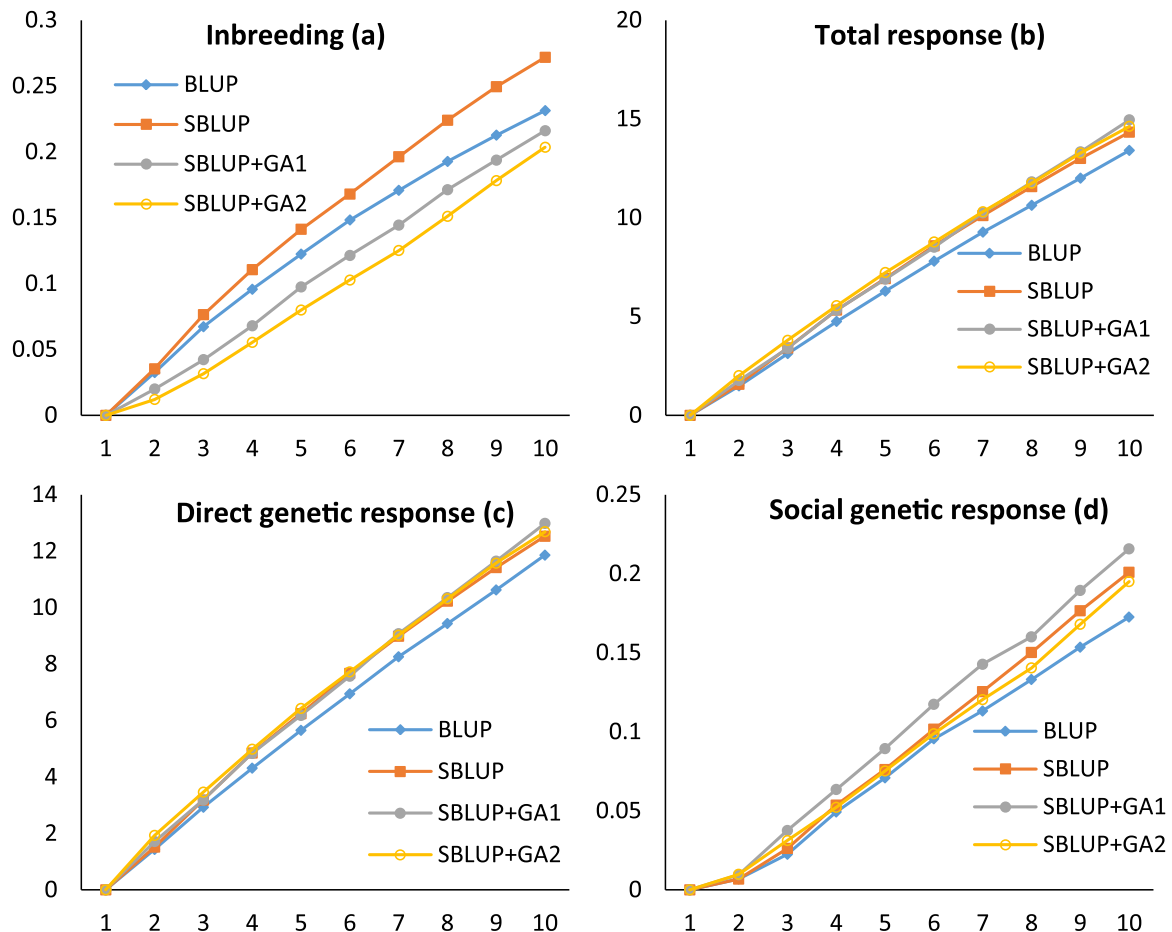


Fig. 1. Average inbreeding coefficients and selection responses under the social selection under the common BLUP selection, social effect selection based on BLUP (SBLUP), SBLUP plus genetic algorithm 1 (SBLUP+GA1), SBLUP plus genetic algorithm 2 (SBLUP+GA2).

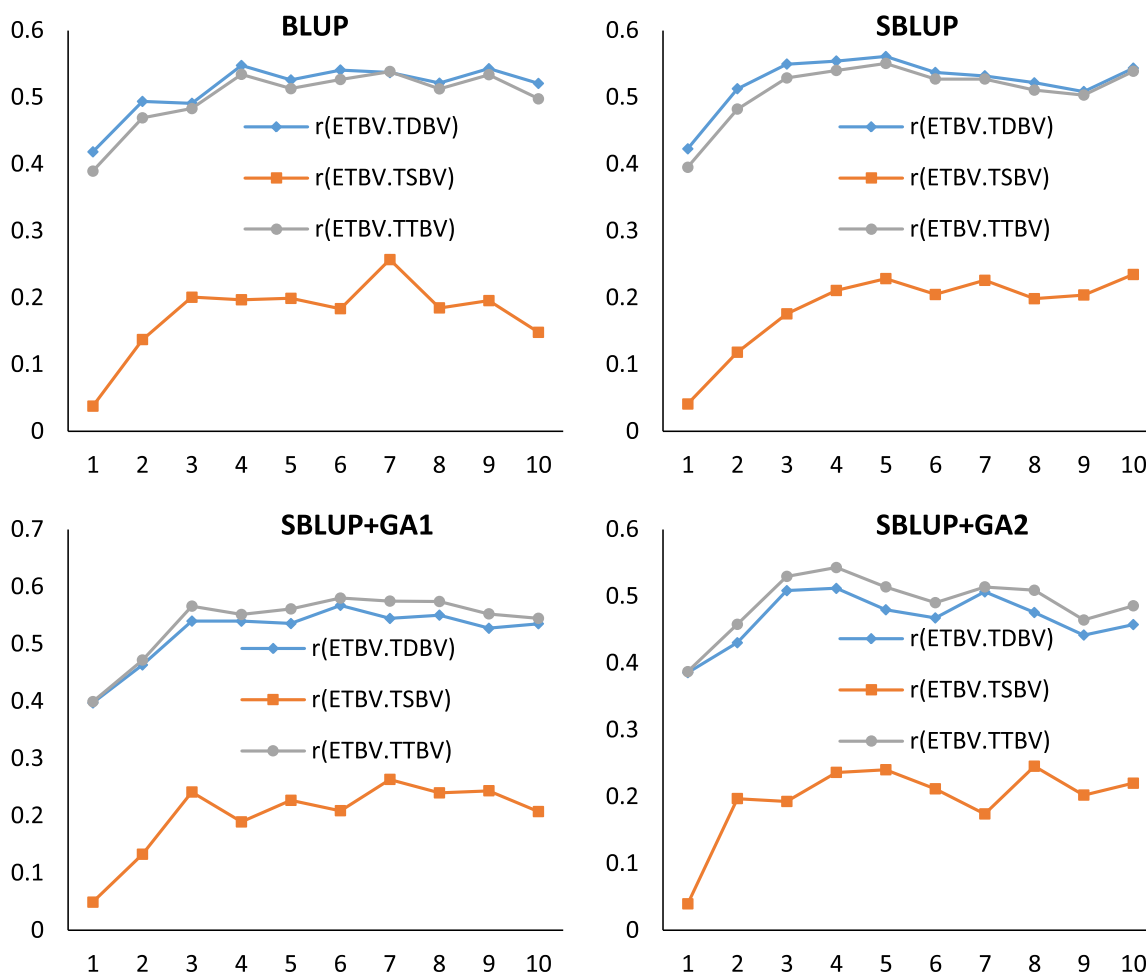


Fig. 2. The correlation between estimated total breeding value and true direct breeding value ($r_{ETBV, TSBV}$), correlation between estimated total breeding value and true social breeding value ($r_{ETBV, TTBV}$), correlation between estimated total breeding value and true total breeding value ($r_{ETBV, TTBV}$) under the common BLUP selection, social effect selection based on BLUP (SBLUP), SBLUP plus genetic algorithm 1 (SBLUP+GA1), SBLUP plus genetic algorithm 2 (SBLUP+GA2).

Table 2
The average inbreeding increment (ΔF), accuracy (r) and genetic gain (ΔG) of direct (A_d), social (A_s) and total effect (A_t) under SBLUP+GA1 and SBLUP+GA2 based on a specified weight ratio between genetic value and relationship.

Method	Ratio (w_1/w_2) ^a	ΔF	$r_{ETBV, TDBV}$ ^b	$r_{ETBV, TSBV}$	$r_{ETBV, TTBV}$	$O_{4,i} = w_i f_i = w_i (p_i x + q_i y + r_i)$ for $i = 1, 2$	ΔG_{A_s}	ΔG_{A_t}
SBLUP+GA1	1/1	0.026	0.490	0.195	0.508	1.223	0.020	1.406
	1/10	0.022	0.520	0.200	0.538	1.298	0.022	1.496
	1/100	0.020	0.526	0.190	0.539	1.305	0.018	1.471
SBLUP+GA2	1/10	0.025	0.473	0.192	0.492	1.263	0.021	1.455
	1/100	0.020	0.466	0.196	0.489	1.269	0.022	1.463
	1/200	0.020	0.467	0.193	0.491	1.259	0.020	1.438

^a w_1 is the weight assigned to average genetic value; w_2 the weight to average relationship.

^b $r_{ETBV, TDBV}$ is the correlation between estimated total breeding value and true direct breeding value; $r_{ETBV, TSBV}$, correlation between estimated total breeding value and true social breeding value; $r_{ETBV, TTBV}$, correlation between estimated total breeding value and true total breeding value.

sex_i is the fixed sex effect; l_j is the litter effect (random); g_k is the random group effect; a_{dm} is the direct additive genetic effect (random) for individual m ; a_{sn} is the social effect for individual n to m ; and e_{ijkm} is the random residual. Because each animal interacts with $n-1$ others in a pen group, the total heritable effect of an animal to the mean trait value of the population is the sum of the animal's direct breeding value and $n-1$ times its social breeding value (Bijma et al., 2007), where n is group size. Thus, the total EBV of an animal was defined as follow,

$$\hat{TBV} = \hat{A}_d + (n-1)\hat{A}_s,$$

where \hat{A}_d and \hat{A}_s are the direct and social EBV of an animal,

respectively.

2.3. Selection accuracy and response

In this study, three accuracies were defined. The correlation of total estimated breeding value (TEBV) and true direct breeding value (TDBV), which judges the selection efficiency of direct additive genetic effect in breeding program using TEBV. The correlation between TEBV and true social breeding value (TSBV), it evaluates the selection efficiency of social genetic effects of individuals. The correlation between TEBV and true total breeding value (TTBV), evaluates the selection accuracy of total genetic

Table 3

The average inbreeding increment (ΔF), accuracy (r) and genetic gain (ΔG) of direct (A_d), social (A_s) and total effect (A_t) under SBLUP, SBLUP+GA1 and SBLUP+GA2 based on a specific ratio of social phenotypic variance (V_s) and direct phenotypic variance (V_d).

V_s/V_d (%)	Method	ΔF	$r_{ETBV.TDBV}$	$r_{ETBV.TSBV}$	$r_{ETBV.TTBV}$	ΔG_{A_d}	ΔG_{A_s}	ΔG_{A_t}
0.3%	SBLUP	0.027	0.524	0.184	0.511	1.253	0.020	1.434
	SBLUP+GA1	0.022(81.48) ^a	0.520	0.200	0.538	1.298(103.59)	0.022(110.00)	1.496(104.32)
	SBLUP+GA2	0.020(74.07)	0.466	0.196	0.489	1.269(101.28)	0.022(110.00)	1.463(102.02)
1%	SBLUP	0.025	0.502	0.206	0.477	1.199	0.038	1.543
	SBLUP+GA1	0.021(84.00)	0.519	0.238	0.555	1.306(108.92)	0.043(113.16)	1.696(109.92)
	SBLUP+GA2	0.017(68.00)	0.456	0.238	0.510	1.225(102.17)	0.041(107.89)	1.594(103.31)
10%	SBLUP	0.026	0.455	0.272	0.405	1.113	0.157	2.523
	SBLUP+GA1	0.020(76.92)	0.466	0.263	0.546	1.179(105.93)	0.145(92.36)	2.481(98.34)
	SBLUP+GA2	0.019(73.08)	0.407	0.296	0.560	1.155(103.77)	0.155(98.73)	2.548(100.99)

^a The values in parentheses denotes the percentages of this value in this row relative to the value under SBLUP.

Table 4

The average inbreeding increment (ΔF), accuracy (r) and genetic gain (ΔG) of direct (A_d), social (A_s) and total effect (A_t) under SBLUP+GA1 and SBLUP+GA2 based on a specified group size (n).

Group size	Method	ΔF	$r_{ETBV.TDBV}$	$r_{ETBV.TSBV}$	$r_{ETBV.TTBV}$	ΔG_{A_d}	ΔG_{A_s}	ΔG_{A_t}
5	SBLUP	0.025	0.569	0.175	0.567	1.330	0.018	1.404
	SBLUP+GA1	0.024(96.00)	0.561	0.204	0.574	1.353(101.73)	0.021(116.67)	1.438(102.42)
	SBLUP+GA2	0.020(80.00)	0.566	0.191	0.579	1.446(108.72)	0.021(116.67)	1.531(109.05)
10	SBLUP	0.027	0.524	0.184	0.511	1.253	0.020	1.434
	SBLUP+GA1	0.022(81.48)	0.520	0.200	0.538	1.298(103.59)	0.022(110.00)	1.496(104.32)
	SBLUP+GA2	0.020(74.07)	0.466	0.196	0.489	1.269(101.28)	0.022(110.00)	1.463(102.02)
15	SBLUP	0.025	0.485	0.175	0.455	1.184	0.018	1.443
	SBLUP+GA1	0.022(88.00)	0.462	0.200	0.496	1.171(98.90)	0.021(116.67)	1.470(101.87)
	SBLUP+GA2	0.018(72.00)	0.424	0.200	0.467	1.200(101.35)	0.021(116.67)	1.490(103.26)

effect. At subsequent each generation, the mean values of direct, social and total true breeding value for all individuals minus the mean values of direct, social and total true breeding value at base generation, and the differences between them were taken as cumulative selection response of direct, social and total genetic effect at current generation, respectively.

2.4. The control of inbreeding rate

Because the selection of social genetic effect will lead to rapid increase of inbreeding, so, the inbreeding level of a population has to be restricted. In this study, the inbreeding was controlled by optimizing the genetic contribution of all selected animals, which was implemented based on a genetic algorithm using an R function *rbga* (R/genalg, 2015 version 0.2.0).

2.4.1. Strategy 1 (GA1)

In this strategy, only the contributions of sires were optimized using genetic algorithm and the contributions of all dams were fixed as $0.5/n_d$, where n_d is the number of dam. A fitness function was modeled as:

$$F = w_1 \mathbf{c}'_s \mathbf{TBV}_s - w_2 (\mathbf{c}'_s \mathbf{A}_{ss} \mathbf{c}_s + 2 \mathbf{c}'_s \mathbf{A}_{sd} \mathbf{c}_d),$$

where \mathbf{c}_s is the vector of genetic contributions of sires; \mathbf{TBV}_s is the vector of estimated total breeding values of sires; \mathbf{A}_{ss} , \mathbf{A}_{sd} are the additive genetic correlation matrixes between sires, sires and dams, respectively; \mathbf{c}_d is the vector of dams' fixed genetic contributions; w_1 , w_2 are the weight assigned to corresponding term. The objective of optimization was to maximize the F value, i.e. to maximize $w_1 \mathbf{c}'_s \mathbf{TBV}_s$ (selection response) and minimize $w_2 (\mathbf{c}'_s \mathbf{A}_{ss} \mathbf{c}_s + 2 \mathbf{c}'_s \mathbf{A}_{sd} \mathbf{c}_d)$ (inbreeding increment). To restrict the sum of sires' contributions equals to 0.5 (sires have half contribution to next generation), a penalty factor was applied to fitness function:

$$F = F + w_1 \left(\left| \sum \mathbf{c}_s - 0.5 \right| \right),$$

where w is the penalty weight.

2.4.2. Strategy 2 (GA2)

In this strategy, the contributions of sires and dams were optimized together. An evaluation function was constructed as follows.

$$F = w_1 \mathbf{c}'_t \mathbf{TBV}_t - w_2 \mathbf{c}'_t \mathbf{A}_t \mathbf{c}_t,$$

where \mathbf{c}_t is the vector of genetic contribution of seedstocks to next generation; \mathbf{TBV}_t is the vector of estimated total breeding value of seedstocks; \mathbf{A}_t is the matrix of additive genetic correlation for all seedstocks; w_1 , w_2 are the weights assigned to corresponding term. As strategy 1, a penalty factor was applied to the fitness function:

$$F = F + w_1 \left(\left| \sum \mathbf{c}_s - 0.5 \right| \right) + w_2 \left(\left| \sum \mathbf{c}_d - 0.5 \right| \right),$$

where w_1 , w_2 are the penalty weight assigned to sires and dams, respectively; \mathbf{c}_s , \mathbf{c}_d are genetic contributions of sires and dams, respectively.

2.5. The comparison of selection scheme

Four types of selection scheme were simulated and compared, and they are described below.

2.5.1. BLUP

In this scheme, the total estimated breeding value (including direct and social genetic effect) of an animal was obtained based on the classical BLUP method with only additive genetic effect. A truncation selection i.e., a fixed number of animals (N_s sire and N_d dams) with the highest total estimated breeding values was selected to be parents of next cycle. Each sire mated randomly to N_d/N_s dams.

2.5.2. SBLUP

In SBLUP, a full model with direct and social genetic effect was constructed and solved using BLUP method. Similar to BLUP, a

fixed number of individuals (N_s sire and N_d dams) with the highest total estimated breeding values were selected as the seedstocks of next generation. Sires mated dams randomly.

2.5.3. SBLUP+GA1

In this scheme, the estimation of EBV and selection of sires and dams were similar to SBLUP. However, the optimal genetic contributions of sires were obtained using genetic algorithm based on **strategy 1** (Section 2.4.1).

2.5.4. SBLUP+GA2

This scheme was similar to SBLUP+GA1. However, the genetic contributions of sires and dams were optimized together using genetic algorithm based on **strategy 2** (Section 2.4.2).

3. Results and discussion

3.1. The comparison of inbreeding level and selection response for different schemes

The inbreeding levels and selection responses for four schemes under base parameters (Table 1) are showed in Fig. 1. As expected, SBLUP+GA1 and SBLUP+GA2 resulted in lower inbreeding coefficient than SBLUP in all generations using genetic algorithm; moreover, these inbreeding levels even were smaller than common BLUP scheme. The SBLUP resulted in the highest average inbreeding coefficient (0.272) in terminal generation, followed by BLUP (0.231), SBLUP+GA1 (0.216) and SBLUP+GA2 (0.204). SBLUP+GA2 resulted in lower inbreeding rate than SBLUP+GA1 in all generations. This was because the contributions of sires and dams in SBLUP+GA2 were optimized simultaneously. Therefore, SBLUP+GA2 had a larger search space of contribution than SBLUP+GA1 due to the dams' contribution, which led to SBLUP+GA2 resulted in lower inbreeding rate than SBLUP+GA1 (Fig. 1). However, the selection response of SBLUP+GA2 was similar to the SBLUP+GA1 in most of cases, which implied the optimization of dams' contribution, had little effect to the total selection response.

Comparing the accuracies in four selection schemes under the base parameters (Fig. 2), the accuracies of total genetic effect in BLUP and SBLUP were smaller than the accuracies of direct genetic effect, contrarily, the accuracies of total genetic effect in SBLUP+GA1 and SBLUP+GA2 were larger than direct genetic effect. This implied that two optimization methods based on genetic algorithm increased indirectly the correlation between estimated total breeding value and true total breeding value by optimizing the genetic contributions of animals selected. Its mechanism needs to be studied further.

3.2. The influence of weight ratio between EBV and average relationship to optimization schemes

In this study, the fitness function of genetic algorithm was constructed by two weights (w_1 assigned to EBV and w_2 assigned to average relationship in Section 2.4). The changes of ratio should have a direct influence on optimization schemes. Table 2 listed the average inbreeding, accuracy and selection response of direct, social and total effect component for SBLUP+GA1 and SBLUP+GA2 under different weight ratios between EBV and relationship. Comparing the results, not only SBLUP+GA1, but also SBLUP+GA2, the average inbreeding rate decreased with the increase of weight assigned to average relationship. However, the inbreeding rate changed little when the weight on mean relationship exceeded a threshold value (a specific value). In addition, both in SBLUP+GA1 and SBLUP+GA2, the genetic gain of

total genetic effect component increased firstly and then decreased. These phenomena demonstrated there is an optimal weight ratio both in SBLUP+GA1 and SBLUP+GA2, which can decrease effectively inbreeding rate and maximize the genetic gain of total genetic effect.

3.3. The influence of social genetic effect size to optimization schemes

The effects of social genetic effect size to three optimization schemes are listed in Table 3. SBLUP+GA1 and SBLUP+GA2 reduced effectively the inbreeding rate in all cases. The percentages of inbreeding rate for SBLUP+GA1 relative to SBLUP at the social genetic size of 0.3%, 1% and 10% were 81.48%, 84.00% and 76.92%, respectively. In SBLUP+GA2, they were 74.07%, 68.00% and 73.08%, respectively. SBLUP+GA2 reduced obviously more inbreeding rate than SBLUP+GA1 due to the optimization of dam's contribution. Comparing the selection responses, the response of direct genetic effects for all selection schemes decreased with the increase of social genetic effect, contrarily, the response of social genetic effect increased with its increase in SBLUP scheme. However, in SBLUP+GA1 and SBLUP+GA2, only the social effect component increased with the increase of social effect. The percentage of total genetic gain in SBLUP+GA1 relative to SBLUP at the social genetic size of 0.3%, 1% and 10% were 104.32%, 109.92% and 98.34%, respectively. In SBLUP+GA2, they were 102.02%, 103.31% and 100.99%, respectively.

3.4. The influence of group size to optimization schemes

Table 4 listed the average inbreeding rate, accuracy and selection response of direct, social and total effect component for SBLUP+GA1, SBLUP+GA2 and SBLUP under different group size. Comparing the inbreeding level, as expected, SBLUP+GA1 and SBLUP+GA2 reduced effectively inbreeding rate relative to SBLUP in three cases. The percentages of inbreeding rate for SBLUP+GA1 relative to SBLUP at the group size of 5, 10 and 15 were 96.00%, 81.48% and 88.00%, respectively. SBLUP+GA2 resulted in lower inbreeding rate than SBLUP+GA1 in all cases. Comparing the selection response, the gain of direct effect component decreased obviously with the increase of group size in three schemes. Two optimization schemes both resulted in more total selection response than SBLUP in all cases. The percentage of total genetic gain in SBLUP+GA1 relative to SBLUP at the group size of 5, 10 and 15 were 102.42%, 104.32% and 101.87%, respectively. In SBLUP+GA2, they were 109.05%, 102.02% and 103.26%, respectively.

4. Conclusions

It was concluded that two optimization methods based on genetic algorithm resulted in substantial more selection response than common social genetic effect selection based on BLUP method in most of cases, furthermore, the average inbreeding of population was also reduced to lower level than the latter.

Conflict of interest

There is no conflict of interest.

Acknowledgments

The financial supports from National Natural Science Foundation of China #C170102, Program for Changjiang Scholars and

Innovative Research Team in University #IRT13083, and Earmarked Fund for China Agriculture Research System #CARS-36-03A are greatly appreciated.

References

- Arango, J., Misztal, I., Tsuruta, S., Culbertson, M., Herring, W., 2005. Estimation of variance components including competitive effects of Large White growing gilts. *J. Anim. Sci.* 83, 1241–1246.
- Bergsma, R., Kanis, E., Knol, E.F., Bijma, P., 2008. The contribution of social effects to heritable variation in finishing traits of domestic pigs (*Sus scrofa*). *Genetics* 178, 1559–1570.
- Bijma, P., Muir, W.M., van Arendonk, J.A.M., 2007. Multilevel selection 1: quantitative genetics of inheritance and response to selection. *Genetics* 175, 277–288.
- Cassady, J.P., Van Vleck, L.D., 2004. Estimation of (co) variance components due to genetic competition effects in pigs. *J. Anim. Sci.* 82 (Suppl. 2), S38.
- Chen, C.Y., Johnson, R.K., Newman, S., Kachman, S.D., Van Vleck, L.D., 2009. Effects of social interactions on empirical responses to selection for average daily gain of boars. *J. Anim. Sci.* 87, 844–849.
- Ellen, E.D., Muir, W.M., Teuscher, F., Bijma, P., 2007. Genetic improvement of traits affected by interactions among individuals: sib selection schemes. *Genetics* 176, 489–499.
- Falconer, D.S., Mackay, T.F.C., 1996. *Introduction to Quantitative Genetics*. Longman, Harlow.
- Gómez, M.D., Varona, L., Molina, A., Valera, M., 2011. Genetic evaluation of racing performance in trotter horses by competitive models. *Livest. Sci.* 140, 155–160.
- Khaw, H.L., Ponzoni, R.W., Bijma, P., 2014. Indirect genetic effects and inbreeding: consequences of BLUP selection for socially affected traits on rate of inbreeding. *Genet. Sel. Evol.* 46, 39.
- Madsen, P., Jensen, J., 2006. *A User's Guide to DMU A Package for Analyzing Multivariate Mixed Models*. Version 6, release 4.6. Danish Institute of Agricultural Sciences, p. 27.
- Muir, W.M., 1996. Group selection for adaptation to multiple-hen cages: selection program and direct responses. *Poult. Sci.* 75, 447–458.
- Muir, W.M., 2005. Incorporation of competitive effects in forest tree or animal breeding program. *Genetics* 170, 1247–1259.
- R/genalg, 2015. Version: 0.2.0.