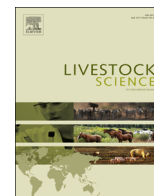




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Short communication

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



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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.

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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.

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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;

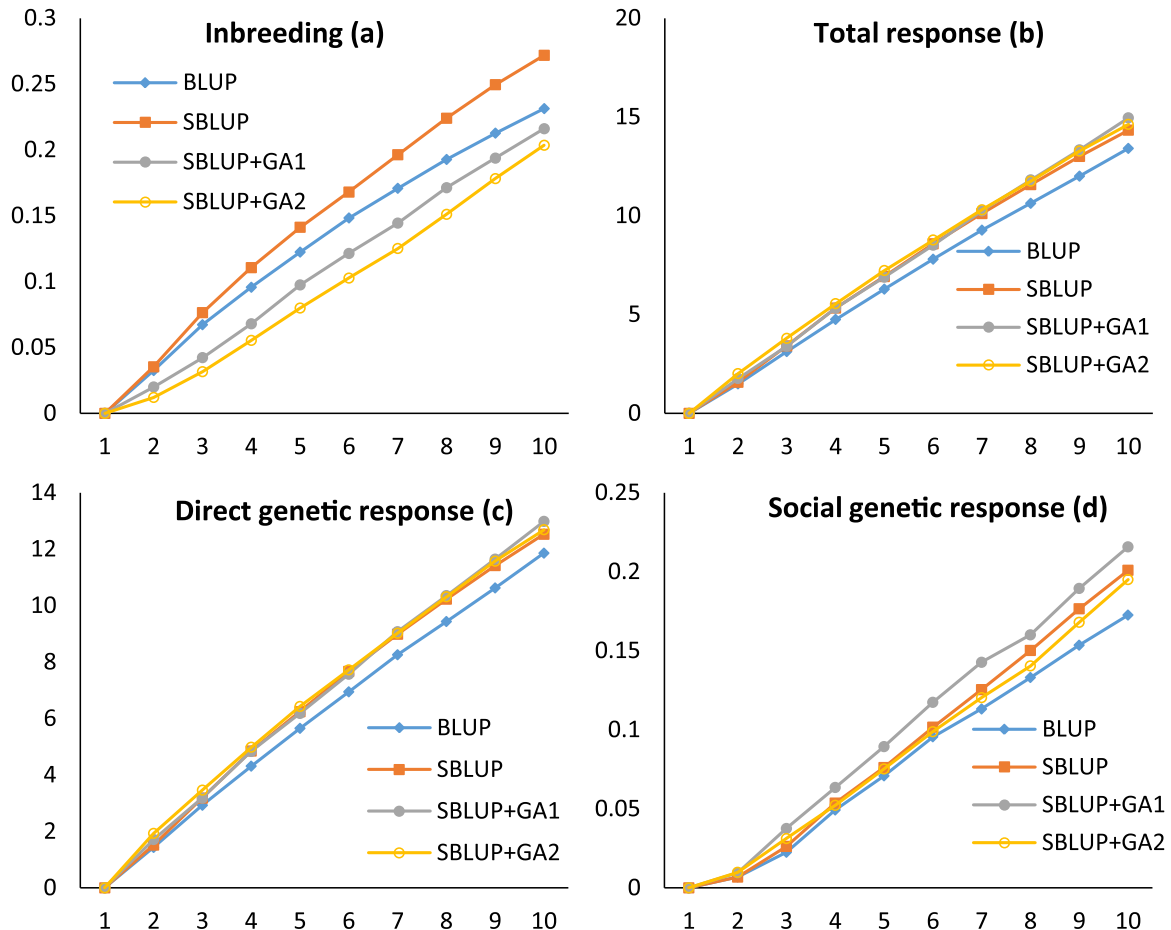


Fig. 1. Average inbreeding coefficients and selection responses under the social selection under the common BLUP selection, social effect selection based on BLUP (SBLUP), SBLUP plus genetic algorithm 1 (SBLUP+GA1), SBLUP plus genetic algorithm 2 (SBLUP+GA2).

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