



Maximizing the Selection Response by Optimal Quantitative Trait Loci Selection and Control of Inbreeding in a Population with Different Lifetimes between Sires and Dams*

G. Q. Tang, X. W. Li**, L. Zhu, S. R. Shuai and L. Bai

College of Animal Science and Technology, Sichuan Agricultural University, Ya'an, 625014, China

ABSTRACT : A rule was developed to constrain the annual rate of inbreeding to a predefined value in a population with different lifetimes between sires and dams, and to maximize the selection response over generations. This rule considers that the animals in a population should be divided into sex-age classes based on the theory of gene flow, and restricts the increase of average inbreeding coefficient for new offspring by limiting the increase of the mean additive genetic relationship for parents selected. The optimization problem of this rule was formulated as a quadratic programming problem. Inputs for the rule were the BLUP estimated breeding values, the additive genetic relationship matrix of all animals, and the long-term contributions of sex-age classes. Outputs were optimal number and contributions of selected animals. In addition, this rule was combined with the optimization of emphasis given to QTL, and further increased the genetic gain over the planning horizon. Stochastic simulations of closed nucleus schemes for pigs were used to investigate the potential advantages obtained from this rule by combining the standard QTL selection, optimal QTL selection and conventional BLUP selection. Results showed that the predefined rates of inbreeding were actually achieved by this rule in three selection strategies. The rule obtained up to 9.23% extra genetic gain over truncation selection at the same rates of inbreeding. The combination of the extended rule and the optimization of emphasis given to QTL allowed substantial increases in selection response at a fixed annual rate of inbreeding, and solved substantially the conflict between short-term and long-term selection response in QTL-assisted selection schemes. (**Key Words :** Selection, Optimization, Quantitative Trait Loci, Inbreeding Restriction)

INTRODUCTION

Following the rapid development of molecular genetics, many studies on the value of gene- and marker-assisted selection (GAS and MAS) in practical breeding programs have been published in recent years. The standard approach for using QTL information in selection schemes is based on a simple index: $I = \alpha + EBV$ (Falconer and Mackay, 1996; Soller, 1978), where α is an estimate of the breeding value for the identified or marked QTL of the individual and EBV is an estimated breeding value of the polygenic effects of the individual. When α and EBV are estimated based on

best linear unbiased prediction (BLUP), α may be as a fixed or random effect. Most studies evaluating GAS have assumed standard truncation (where all selected parents contribute equally to the next generation) and equal emphasis on α and EBV (e.g. Gibson, 1994; Ruane and Colleau, 1995; Larzul et al., 1997; Pong-Wong and Woolliams, 1998; Abdel-Azim and Freeman, 2002; Kim and Farnir, 2006). The general finding has been that extra gains are expected from GAS in the early generations of selection, as described by Gibson (1994), however, these extra gains are not maintained in the long term. This paradox has become known as the Gibson effect.

Dekkers and van Arendonk (1998) developed a model to optimize selection on an identified QTL over a planning horizon of multiple generations, and solved the problem of loss of longer term response. Chakraborty et al. (2002) extended the method of Dekkers and van Arendonk (1998) to selection programs with different selection strategies for males and females, maximizing a weighted combination of short and longer term responses, and to multiple identified

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** Corresponding Author: X. W. Li. Tel: +86-0835-2886000, Fax: +86-0835-2886080, E-mail: lixuewei9125@126.com

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QTL, allowing for non-additive effects at the QTL, including dominance, epistasis and gametic imprinting. However, the model of Chakraborty et al. (2002) was restricted to one quantitative trait with multiple identified QTL, and in a population with discrete generations. These assumptions are too restrictive for application to practical breeding programs. Thus, Tang and Li (2006) extend the method of Chakraborty et al. (2002) to allow optimization of selection on multiple traits with multiple QTL in a population with overlapping generations. All these methods optimized relative weight on the QTL to maximize response of selection over multiple generations, but assumed equal contributions of selected candidates and infinite population sizes without accumulation of inbreeding.

Optimum contribution (OC) selection algorithms for simultaneously maximizing genetic gain and constraining the rate of inbreeding have been developed during the past decade (Eisen, 2007). Meuwissen (1997) and Grundy et al. (1998) suggested a method to maximize genetic response while restricting the rate of inbreeding per generation to a predefined value in a population with discrete generations. The methods of Meuwissen (1997) and Grundy et al. (1998) were extended to populations with overlapping generations by Meuwissen and Sonesson (1998) and Grundy et al. (2000), respectively. They optimized genetic contributions of individuals over age classes. In general, the lifetimes of sires and dams are, however, different in practical breeding schemes, but these two methods are based on the same lifetime for sires and dams. Thus, they are too restrictive for application to practical breeding schemes. Villanueva et al (1999) used BLUP evaluation and OC selection algorithms in GAS schemes. The emphasis given to the QTL EBV relative to the polygenic EBV was, however, equal. It yielded more genetic gain than truncation selection schemes that account for the QTL in the short and the long term, but these authors also showed that the Gibson effect occurred for OC selection when used as a one-generation scheme (i.e. estimates of polygenic and QTL effect have equal weights) (Villanueva et al., 1999, 2002). Therefore, Villanueva et al. (2004) tried to combine the method of Dekkers and van Arendonk (1998) with OC selection, and to further increase the benefits from GAS in finite population sizes.

The objective of this paper is to extend the rule of optimal contribution proposed by Meuwissen and Sonesson (1998) to populations with overlapping generations and different lifetimes between sires and dams. Moreover, this extended OC selection rule is combined with the methods of Tang and Li (2006) that optimizes the relative emphasis given to multiple QTL for multiple traits in a population with overlapping generations, and further increases the selection response.

METHODS

The constraint on $r' \overline{A}_{t+1} r$

At any time, there are animals of different sex and ages in a population with different lifetimes for sire and dam. The animals will be divided into sex-age classes. Here, the interval of age is different from the common year, and an age class is defined as the time period between two consecutive rounds of selection. For convenience, this time period will be assumed to equal one year. Following the theory of Meuwissen and Sonesson (1998), when selecting parents in year t, we want to limit the increase of average inbreeding coefficient of future individuals, which is limited by constraining the $r' \overline{A}_{t+1} r$ term in year t+1; where r is a weight vector of age classes; r_i denotes the long-term contribution of age class i (until lifetime is reached); \overline{A}_{t+1} is a matrix with the average additive genetic relationships within age classes on the diagonals and between age classes on the off-diagonals. For optimizing the contribution of selected parents in a population with different lifetimes between sires and dams, these animals have to be divided into sex-age classes according to the method of Hill (1974). Now, \overline{A}_{t+1} is arranged according to the order of transmission matrix P:

$$\overline{A}_{t+1} = \begin{pmatrix} \overline{A}_{1,1} & \overline{A}_{1,2} & \overline{A}_{1,3} & \overline{A}_{1,4} \\ \overline{A}_{2,1} & \overline{A}_{2,2} & \overline{A}_{2,3} & \overline{A}_{2,4} \\ \overline{A}_{3,1} & \overline{A}_{3,2} & \overline{A}_{3,3} & \overline{A}_{3,4} \\ \overline{A}_{4,1} & \overline{A}_{4,2} & \overline{A}_{4,3} & \overline{A}_{4,4} \end{pmatrix}, \quad r = \begin{pmatrix} r_1 \\ r_2 \\ r_3 \\ r_4 \end{pmatrix} \quad (1)$$

where, subscript 1 and 2 denote age 1 and other ages (except for age 1) of sire, respectively; subscript 3 and 4 is age 1 and other ages of dam, respectively. The population of year t+1 is formed from that in year t. Namely, age class 2, 3, ..., q are formed by aging from the age class 1, 2, ..., q-1 in year t, respectively, because the age of animal increases one from year t to t+1, but the age class has no change. Age class 1 is newly formed in year t+1. It is formed by mating within the selected parent's population in year t. Thus, $r' \overline{A}_{t+1} r$ of all age classes can be split into different terms:

$$\begin{aligned} r' \overline{A}_{t+1} r = & r'_1 \overline{A}_{11} r_1 + r'_2 \overline{A}_{21} r_1 + r'_3 \overline{A}_{31} r_1 + r'_4 \overline{A}_{41} r_1 + r'_1 \overline{A}_{12} r_2 + r'_2 \overline{A}_{22} r_2 + r'_3 \overline{A}_{32} r_2 \\ & + r'_4 \overline{A}_{42} r_2 + r'_1 \overline{A}_{13} r_3 + r'_2 \overline{A}_{23} r_3 + r'_3 \overline{A}_{33} r_3 + r'_4 \overline{A}_{43} r_3 + r'_1 \overline{A}_{14} r_4 \\ & + r'_2 \overline{A}_{24} r_4 + r'_3 \overline{A}_{34} r_4 + r'_4 \overline{A}_{44} r_4 \end{aligned} \quad (2)$$

Then, combining these terms of formula [2] according to age class 1 (subscript a) and other age classes (subscript b), and to form a new matrix formula:

$$r' \overline{A}_{t+1} r = r'_a \overline{A}_{t+1(a,a)} r_a + 2r'_a \overline{A}_{t+1(a,b)} r_b + r'_b \overline{A}_{t+1(b,b)} r_b \quad (3)$$

where:

$$r_a = \begin{pmatrix} r_1 \\ r_3 \end{pmatrix}, \quad \overline{A_{t+1(a,a)}} = \begin{pmatrix} \overline{A_{11}} & \overline{A_{31}} \\ \overline{A_{13}} & \overline{A_{33}} \end{pmatrix}, \quad r_b = \begin{pmatrix} r_2 \\ r_4 \end{pmatrix}$$

$$\overline{A_{t+1(a,b)}} = \begin{pmatrix} \overline{A_{12}} & \overline{A_{14}} \\ \overline{A_{32}} & \overline{A_{34}} \end{pmatrix}, \quad \overline{A_{t+1(b,b)}} = \begin{pmatrix} \overline{A_{22}} & \overline{A_{24}} \\ \overline{A_{42}} & \overline{A_{44}} \end{pmatrix}$$

The formula (3) is similar to the formula (4) of Meuwissen and Sonesson (1998). The latter is more general, the former is a special case for application in this paper. The $r_b' \overline{A_{t+1(b,b)}} r_b$ term in equation (3) does not depend on the selected parents, because animals in age classes 2 to q in year t+1 are identical to those in age class 1, to q-1 in year t (all individuals of age class i transfer to age class i+1 from year t to t+1). It is calculated from $\overline{A_t}$ and r_b . The terms $r_a' \overline{A_{t+1(a,a)}} r_a$ and $r_a' \overline{A_{t+1(a,b)}} r_b$ are influenced by selection in year t, where the former represents the average additive genetic relationship among new progenies, and the second term represents the average additive genetic relationship between new progenies and other older animals (age class 2 to q). Following the description of Meuwissen and Sonesson (12):

$$\overline{A_{t+1(a,a)}} = c_t' A_t c_t \tag{4}$$

$$\overline{A_{t+1(a,b)}} = c_t' A_t J \tag{5}$$

where, A_t denotes the matrix of additive genetic relationship among animals in year t; c_t denotes the vector of genetic contribution of individuals in year t to age class 1 in year t+1 (contributions of animals not selected are 0; male or female contributions sum to 0.5); $\overline{A_{t+1(a,a)}}$ denotes the average additive genetic relationship of individuals within age class 1 in year t+1 (i.e. the mean value of all elements of $\overline{A_{t+1(a,a)}}$); $\overline{A_{t+1(a,b)}}$ is the vector of average additive genetic relationship of individuals between age class 1 and other age classes in year t+1 (the vector of mean value of each column of $\overline{A_{t+1(a,a)}}$); J is the matrix that averages these additive genetic relationships of individuals within every age class (i.e., the j^{th} column of J has the n elements that correspond to animals in age class j equal to $1/n$ and all other elements equal to 0, where n is equal to the number of animals per sex-age class. The columns of J include all other age class except for the age class 1 of sire and dam). For details, see Meuwissen (1998).

Inbreeding increases on average within new progenies

equal half the increase of the average additive genetic relationship among selected parents (Falconer and Mackay, 1996). Hence, these selected animals in year t such that the average relationship of population in year t+1 does not exceed the constraint (1998):

$$C_{t+1} = C_t + 2\Delta F(1 - 1/2C_t) \tag{6}$$

Combining equation (3), (4), (5) and (6) yields a restriction on the average additive genetic relationship in a population with different lifetimes between sire and dam:

$$C_{t+1} \leq (r_1 + r_3)^2 c_t' A_t c_t + 2(r_1 c_t' A_t J r_b + r_3 c_t' A_t J r_b) + r_b' \overline{A_{t+1(b,b)}} r_b \tag{7}$$

The optimization problem

In the round of selection, we want to maximize genetic value of new animals in the next selection cycle. In other words, we want to choose c_t so that the expected genetic merit of offspring is as high as possible. The general optimization problem:

$$\text{Max: } c_t' EBV_t \tag{8}$$

Subject to:

$$C_{t+1} \leq (r_1 + r_3)^2 c_t' A_t c_t + 2(r_1 c_t' A_t J r_b + r_3 c_t' A_t J r_b) + r_b' \overline{A_{t+1(b,b)}} r_b \tag{8a}$$

$$Q' c_t = s \tag{8b}$$

Where, Q' is the incidence matrix relating the animal to sex, and its column is sex-age classes arranged according to the order of $\overline{A_{t+1}}$; s is contribution vector of every sex-age class. The above optimization problem can be solved using the Lagrange multiplier method to transform the extremum problem with condition constraints into no restriction extremum problem. The Lagrange objective function is:

$$H(c) = c_t' EBV_t - \lambda_0 [(r_1 + r_3)^2 c_t' A_t c_t + 2(r_1 + r_3) c_t' A_t J r_b - K] - (c_t' Q - s)' \lambda \tag{9}$$

where, λ_0 and λ are the Lagrange multipliers for the constraints (8a) and (8b); $K = C_{t+1} - r_b' \overline{A_{t+1(b,b)}} r_b$.

Equating the first derivative of $H(c)$ with respect to the contribution vector c_t to zero yields

$$c_t = A_t^{-1} [EBV_t - 2\lambda_0 (r_1 + r_3) A_t J r_b - Q\lambda] / 2\lambda_0 (r_1 + r_3)^2 \tag{10}$$

From the constraint (8a) to get λ :

$$\lambda = (Q' A_t^{-1} Q)^{-1} \{Q' A_t^{-1} [EBV_t - 2\lambda_0 (r_1 + r_3) A_t J r_b] - 2\lambda_0 (r_1 + r_3)^2 s\} \tag{11}$$

From the constraint (8b) to get λ_0 :

$$\lambda_0^2 = 1/4(EBV_1'R(EBV_1) / [K + (r_1 + r_3)^2 r_b^2 J_1' R_1 J_1 r_b - (r_1 + r_3)^2 s' (Q_1' A_1^{-1} Q_1)^{-1} Q_1' A_1^{-1} Q_1 (Q_1' A_1^{-1} Q_1)^{-1} s - 2(r_1 + r_3) s' (Q_1' A_1^{-1} Q_1)^{-1} Q_1' J_1 r_b]) \quad (12)$$

where, $R = (A_1^{-1} - A_1^{-1} Q_1 (Q_1' A_1^{-1} Q_1)^{-1} Q_1' A_1^{-1}) / (r_1 + r_3)^2$. The value for λ_0 from equation (12) is used in equation (11) to obtain λ . Now, λ_0 and λ are used in equation (10) to obtain optimal c_t . If genetic contributions of some individuals of c_t are fixed, the above formulas can be split according to the method described by Meuwissen (1997), and these corresponding formulas as following:

$$H(c) = c_1' EBV_1 - \lambda_0 \{ (r_1 + r_3)^2 c_1' A_1 c_1 + c_1' [2(r_1 + r_3)^2 A_2 c_2 + 2(r_1 + r_3) A_1 J_1 r_b + 2(r_1 + r_3) A_2 J_2 r_b] - K \} - (c_1' Q_1 - s') \lambda \quad (13)$$

$$K = C_{t+1} - (r_1 + r_3)^2 c_2' A_2 c_2 - 2(r_1 + r_3) c_2 A_2 J_1 r_b - 2(r_1 + r_3) c_2 A_2 J_2 r_b - r_b^2 A_{t+1(b,b)} r_b \quad (14)$$

$$c_1 = A_1^{-1} \{ EBV_1 - \lambda_0 [2(r_1 + r_3)^2 A_2 c_2 + 2(r_1 + r_3) A_1 J_1 r_b + 2(r_1 + r_3) A_2 J_2 r_b] - Q_1 \lambda \} / 2\lambda_0 (r_1 + r_3)^2 \quad (15)$$

$$\lambda = (Q_1' A_1^{-1} Q_1)^{-1} \{ Q_1' A_1^{-1} [EBV_1 - \lambda_0 (2(r_1 + r_3)^2 A_2 c_2 + 2(r_1 + r_3) A_1 J_1 r_b + 2(r_1 + r_3) A_2 J_2 r_b)] - 2\lambda_0 (r_1 + r_3)^2 s' \} \quad (16)$$

$$\lambda_0^2 = 1/4(EBV_1'R(EBV_1) / [K + P'RP - (r_1 + r_3)^2 s' (Q_1' A_1^{-1} Q_1)^{-1} Q_1' A_1^{-1} Q_1 (Q_1' A_1^{-1} Q_1)^{-1} s - 2s' (Q_1' A_1^{-1} Q_1)^{-1} Q_1' A_1^{-1} P]) \quad (17)$$

$$P = (r_1 + r_3)^2 A_2 c_2 + (r_1 + r_3) A_1 J_1 r_b + (r_1 + r_3) A_2 J_2 r_b$$

$$R = (A_1^{-1} - A_1^{-1} Q_1 (Q_1' A_1^{-1} Q_1)^{-1} Q_1' A_1^{-1}) / (r_1 + r_3)^2 \quad (18)$$

Where, subscript 1 denotes candidates which will be optimized; subscript 2 denotes candidates with fixed contribution.

Determining the contribution of the sex-age classes

In the previous selection, weight vector r was assumed known. This vector was calculated from the transmission matrix P, and depended on the contribution of each sex-age class to sex-age class 1. This contribution depends, however, on the selected animals (c_t). These are unknown when parents are selected in year t, but can be calculated from c_t while limiting inbreeding. The optimized c_t depends, however, on r (equation (10)), so, we need to find optimal c_t and r simultaneously. This may be solved by an iteration method or simulated annealing algorithm (Meuwissen and Sonesson, 1998; Grundy et al., 2000). In practical breeding schemes, breeders sometimes need to fix the proportion of genetic contribution of each sex-age class to new progenies in advance (i.e. the sum of genetic contributions of all

animals in each sex-age class is the same over years). The number of animals and the contribution of each animal may be variable within sex-age class, but its sum is fixed. In such a population, the first row (i.e. row for reproduction) of transmission matrix P is fixed, and r can be computed by the formula $r^{(i)} = (\sum_{j=1}^q P(i,j)) / \bar{L}$ (Meuwissen and Sonesson, 1998), where q is number of sex-age classes and \bar{L} is average generation interval of the sires and dams. Then, the objects of optimization are number of animals selected and genetic contribution of each animal in every sex-age class. Referring to the method of Grundy et al. (2000), contribution proportions of sex-age classes can be restricted by s (equation (8b)). For example, the structure of a population is defined as: 80% of the paternal contribution to next round of selection derives from the 2 year-old boar, 20% of the paternal contribution derives from 3 year-old boar, 60% maternal contribution to next round of selection derives from 2 year-old sow, 30% of the maternal contribution derives from 3 year-old sow, 10% of the maternal contribution derives from 4 year-old sow, then, $s = (0.4 \ 0.1 \ 0.3 \ 0.15 \ 0.05)'$, and the corresponding $r = (0.21 \ 0.04 \ 0.21 \ 0.09 \ 0.02)'$.

Genetic model and simulation procedure

The genetic gains obtained by optimizing both the emphasis given to the QTL in the selection criterion and the contributions of candidates over generations were modeled using stochastic computer simulations. Considering a breeding scheme of a nucleus population for pigs, days to 100 kg (D100) and backfat to 100 kg (BF) were improved in this scheme. These two traits under selection were genetically controlled by an infinite number of additive loci, each with infinitesimal effect (polygene effect), plus two identified biallelic QTL (A1, A2 and B1, B2). The A1 and B1 were favorable to D100 and BF. Parameters of this scheme are listed in Table 1.

The base population (t = 0) was composed of 10,000 unrelated individuals (5,000 males and 5,000 females), and was created by one generation of random selection. The initial frequencies of the favorable alleles (A1 and B1) were 0.15 for both QTL of D100 and BF. The QTL genotypes of individuals in the base population were determined using the random number generator of uniform distribution u(0,1) according to the initial frequency p of the favorable allele. In the base population, the polygene effect u_i for each individual was obtained randomly from a normal distribution $N(0, \sigma_u^2)$. The QTL and polygenes were in gametic phase equilibrium. For an additive model, the genotypic value v_i of QTL was $\sqrt{\sigma_q^2 / 2p(1-p)} \cdot -\sqrt{\sigma_q^2 / 2p(1-p)}$ and 0 for an individual with favorable, unfavorable and heterozygous genotype, respectively (Falconer and Mackay,

Table 1. Parameters of the nucleus breeding schemes for pigs

Size of base population	♂: 5,000, ♀: 5,000
Size of sow population	100
Size of boar population for truncation selection	20
Number of years evaluated	15
Genetic contribution proportion of boar-age class	0, 0.8 and 0.2
Genetic contribution proportion of sow-age class	0, 0.5, 0.3 and 0.2
Traits evaluated and SD (in parenthesis)	BF (2.5 mm) and D100 (16.7 d)
Economic weight of trait	BF: -1, D100: -0.7
Value of season effect (spring-summer and autumn - winter)	BF: -0.1 and 0.1 mm, D100: -5 and 5 d
Value of sex effect (male and female)	BF: -1 and 1 mm, D100: -7 and 7 d
Proportion of genetic, litter, year, and residual variance of BF relative to phenotypic variance	0.5, 0.1, 0.05 and 0.35
Proportion of genetic, litter, year, and residual variance of D100 relative to phenotypic variance	0.3, 0.26, 0.04 and 0.4
Number of QTL and QTL allele (in parenthesis)	BF: 2 (2), D100: 2 (2)
Initial QTL favorable allele frequency of BF and D100	0.15 (QTL1) and 0.15 (QTL2)
Proportion of QTL variance of BF and D100 relative to genetic variance	15% (QTL1) and 10% (QTL2)
Genetic distance between QTL1 and QTL2	6 cM

BF and D100 denote backfat to 100 kg and days to 100 kg, respectively.

1996), where σ_q^2 was the genetic variance of QTL. Thus, the genetic value for individual i was: $a_i = u_i + v_{i1} + v_{i2}$, where v_{i1} and v_{i2} denote the genotypic value of QTL1 and QTL2, respectively. The phenotypic values of BF and D100 for an individual were calculated based on the linear model:

$$y_{ikl} = \mu + h_i + l_k + a_{ikl} + e_{ikl} \quad (19)$$

where, h_i denotes the management class effect (including year, season and sex effect, etc.); l_k denotes the litter effect; e_{ikl} denotes the residual effect. The year, litter and residual effect were obtained randomly from the normal distribution $N(0, \sigma^2)$ based on these corresponding variances, respectively (Table 1). The effects of sex and season were determined according to Table 1.

In subsequent generations, the offspring were generated by parents according to the mating system. The number of progeny for each mating was obtained randomly from the normal distribution $N(10, 6.25)$ (for dynamic selection, the number of progeny of the dam was fixed as 10). The sex of an individual was determined by $u(0,1)$ based on equal frequency (0.5 for both male and female). The first allele of the QTL1 for offspring was derived randomly from the two alleles of the sire, and the second allele of QTL1 was

derived randomly from the two alleles of the dam. The allelic origin of QTL2 depends on the linkage phase of parents, the allelic origin of QTL1 and the recombination rate r . When the allelic origin of QTL1 was determined, the probability of allelic origin of QTL2 from parents was obtained based on Table 2. Then, using the uniform distribution $u(0,1)$ based on the previous probability the genotype of QTL2 was obtained. The polygenic effect of the offspring was generated based on the formula $u_i = 1/2u_s + 1/2u_d + m_i$, where u_s and u_d are the polygenic effects of sire and dam, respectively; m_i is the random Mendelian deviation. The latter was sampled from a normal distribution with mean zero and variance $0.5\sigma_a^2(1 - 0.5(F_s + F_d))$, where F_s and F_d are the inbreeding coefficients of the sire and dam, respectively. The QTL alleles were transmitted from parents to offspring in classical Mendelian fashion. The phenotypic value for a progeny was calculated according to the model described in the base population.

For generating a population with overlapping generations, we simulated three years in advance based on random selection. The sires and dams were selected using the uniform distribution $u(0,1)$ based on equal frequency for all candidates. Then, all these schemes were implemented again over 15 years based on the population with

Table 2. The probability of origin of alleles at the second QTL from the allele of parents

Origin of allele	$Q_1^{2,1} = Q_2^{2,1}$	$Q_1^{2,1} = Q_2^{2,2}$	$Q_1^{2,2} = Q_2^{2,1}$	$Q_1^{2,2} = Q_2^{2,2}$
$Q_1^{1,1} = Q_2^{1,1}$	1-r	r	0	0
$Q_1^{1,1} = Q_2^{1,2}$	r	1-r	0	0
$Q_1^{1,2} = Q_2^{1,1}$	0	0	1-r	R
$Q_1^{1,2} = Q_2^{1,2}$	0	0	r	1-r

Subscript i , s and d denote individual, sire and dam, respectively.

The first number of superscript denotes the QTL, and the second number denotes the allele.

overlapping generations. All these cases were replicated 50 times. The end results were the mean values of all these replicates and standard errors were calculated from the variance among replicates.

Estimation of breeding values

All candidates were phenotyped and genotyped for the QTL prior to selection. Three types of schemes for estimation of breeding value were compared, and they are described below:

Conventional BLUP selection (CBLUPS) : When the information on the QTL was not used, genetic evaluations were entirely based on phenotypic and pedigree information. The total estimated breeding value (including QTL and polygene) for an individual i (EBV_i) was obtained from standard BLUP using the total additive genetic variance ($\sigma_q^2 + \sigma_u^2$) and the phenotypic values uncorrected for the QTL effect. In this case, the estimated breeding value was:

$$EBV_i = \hat{g}_i \quad (20)$$

where, \hat{g}_i is total estimated breeding value of individual i . If there are multiple quantitative traits in selection schemes, then, the EBVs of multiple traits are aggregated with the corresponding economic weight. Therefore, the selection criterion in simulated populations was:

$$I = w_{BF} EBV_{BF} + w_{D100} EBV_{D100} \quad (21)$$

Standard QTL-assisted selection (SQS) : In schemes selecting directly on the QTL, it was assumed that all individuals had a known genotype for the QTL, and its effect was known without error (as the fixed effect). In these assumptions, the estimated breeding value was:

$$EBV_i = \hat{u}_i + q_i \quad (22)$$

where, \hat{u}_i is the estimate of polygenic breeding value; q_i is the sum of the breeding value due to the QTL effect. The estimate \hat{u}_i was obtained from standard BLUP using the polygenic variance (σ_u^2) and the phenotypic values corrected for the QTL effect ($y_i' = y_i - q_i$). For an additive model, the breeding value of the QTL with two alleles was $2(1-p)a$, $-2pa$ and $((1-p)-p)a$ for individuals with genotype A1A1, A2A2 and A1A2 respectively (Falconer and Mackay, 1996). The frequency p was updated each cycle of selection to obtain q_i . If there were multiple traits, EBV was calculated according to formula (21).

Optimal QTL-assisted selection (OQS) : In OQS

schemes, the objective was to maximize the cumulative response in the terminal generation, and the selection criterion was:

$$EBV_i = \hat{u}_i + \lambda q_i \quad (23)$$

where, \hat{u}_i is the estimate of polygenic breeding value; λ is the optimal weight given to q_i . According to the theory of Chakraborty et al. (2002), the optimization program provides an optimal vector of proportion selected for all sex, genotypes and generations. Based on the standard normal distribution theory, these proportions can be used to derive the standardized truncation point that is associated with genotype. Following Dekkers and van Arendonk (1998), differences in truncation point between genotypes were translated to the differences between means between genotypes:

$$\theta_{k,t} - \theta_{ref,t} = (X_{ref,t} - X_{k,t})\sigma_j \quad (24)$$

where ref refers to an arbitrary reference genotype. The means derived by (24) quantify the emphasis (λ) that is put on each QTL genotype in (23) relative to reference genotype. These will be referred to as optimal genotype values (λq_i). Then, the selection index was:

$$I_{ijkt} = \theta_{ref,t} + (X_{ref,t} - X_{k,t})\sigma_j + EBV_{ijkt} \quad (25)$$

where EBV_{ijkt} is the polygenic EBV of animal i and was obtained as SQS; $X_{k,t}$ is the truncation point of the k^{th} genotype in year t and was obtained by the method of Tang and Li (2006) in a population with two quantitative traits and overlapping generations. Finally, the aggregate EBV was calculated according to the formula (21).

Selection procedure

For three types of breeding value estimation method described above, two types of selection procedures were considered in selection schemes.

Standard truncation selection (TS) : A fixed number of individuals (N_s males and N_d females) with the highest estimated breeding values were selected to be parents of the next cycle. Each sire mated at random to N_d/N_s dams, and each dam mated to a single sire.

Dynamic selection (DS) : The number of parents and their contributions to the next generation are dynamic. Selection on a quadratic index that optimizes the number of animals selected and their contribution maximizes the genetic gain while restricting the rate of inbreeding to a predefined value in a population with different lifetimes for sires and dams. The detailed method of optimization was described previously (section 2.1. and 2.2.). In a time period

Table 3. Annual genetic gains (ΔG) and annual rates of inbreeding (ΔF) on truncation selection and dynamic selection for OQS, SQS and CBLUPS

Selection strategy	Response component	Truncation selection					Dynamic selection				
		N_s	ΔG_{BF}	ΔG_{D100}	ΔG_{ABV}	ΔF_{year}	N_s	ΔG_{BF}	ΔG_{D100}	ΔG_{ABV}	ΔF_{year}
OQS	Polygene	20	-0.30 (91.90) ³	-3.19 (92.73)	2.54 (92.63)	0.0111	14.42	-0.31 (103.18)	-3.51 (101.69)	2.77 (101.86)	0.0113
	QTL		-0.30 (202.92)	-1.57 (118.72)	1.40 (130.30)			-0.24 (173.38)	-1.44 (103.74)	1.25 (112.57)	
	Total		-0.60 (126.08)	-4.76 (99.94)	3.94 (103.22)			-0.56 (125.42)	-4.96 (102.28)	4.03 (104.97)	
SQS	Polygene	20	-0.28 (83.80)	-2.87 (83.35)	2.29 (83.40)	0.0131	12.32	-0.29 (94.25)	-3.19 (92.28)	2.52 (92.50)	0.0132
	QTL		-0.27 (184.74)	-1.62 (122.36)	1.40 (130.93)			-0.24 (170.75)	-1.65 (118.36)	1.39 (125.00)	
	Total		-0.55 (114.87)	-4.49 (94.17)	3.69 (96.77)			-0.53 (118.48)	-4.83 (99.76)	3.91 (101.94)	
CBLUPS	Polygene	20	-0.33	-3.44	2.74	0.0075	20.62	-0.30	-3.46	2.72	0.0076
	QTL		-0.15	-1.32	1.07			-0.14	-1.39	1.11	
	Total		-0.48	-4.77	3.82			-0.45	-4.85	3.84	

N_s denotes the average annual optimal number of sires.

Subscript BF, D100 and ABV denote backfat to 100 kg, days to 100 kg, and aggregate breeding value, respectively

In parenthesis, response for OQS and SQS are also expressed relative to response for CBLUPS.

The sampling standard errors ranged from 0.03 to 0.09 for ΔG_{BF} , from 0.09 to 0.33 for ΔG_{D100} , from 0.08 to 0.26 for ΔG_{ABV} and from 1.06 to 1.29 for N_s in all cases. The standard error for ΔF_{year} ranged from 0.0002 to 0.0005 in dynamic selection and 0.0007 to 0.0017 in truncation selection.

of selection, a boar can mate with several sows, and a sow has to mate with a boar because a sow procreates generally once. For the breeders, they want every dam to be mated in a reproduction period. In this case, the optimization of contribution on sow has little meaning. Thus, the contributions of sows were fixed in this paper, and the contributions of boars were optimized according to formula (15), (16) and (17). For purposes of comparison, the rate of inbreeding in dynamic selection was restricted to be the same as the mean annual rate of inbreeding in truncation selection over the planning horizon. Following Villanueva (2004), selection decisions for OQS-DS were optimized in two steps. Firstly, the SQS-DS scheme was run, and the optimal number of males and females selected and the accuracies of EBV for both sexes obtained from this scheme were used as the inputs for OQS to obtain the optimal QTL genotype value over generations (Tang and Li, 2006). Secondly, contributions of candidates were optimized based on OQS.

RESULTS

Selection response and rate of inbreeding

Annual genetic gain and annual rate of inbreeding over 15 years on standard truncation selection and dynamic selection for OQS, SQS and CBLUPS are listed in Table 3. As expected, under DS, the annual genetic gains of the total component for aggregate breeding value (ABV) for three selection strategies were greater than the corresponding TS. DS in the SQS scheme resulted in the greatest increment of gain, followed by OQS and then CBLUPS. From Table 3,

for three selection strategies DS increased mainly the genetic gain of D100. The selection response of BF for DS was not as good as TS because the QTL response of BF was decreased in DS. As TS, under DS, OQS mitigated substantially the Gibson effect and obtained the greatest selection response in three selection strategies. The combination for OQS and DS further increased the selection response.

For three selection strategies, the annual rate of inbreeding on dynamic selection was restricted successfully as the annual rate of inbreeding on truncation selection (Table 3 and Figure 1). From Table 3, SQS resulted in the greatest annual rate of inbreeding, followed by OQS. CBLUPS resulted in the smallest annual rate of inbreeding. The optimal numbers of boars on DS for SQS and OQS were smaller than the numbers of boars on TS (fixed number), but the number for CBLUPS was a little larger than that on TS. They all decreased with the increase of annual rate of inbreeding.

The trends of cumulative gain about ABV and average inbreeding coefficient for OQS, SQS and CBLUPS in two selection procedures are illustrated in Figure 1. The increase of inbreeding was strictly controlled by DS, which increased following an approximate beeline using the fixed rate in the three selection schemes. SQS resulted in the greatest difference of movement trend for inbreeding coefficient between DS and TS, followed by OQS. The smallest was CBLUPS, and its inbreeding curve in TS increased according to a fixed rate that was similar to DS. For three selection strategies, the cumulative gain was improved more rapidly in the forepart and then slower in

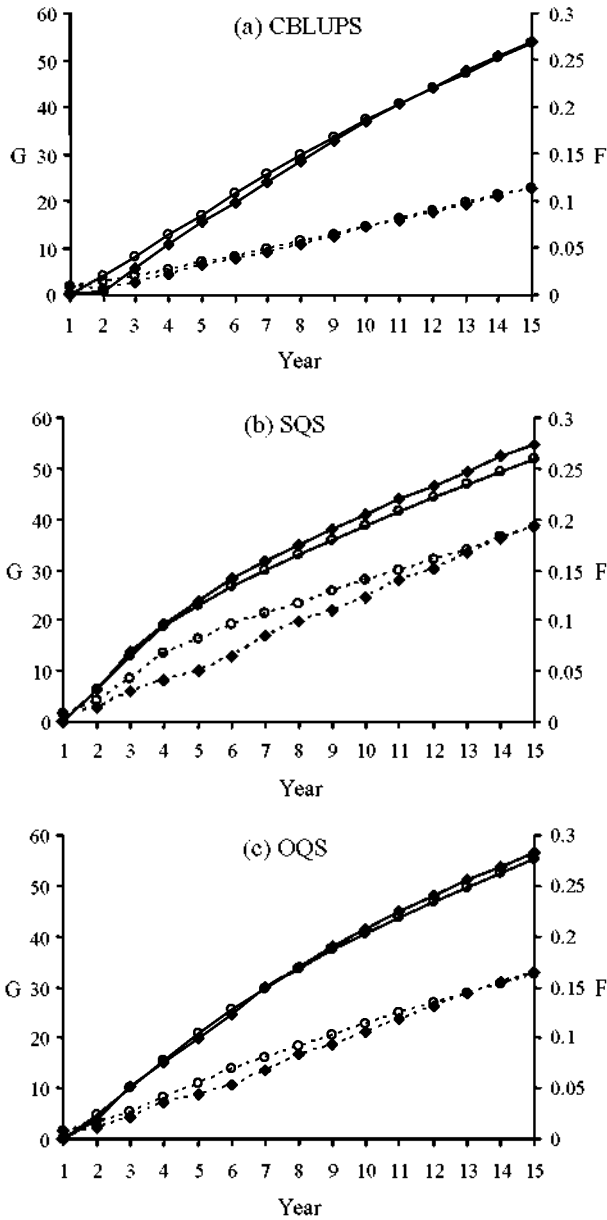


Figure 1. Cumulative gains (–) of ABV and average inbreeding coefficients (---) for dynamic selection (♦) and truncation selection (◊) for SQS, OQS and CBLUPS.

back-part because genetic variance was decreased owing to the increase of inbreeding.

QTL haplotype frequencies

The curves in frequencies for three QTL haplotypes of BF and D100 are displayed in Figure 2 for SQS, OQS and CBLUPS. As described by Dekkers et al. (2002), for all these schemes the trends of frequency for the favorable haplotype A1B1 and the unfavorable haplotype A2B2 were to fixation and zero, respectively. The frequency for the haplotype A1B2 in the repulsion phase was, however, increased initially before reducing to zero. These trends for

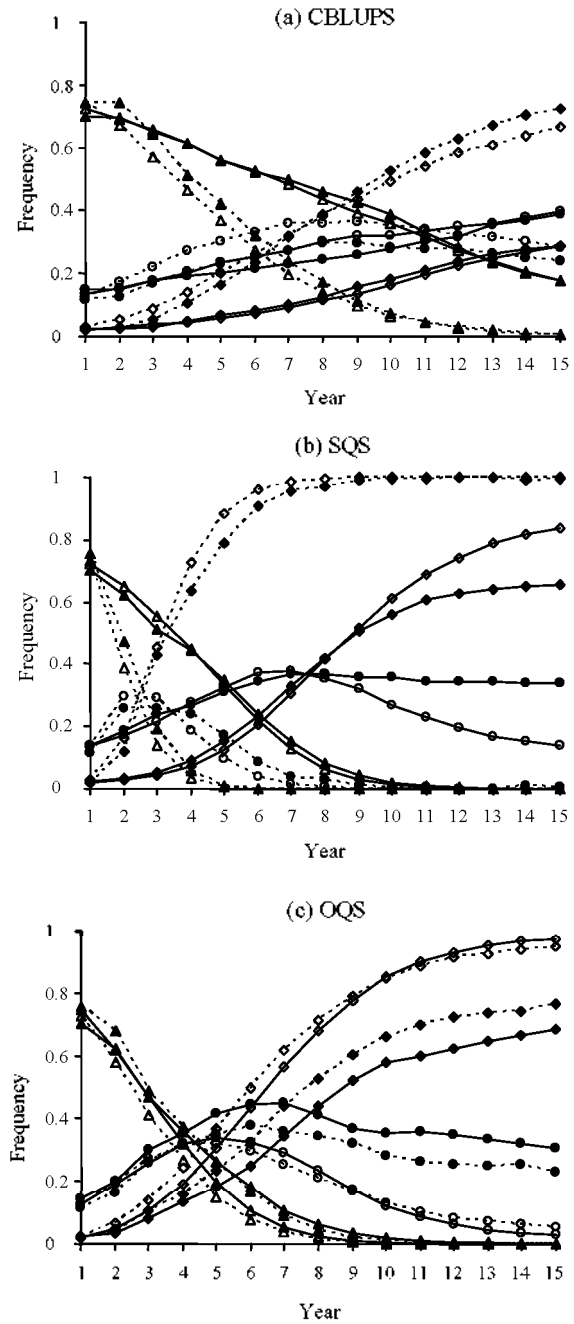


Figure 2. Frequencies of A1B1 (dynamic: ♦, truncation: ◊), A1B2 (dynamic: ●, truncation: ○), and A2B2 (dynamic: ▲, truncation: △) of BF (–) and D100 (---) for SQS, OQS and CBLUPS.

D100 in the SQS scheme were most rapid (Figure 2b), followed by the OQS scheme and then the CBLUPS scheme. These trends for BF in the OQS scheme were however, most rapid, followed by SQS and CBLUPS. Relative to TS, DS resulted in a slower movement trend for three haplotypes in the SQS and OQS schemes. Furthermore, they are more obvious in the OQS scheme.

Quite different trends in haplotype frequencies are observed for OQS and SQS schemes (Figure 2). In the SQS

Table 4. Annual genetic gains (ΔG) and annual rates of inbreeding (ΔF) on truncation selection and dynamic selection for OQS, SQS and CBLUPS with different contributions of sire-age classes

S	Selection strategy	Truncation selection					Dynamic selection				
		N_s	ΔG_{BF}	ΔG_{D100}	ΔG_{ABV}	ΔF_{year}	N_s	ΔG_{BF}	ΔG_{D100}	ΔG_{ABV}	ΔF_{year}
(0.35, 0.15)	CBLUPS	20	-0.47	-4.80	3.83	0.0080	18.11	-0.40	-4.76	3.73	0.0083
	SQS	20	-0.55	-4.40	3.63	0.0138	11.17	-0.51	-4.61	3.74	0.0145
	OQS	20	-0.60	-4.69	3.88	0.0118	13.29	-0.54	-4.73	3.85	0.0124
(0.4, 0.1)	CBLUPS	20	-0.48	-4.77	3.82	0.0075	20.62	-0.45	-4.85	3.84	0.0076
	SQS	20	-0.55	-4.49	3.69	0.0131	12.32	-0.53	-4.83	3.91	0.0132
	OQS	20	-0.60	-4.76	3.94	0.0111	14.42	-0.56	-4.96	4.03	0.0113
(0.45, 0.05)	CBLUPS	20	-0.51	-4.90	3.94	0.0072	23.19	-0.46	-5.03	3.98	0.0071
	SQS	20	-0.56	-4.53	3.74	0.0130	13.99	-0.54	-5.06	4.08	0.0127
	OQS	20	-0.62	-4.77	3.96	0.0107	16.00	-0.58	-5.13	4.17	0.0106

S denotes the vector restricted for contributions of sire-age classes.

The standard errors ranged from 0.03 to 0.09 for ΔG_{BF} , from 0.09 to 0.38 for ΔG_{D100} , from 0.08 to 0.27 for ΔG_{ABV} and from 1.06 to 1.60 for N_s in all cases; the standard error for ΔF_{year} ranged from 0.0002 to 0.0005 in dynamic selection and 0.0007 to 0.0021 in truncation selection.

scheme, the haplotype frequency for D100 rapidly trended to fixation or zero, the haplotype frequency for BF slowly trended, however, to fixation or zero. On the contrary, in the OQS scheme for both TS and DS the changing trends of haplotype frequency for D100 were more gradual than in the SQS scheme, but the trends for BF were more rapid. This showed that the optimization of emphasis given to QTL balanced substantially the relative weight between QTL and polygene in the selection criterion. Relative to SQS and OQS schemes, the movement trends of QTL haplotype frequencies were gentler in the CBLUPS scheme under TS. But under DS, unlike the SQS and OQS, the trends of QTL haplotype frequencies of D100 were more rapid in the CBLUPS scheme, and the trends of BF were similar to SQS and OQS.

Effects of contribution of sire-age class

A comparison of the rates of response and inbreeding obtained with truncation selection and dynamic selection with different contributions of sire-age classes for CBLUPS, SQS and OQS is shown in Table 4. The annual gains of ABV for SQS and OQS increased gradually following the increase of contribution of the first sire-age class (i.e. the generational interval decreased) in TS. The increment of gain for D100 was larger than that for BF. When $s = (0.35, 0.15)$ or $s = (0.45, 0.05)$, DS resulted in more response than TS in CBLUPS, SQS and OQS. However, when $s = (0.35, 0.15)$ the annual gains of ABV for CBLUPS and OQS were smaller in DS than in TS and only the gain of ABV for SQS was larger. As expected, the annual rates of inbreeding decreased gradually following the increase of contribution of the first sire-age class in TS. When $s = (0.35, 0.15)$ or $s = (0.45, 0.05)$, DS successfully maintained annual rates of inbreeding at the corresponding value which resulted in TS for CBLUPS, SQS and OQS. However, when $s = (0.35, 0.15)$, annual rates of inbreeding for the three selection strategies were not restricted substantially as the corresponding value. This shows the constraints for s and

rate of inbreeding will be more difficult following the increase of contribution of the second sire-age class.

Effects of annual rate of inbreeding

For OQS, SQS and CBLUPS, the average annual genetic gains and the cumulative terminal gains in DS with different annual rates of inbreeding (Kim et al., 2006) are listed in Table 4. At the same annual rate of inbreeding, SQS resulted in the greatest optimal number of sires, followed by OQS. The smallest was CBLUPS. The optimal number of sires was decreased obviously with the increase of annual rate of inbreeding that was defined in advance (Table 4). Both the average annual genetic gain and the cumulative terminal gain for SQS were improved following the increase of the annual rate of inbreeding. They were decreased, however, following the increase of the annual rate of inbreeding in the CBLUPS scheme. OQS resulted in the greatest annual genetic gain and cumulative terminal gain when the annual rate of inbreeding equaled 0.02, followed by equaling to 0.03 and 0.01.

Figure 3 shows the cumulative genetic gain and average inbreeding coefficient for SQS, OQS and CBLUPS in DS with different annual rates of inbreeding. The annual rates of inbreeding for three selection strategies were restricted to a predefined value by DS, and the inbreeding coefficient in the terminal generation were similar for SQS, OQS and CBLUPS. The rate of inbreeding in the CBLUPS scheme was controlled more easily, followed by OQS and SQS schemes. The curve of average inbreeding coefficient in OQS and SQS schemes represents slight fluctuation. Comparing these curves for SQS, OQS and CBLUPS, the rate of inbreeding can be controlled more easily by DS to a smaller predefined value. For all three selection strategies, while annual rate of inbreeding equaled 0.01, the cumulative gain was improved most slowly in the forepart, then the followed was to equal 0.01 and 0.02. This is because the larger annual rate of inbreeding is favorable to select those animals with closer coancestry, furthermore,

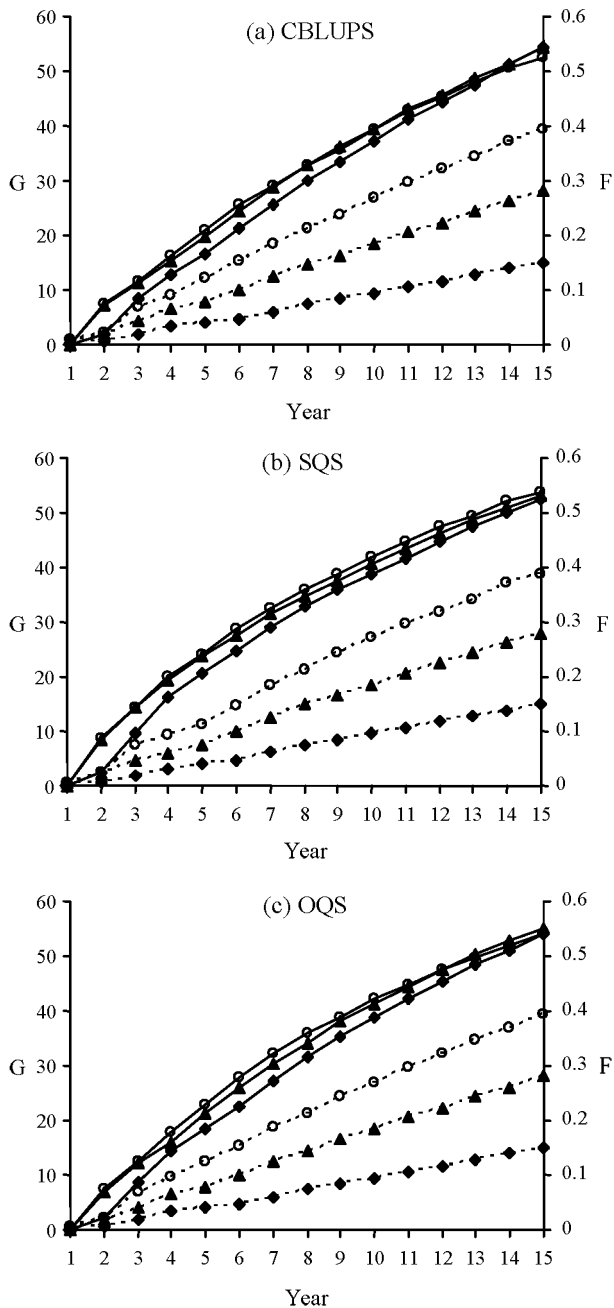


Figure 3. Cumulative genetic gains (—) of ABV and average inbreeding coefficients (---) for dynamic selection for three selection strategies with rate of inbreeding equaling to 0.01 (◆), 0.02 (▲), and 0.03 (○).

these animals have similar genetic levels because of their coancestry. So, the corresponding cumulative gain of ABV was improved more rapidly following the increase of annual rate of inbreeding in the forepart. However, the genetic variation was decreased gradually following the increase of inbreeding. So, the increment of cumulative gain was decreased more rapidly in the back-part with the increase of inbreeding. Finally, the cumulative gains for three annual rates of inbreeding were similar in the terminal year for

CBLUPS, SQS and OQS.

DISCUSSION

In this paper, a method was developed to optimize the genetic contribution of individuals in a population with overlapping generations and different lifetimes for sires and dams. This rule maximizes genetic merit of selected individuals while restricting the rate of inbreeding to a predefined value. As described by Meuwissen and Sonesson (1998), this paper also controls the increase of average additive genetic relationship for parents selected by constraining the $r'A_{t+1}r$ term of year $t+1$, and further restricts the increase of average inbreeding for new offspring. However, for optimizing the contribution of selected parents in a population with different lifetimes between sires and dams, the population has to be divided into sex-age classes according to the method of Hill (1974) and not be divided into age classes based on the methods described by Meuwissen and Sonesson (1998) and Grundy et al. (2000). Then, the long-term contribution vector r and average additive genetic relationship $\overline{A_{t+1}}$ need to be defined again in terms of sires and dams, respectively. Under these conditions, the Lagrange function of the optimization problem was further reconstructed, and obtained the corresponding formulas of Lagrange multipliers and optimal c_t .

As described by Meuwissen and Sonesson (1998), this extended rule was also based on the year to constrain the increase of annual rate of inbreeding. It is favorable to practical breeders, because they want to control the inbreeding depression, variance reduction due to inbreeding and the risk of the breeding scheme in a fixed number of years (for example five years), and not in a fixed number of generations, consequently to maximize the economic profit of breeding over years. However, from a theoretical and long-term perspective, a limit on the inbreeding per generation may be more appropriate because those factors that counteract the detrimental effects of inbreeding occur on a per-generation basis. Classical examples of these factors are natural selection and mutations that occur during meiosis. After comparison between the method of Meuwissen and Sonesson (1998), based on the constraint of inbreeding per year, and the method of Grundy et al. (2000), based on the restriction of inbreeding per generation, Sonesson et al. (2000) found that constraint of inbreeding on a per generation basis resulted in shorter generation interval. This enhances the chance to cull animals at younger ages. It is favorable to increase the transmission rate of gain. However, it also leads to an increase in breeding cost, and may not be appropriate for practical breeders. In addition, the "year" in the extended rule

Table 5. Annual genetic gains and terminal cumulative gains on dynamic selection for OQS, SQS and CBLUPS with different rates of inbreeding

Selection strategy	Response component	Annual rate of inbreeding								
		0.01			0.02			0.03		
		N_s	ΔG_{ABV}	ΔG_{15}	N_s	ΔG_{ABV}	ΔG_{15}	N_s	ΔG_{ABV}	ΔG_{15}
OQS	Polygene	16.98	2.66	37.30	6.82	2.72	38.15	4.58	2.68	37.49
	QTL		1.19	16.67		1.20	16.79		1.18	16.49
	Total		3.85	53.97		3.92	54.94		3.86	53.98
SQS	Polygene	18.07	2.38	33.37	7.56	2.42	33.82	5.00	2.48	34.65
	QTL		1.38	19.28		1.38	19.25		1.37	19.24
	Total		3.76	52.64		3.79	53.07		3.85	53.89
CBLUPS	Polygene	15.31	2.81	39.29	6.15	2.84	39.70	4.12	2.78	38.92
	QTL		1.08	15.17		1.05	14.66		0.98	13.72
	Total		3.89	54.46		3.88	54.36		3.76	52.64

G_{15} denotes the terminal cumulative response of ABV.

The standard errors ranged from 0.23 to 0.54 for ΔG_{ABV} , from 0.60 to 1.47 for N_s and from 3.30 to 7.64 for G_{15} in all cases.

implies an interval of selection period (from the selection of parents to the selection of new offspring), and changes following a change of livestock (such as 6 months for pigs, 1 year for cattle). For convenience, it was assumed to be one year. Therefore, the extended dynamic rule constrained the rate of inbreeding based on per selection period, and so it also considered these factors based on the generation in a breeding scheme.

In a selection period, a sire may mate with multiple dams and a dam has to mate commonly with a sire. In other words, a dam only procreates one time in a reproduction cycle. Following the rapid development of reproductive biotechnology, now a dam can also procreates multiple times (such as multiple ovulation and embryo transfer, MOET). Unfortunately, these biotechnologies are not implemented on a large scale in a practical breeding scheme. In addition, practical breeders generally let the number of dams denote the size of the population, and let every dam have the same contribution to offspring. In this case, the contributions of the dams do not need to be optimized, and the optimization of contributions for the sires has the more important value. Thus, for matching to a practical breeding program, this paper only optimized the number and contributions of sires selected, and the number and contributions of dams were determined in advance. Certainly, this strategy inevitably causes some loss of selection response, because the dams also have half contributions to offspring in a breeding scheme.

Meuwissen and Sonesson (1998) and Grundy et al. (2000) optimized the long-term contribution vector r using iteration method and annealing method, respectively. However in a small simulated population, if EBVs of the animals in some sex-age classes are too large or too small, it will cause the animals of some sex-age classes to be fully selected or eliminated in the optimization process. For example, if the lifetime of an animal is 3 years, and the EBVs of animals for sex-age class 3 are very large, these animals will be totally selected by DS. Furthermore, the

optimal contributions for them will be very large. In this case, the animals of sex-age class 2 may be eliminated entirely, but the animals of sex-age class 3 also have to be fully eliminated the next year (surpassing the service lifetime of the animal). So, it inevitably causes the population to fluctuate in the planning horizon. This case was met by the author in optimizing simultaneously r and c_i using an iteration method (results not shown). For avoiding this case, the sum of contributions for each sex-age class can be restricted to a fixed proportion by s according to the method described by Grundy et al. (2000). Then, the genetic contributions of all these sex-age classes will be determined in advance.

Although only a limited number of scenarios were investigated, the results indicate that the extended rule can strictly constrain the annual rate of inbreeding to a predefined value for SQS, OQS and CBLUPS, and can obtain greater selection response than TS in a population with overlapping generations and different lifetimes between sires and dams. This paper also shows that the combination of the extended rule and the optimization of emphasis given to QTL can further increase the selection response, and substantially solve the conflict between short-term and long-term selection response for GAS. A similar increment for gain was produced by optimizing contributions of selection candidates and emphasis given to QTL, respectively. Optimization of the emphasis given to QTL over years had, however, a greater impact on avoiding the long-term loss usually observed in these schemes.

Most results indicated that SQS resulted in the greatest relative advantage for DS over TS, followed by OQS and then CBLUPS (Tables 3 and 4; Figure 1). Furthermore, most increase of these relative advantages for the three selection strategies was produced from the polygenic component, and the top-down order of increment size was SQS, OQS and CBLUPS. It is known that SQS results in the loss of long-term selection response (Gibson, 1994; Ruane and Colleau, 1995; Pong-Wong and Woolliams,

1998). The cause of loss for the long-term selection response is that QTL is given high emphasis in early generations, and reduces the selection intensity of polygenes, consequently resulting in a reduced early response at polygenes. This loss is not fully recovered during the later generations of selection due to the non-linear relationship between selection pressure and selection response in a finite population with an infinitesimal model. According to the illustration by Villanueva et al. (2004), dynamic selection that obtains the optimal contributions attempts to i) make the contribution of a candidate to the next generation equal to its desired long term contribution conditional on the observed information, and ii) uses the estimated Mendelian sampling term as the selective advantage and not the breeding value. Therefore, in each generation of selection, a considerable part of the selection pressure will be within families by DS, and between-family selection will be kept to the minimum. The probability of identity for the favorable QTL genotype between animals is very large when a family has high favorable QTL allele frequency. Then, the selection of parents will mainly depend on the size of polygenic effect (high emphasis given to polygenes), and within-family selection will give little or no decrease of selection intensity for polygenes. Thus, to a certain extent, it can reduce the loss of early polygenic response. In other words, following the increase of favorable QTL allele frequency in a family, the selection within family will gradually enhance the selection pressure given to the polygenic component in the process of DS. In the SQS-DS scheme, because the frequencies of favorable QTL alleles rapidly reach fixation in early generations (within 6 generations), so, the early polygenic selection pressure under DS has little reduction, which finally results in more polygenic response over the planning horizon. In the OQS-DS scheme, the weight given to the polygene has been increased by the optimization of relative emphasis given to QTL in the first step and, to a certain extent, the loss of early polygenic response has been lessened. Thus, in the second step, the space for increasing the frequency of a favorable QTL allele to reduce the loss of early polygenic response under DS is smaller than the corresponding SQS scheme. For the CBLUPS, there is nearly no loss of early polygenic response, so the extra early polygenic response under DS is very little.

Several interesting features were observed from these simulated results, which deserve further discussion. First, SQS resulted in the greatest annual rate of inbreeding, and obtained the smallest genetic gain in the long term under TS (Table 3). Second, SQS resulted in the largest optimal number of sires, and CBLUPS resulted in the smallest optimal number of sires while constraining the annual rate of inbreeding to a given value under DS (Tables 3 and 4). In the process of TS, within-family and between-family

selection are given equal selection pressure by SQS, but the selection intensity given to QTL is larger than polygenes. For a favorable QTL allele, from the starting of mutation, it has been given very high selection intensity by SQS that maximizes the selection response from current generation to next generation. In this process of selection, other polygenes are given a little emphasis (i.e. all individuals with this favorable QTL allele are selected, and the size of polygenic effect not considered), which finally results in the loss of early polygenic response. However, these individuals with this QTL allele come from a common ancestor that produces this QTL allele; so, there is some kindredship between them. In this case, SQS resulted in a rapid increase of inbreeding, and obtained the smallest selection response. For CBLUPS, an individual is selected based on the EBV of this individual (including QTL and polygenes). This selection criterion may put more emphasis on polygenes, because the polygenic effects are generally larger. Therefore, CBLUPS did not result in the extra increase of inbreeding due to the QTL component, and obtained a high selection response in the long term. For the same reason, while constraining the rate of inbreeding to a given value, DS needs to select more animals with a little kindredship to reduce the increase of inbreeding in the SQS scheme and needs fewer animals in the CBLUPS scheme, because the average relationship of animals selected in the CBLUPS scheme is smaller than that in the SQS scheme.

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