Determination of the Optimum Mating Design with Constraints on Inbreeding Level and Mating Frequency of Sires *via* a Simple Genetic Algorithm

Kenji OYAMA and Fumio MUKAI*¹⁾

Graduate School of Science and Technology, Kobe University,
Nada-ku, Kobe-shi 657-8501

* Faculty of Agriculture, Kobe University, Nada-ku, Kobe-shi 657-8501

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Abstract Using predicted breeding values (PBV) of an actual beef cattle population, application of a simple genetic algorithm (GA) was done to design the optimum mating, with constraints on inbreeding coefficient of each progeny, inbreeding level of the next generation, and mating frequency of sires. As the breeding stock, 15 sires and 400 dams were selected according to PBV of judging score for breeding females (JS-Data) or beef carcass marbling score (BMS-Data). Aggregate genetic merit (AGM) of eight traits (judging score, two reproductive traits, and five carcass traits) weighing differently was regarded as the breeding objective. When appropriate operator values were used, GA found satisfactory mating designs under pre-determined constraints. The losses in gains of AGM by imposing the constraint of 0.30 on mating frequency were only 31.3% in JS-Data and 35.6% in BMS-Data compared with the mating designs without constraints. Genetic gain of beef marbling score was 28.3% higher in the evaluation from BMS-Data than JS-Data. Efficiencies of GA to design mating were demonstrated.

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Key words : Mating design, Genetic merit, Inbreeding, Mating frequency, Genetic algorithm

Selection and mating schemes giving reasonable genetic gains and acceptable inbreeding levels are of primary interest in animal breeding. Several methods to reduce rates of inbreeding have been proposed through selection decisions^{2,15,17}. Mating schemes were also investigated to maintain inbreeding at lower level^{3,4}. Although these methods were effective, evaluation on all possible mating for many candidates becomes difficult. The lack of information on pairing the individuals causes a problem under the practical breeding.

In selection index, Allaire¹⁾ justified the use of mate selection when a nonlinear relationship

exists between at least one trait in the index and merit. Furthermore linear⁸⁾ or quadratic⁹⁾ programming techniques were applied to optimize mating design. Toro and Pérez-Enciso¹⁶⁾ also proposed the mate selection that could maximize the response restricting the increase in inbreeding. Those techniques are computationally demanding and can not be applied to large breeding population.

On the other hand, optimizing procedures, genetic algorithms⁶⁾ (GAs) can adopt for various constraints once the problem and a solution are expressed in a function and string, respectively. The GAs are relatively new

¹⁾ Corresponding author.

approaches in animal science, and few researches to optimize a sheep breeding industry⁷⁾ and mating design of cattle population¹³⁾ have been reported. In the latter study, the mating pairs which produce the maximum gain were determined subject to average inbreeding of the next generation. However the attempt raises problems, such as excessive utilization of particular sire and excessive inbreeding in some progeny even though the average level is low. The first problem would likely occur with migration of superior genes (sires) and result in closely related progeny and less genetic diversity in later generation. The present study described how a simple GA can be used to select mating pairs, which maximize genetic gain at the next generation while restricting three different factors, *i.e.* average inbreeding of the next generation, mating frequency of sires to maintain diversity in later generation, and inbreeding coefficient of each progeny.

Materials and Methods

A simple genetic algorithm

The algorithm used in this study was basically the same as the GA used in the previous report¹³⁾. Let S and D express numbers of sires and dam selected respectively, then expected genetic level of the subsequent generation in k -th trait can be written as

$$m_k = \frac{1}{2} \{ \mathbf{1}'_D \mathbf{P}'_{SD} \mathbf{u}_{Sk} + \mathbf{1}'_S \mathbf{P}_{SD} \mathbf{u}_{Dk} + d_k \\ \times \text{tr}(\mathbf{P}_{SD} \mathbf{A}'_{SD}) \}$$

where

$\mathbf{1}_S$ and $\mathbf{1}_D$: vectors of ones with orders of S and D , respectively,

$\mathbf{u}_{Sk}$ and $\mathbf{u}_{Dk}$: vectors of predicted breeding values (PBV) of k -th trait with orders of S and D , respectively,

$\mathbf{P}_{SD}$: matrix of mating design with order of $S \times D$,

d_k : coefficient of inbreeding depression, and

$\mathbf{A}_{SD}$: additive relationship matrix between sires and dams with order of $S \times D$.

In GA a mating design was expressed as a string form called chromosome. Using above m_k as elements in vector $\mathbf{m}_j$, the fitness of the j -th chromosome was calculated as

$$a_j = \mathbf{b}' \mathbf{L}^{-1} \mathbf{m}_j,$$

where $\mathbf{b}$ is the vector of weighting coefficients on objective traits, $\mathbf{G} = \mathbf{L}\mathbf{L}'$ being $\mathbf{G}$ as the matrix of genetic variances and covariances. The amount of depression due to inbreeding was already taken into consideration in $\mathbf{m}_j$. The a_j was the sum of generalized weighted genetic level in objective traits and regarded as the aggregate genetic merit (AGM) of the j -th chromosome. Only the fitness with penalty was improved to handle one of the additional constraints, mating frequency of sires, as follows:

$$a'_j = a_j + t \left\{ x_j \left(\frac{F_j - F_c}{F_c} \right) + \sum_{i=1}^s z_{ij} \left(\frac{s_{ij} - s_c}{s_c} \right) \right\},$$

where

t : penalty coefficient decided arbitrarily,

F_j and s_{ij} : expected inbreeding level and mating frequency of the i -th sire in the j -th chromosome, respectively,

F_c and s_c : pre-determined constraint values on inbreeding level and mating frequency of sires, respectively, and

x_j and z_{ij} : dummy variables for inbreeding level and mating frequency, respectively.

Constraint on inbreeding coefficient of each progeny was simply achieved by prohibiting the mating, which would result in equal or greater inbreeding coefficient than the pre-determined value.

Selection of sires and dams

The PBV of an actual beef cattle population were used to examine the efficiency of the algorithm. The traits included in the mating design were judging score (JS) for breeding females, carcass weight (CW), *longissimus* muscle area (LMA), rib thickness (RT), subcutaneous fat thickness (SFT), and beef marbling score (BMS) recorded in the slaughter house. Beef marbling was scored by 12 steps from 0 (null) to 5 (very abundant). Certified graders

of Japan Meat Grading Association scored and recorded all carcass measurements. Since selection and mating design based on carcass traits might affect reproductive performances unfavorably, two reproductive traits, age at the first calving (AFC) and average calving interval (ACI), were also included in mating design to examine its influence. Weighting coefficients, inbreeding depressions, and genetic variances and covariances among traits are shown in Table 1. No weights were placed on two reproductive traits and JS. The genetic parameters were cited from Oyama *et al.*¹²⁾, estimated by using field carcass and reproductive records of Japanese Black cattle in the Hiroshima prefecture. Breeding values were predicted by BLUP⁵⁾ under animal models using the parameters. The linear models for predicting breeding values and genetic base year were the same as those in the REML estimation¹²⁾. The AGM was also defined for each sire and dam by replacing $\mathbf{m}_j$ with the vector containing PBV of each animal.

Inclusion of older animals in mating design did not seem realistic. Therefore sires and dams, which were included in design were restricted to those born from 1980 and 1985 onward, respectively. Fifteen sires and 574

dams satisfied the conditions. The GA designates the mating sire for each dam. Therefore animals in the mating design must be selected as breeding stock in advance. Selection based on PBV was initially conducted. However only 15 sires were available for candidates, selection could be applied only on dams. Two different selection criteria, PBV of JS and BMS, were examined. The selection on JS represented the traditional female selection in Japanese Black, and the selection on BMS simulated prospective beef improvement system. Four hundred dams from 574 candidates were selected ($P=0.697$) for a trial. The data selected by JS and BMS were called JS-Data and BMS-Data, respectively. Hence there are 15^{400} possible mating designs in each data set. Average inbreeding coefficients of selected animals were 0.0282 in JS-Data and 0.0252 in BMS-Data. If random mating among selected animals was assumed, inbreeding levels of the next generation would be 0.0520 in JS-Data and 0.0517 in BMS-Data.

Operator and constraint values

We conducted the preparatory experiments, and as a result the number of chromosomes per generation (N), recombination frequency between adjacent loci, mutation rate at each

Table 1. Weighting coefficients (b), coefficients of inbreeding depression (d, per 1% increase in inbreeding), and genetic variances (diagonal) and covariances (upper diagonal) among traits considered in mating design

Trait, unit	b	d	Genetic variance and covariance							
			JS	AFC	ACI	CW	LMA	RT	SFT	BMS
JS, point	± 0	-0.0210	1.156	-0.307	-0.004	2.613	0.350	-0.018	-0.046	-0.024
AFC, mo	± 0	0.0010		0.402	0.054	-4.310	-0.853	0.056	0.061	-0.088
ACI, mo	± 0	0.0030			0.262	-2.009	-0.434	-0.022	-0.042	0.054
CW, kg	+1	-0.2999				693.375	67.675	7.578	6.782	1.666
LMA, cm ²	+1	-0.0303					21.913	0.911	0.063	0.379
RT, cm	+1	-0.0051						0.219	0.128	0.088
SFT, cm	-2	-0.0014							0.371	-0.007
BMS	+2	-0.0033								0.217

JS : judging score, AFC : age at first calving, ACI : average calving interval, CW : carcass weight, LMA : longissimus muscle area, RT : rib thickness, SFT : subcutaneous fat thickness, BMS : beef marbling score (0 to 5).

locus, and number of generations¹³⁾ seemed appropriate at 2,000, 0.01, 0.002, and 3,000, respectively to search for the optimum mating design. Two thousand chromosomes for the base generation were generated randomly. Only the penalty coefficient (t) was varied from -1.4 to -0.2 . Three different upper limits on mating frequency of sires, 0.10, 0.20, and 0.30, were examined. If the 15 sires are utilized equally, the mating frequency will be 0.067. In practice, highly proven sires have higher mating frequencies, and therefore it seemed these values were realistic. Constraints on inbreeding level and inbreeding coefficient were initially fixed at 0.05 and 0.20, respectively. The constraint of 0.20 allows mating between half-sibs, but does not allow mating between full-sibs or parent-offspring.

Diversity index of sires (D_j) and effective number of sires (N_{ej}) for the j -th chromosome were calculated by

$$D_j = 1 - \sum_{i=1}^s s_{ij}^2 \text{ and } N_{ej} = 1 / \sum_{i=1}^s s_{ij}^2,$$

respectively. The usefulness of above statistics is discussed in Lindgren¹⁰⁾.

Calculation was carried out on a personal computer with DEC Alpha 21164 A (433 MHz) CPU.

Results and Discussion

When no constraint was applied, the best mate for each dam could be easily found. Repeating this process for all dams naturally leads to the optimum design. In this case GA was not necessary to find the optimum. In both JS- and BMS-Data only one sire with the highest AGM was allowed to mate with dams when no constraint was applied. This was due to low additive relationships between the sire and dams. This could be regarded as the migration of superior genes, and using only one sire would result in at least half-sib non-inbred population. The genetic gains by GA in AGM were 3.791 and 3.379 with expected inbreeding levels of 0.0013 and 0.0020 in JS- and

BMS - Data, respectively. These expected gains were maximal and no other mating design could produce more gain in these data sets. Although expected inbreeding levels were low, these were the designs without regard to the future breeding structure. Therefore various constraint values were applied on mating frequency hereafter and in those cases the optimum mating design turned to unknown. The constraint on inbreeding level had little effect in this population and was fixed at 0.05 in both data sets throughout the searches.

Table 2 shows genetic gains by GA in AGM with various penalty coefficients and constraints on mating frequency. All these results satisfied three constraints and it took approximately 25 minutes to calculate each combination using the personal computer. The values were the proportions of expected gains by GA to the maximum expected gain by GA in AGM, which was mentioned above, in each data set. The highest gains were searched when the penalty coefficient $t = -0.6$ in mating frequencies of 0.10 and 0.20, and when $t = -1.0$ in the frequency of 0.30 in both data sets. Although the appropriate operator values required in GAs are problem specific¹⁴⁾, the same penalty coefficients gave the highest gains because most of the animals were similar in the two data sets. At the constraint of 0.20 a rapid increase in gain was observed when the penalty coefficient decreased from -0.4 to -0.6 . The same phenomena were observed in all constraint values. It seemed that there was a critical region in each constraint. The highest gains were located near the critical regions, and as the penalty coefficient decreased, *i.e.* penalty being intensified, gains also decreased gradually.

As the mating frequency became smaller, *i.e.* the constraint being intensified, the highest gain decreased. However the losses in gains by imposing the constraint of 0.30 on frequency were only 31.3% in JS-Data and 35.6% in

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Table 2. Genetic gains^a found by genetic algorithm with various amount of penalties

Penalty coefficient	JS-Data			BMS-Data		
	0.10 ^b	0.20	0.30	0.10 ^b	0.20	0.30
-0.2	0.213	0.339	0.477	0.093	0.282	0.409
-0.4	0.311	0.313	0.437	0.237	0.280	0.405
-0.6	<u>0.333</u>	<u>0.571</u>	0.494	<u>0.248</u>	<u>0.519</u>	0.450
-0.8	0.328	0.569	0.685	0.239	0.515	0.643
-1.0	0.323	0.568	<u>0.687</u>	0.235	0.515	<u>0.644</u>
-1.2	0.319	0.566	0.685	0.231	0.511	0.642
-1.4	0.315	0.563	0.684	0.234	0.508	0.641

^a Genetic gains are expressed as the proportions of expected genetic gains in aggregate genetic merit to the maximum genetic gain in each data set without any constraint (3.791 in JS-Data and 3.379 in BMS-Data). The highest gains are underlined.

^b Constraint on mating frequency of sires.

Table 3. Expected genetic gains and inbreeding level found by genetic algorithm

	JS-Data				BMS-Data			
	Current ^a	0.10 ^b	0.20	0.30	Current ^a	0.10 ^b	0.20	0.30
AGM	2.578	1.261	2.163	2.603	3.407	0.838	1.753	2.176
JS, point	0.878	-0.042	-0.025	-0.022	0.568	0.092	0.124	0.118
AFC, mo	-0.131	-0.002	-0.075	-0.131	-0.068	-0.033	-0.102	-0.161
ACI, mo	-0.082	-0.035	-0.067	-0.072	-0.058	-0.045	-0.078	-0.082
CW, kg	-9.012	5.695	9.581	14.564	-7.540	4.797	8.488	13.625
LMA, cm ²	0.915	0.746	0.826	0.956	1.282	0.528	0.637	0.775
RT, cm	-0.022	-0.065	-0.081	-0.022	0.017	-0.086	-0.104	-0.047
SFT, cm	-0.395	-0.146	-0.187	-0.074	-0.402	-0.144	-0.191	-0.078
BMS, unit	0.192	-0.005	0.080	0.187	0.301	-0.056	0.024	0.130
Inbreeding level		0.012	0.010	0.007		0.014	0.012	0.010
Minimum		0.000	0.000	0.000		0.000	0.000	0.000
Maximum		0.043	0.039	0.051		0.060	0.047	0.062

AGM : aggregate genetic merit, JS : judging score, AFC : age at first calving, ACI : average calving interval, CW : carcass weight, LMA : *longissimus* muscle area, RT : rib thickness, SFT : subcutaneous fat thickness, BMS : beef marbling score (0 to 5).

^a Current genetic merit after selection.

^b Constraint on mating frequency of sires.

BMS-Data compared with the maximum gains. The degree of decrease would be influenced by the differences of AGM between the best sire and the others. On the other hand, diversity indices of sires given in Table 4 increased from 0 attained when using only one sire to 0.7214 in JS-Data and to 0.7249 in BMS-Data. Therefore determination of the constraint on mating

frequency is the tradeoff between genetic gain and diversity of the population.

Tables 3 and 4 show expected genetic gains by GA in the traits considered and mating frequency of sires, respectively, obtained from the highest gains which are underlined in Table 2. Gains in CW, LMA, and BMS favorably increased with the increase in mating

Table 4. Aggregate genetic merit (AGM), mating frequency of sires, and average additive relationships with dams ($\bar{a}$)

	AGM	JS-Data				BMS-Data			
		$\bar{a}$	0.10 ^a	0.20	0.30	$\bar{a}$	0.10 ^a	0.20	0.30
Sire 1	10.037	0.003	0.1000	0.2000	0.3000	0.004	0.1000	0.2000	0.3000
Sire 2	7.068	0.111	0.0975	0.2000	0.3000	0.112	0.1000	0.2000	0.3000
Sire 3	6.735	0.162	0.1000	0.1975	0.3000	0.174	0.1000	0.2000	0.2925
Sire 4	5.948	0.092	0.1000	0.2000	0.0925	0.087	0.1000	0.1950	0.0975
Sire 5	4.885	0.123	0.1000	0.1550	—	0.114	0.0975	0.1675	0.0050
Sire 6	4.651	0.160	0.0975	0.0125	—	0.167	0.0925	0.0100	—
Sire 7	4.066	0.002	0.0875	0.0300	0.0050	0.002	0.0975	0.0175	0.0050
Sire 8	3.804	0.071	0.1000	—	0.0025	0.068	0.0975	0.0075	—
Sire 9	3.336	0.152	0.0975	—	—	0.155	0.0900	0.0025	—
Sire 10	1.343	0.100	0.0425	—	—	0.095	0.0525	—	—
Sire 11	1.283	0.154	0.0125	0.0025	—	0.164	0.0150	—	—
Sire 12	1.275	0.088	0.0475	—	—	0.081	0.0425	—	—
Sire 13	0.756	0.092	0.0125	0.0025	—	0.087	0.0075	—	—
Sire 14	-0.208	0.138	0.0050	—	—	0.144	0.0050	—	—
Sire 15	-2.209	0.112	—	—	—	0.098	0.0025	—	—
Diversity index			0.9094	0.8159	0.7214		0.9100	0.8135	0.7249
Effective number			11.0375	5.4318	3.5894		11.1111	5.3619	3.6350

^a Constraint on mating frequency of sires.

frequency. However RT and SFT did not correspond to constraint values. Because the GA did not work on each component trait separately, some traits might change unfavorably in some cases. It is affected by PBV (components of AGM) of sires mainly utilized in each constraint value. Gains in reproductive traits were consistently favorable in both data sets. This suggests that mating designs based on carcass traits, which have no bad influence on reproductive traits, can be made up in this prefecture. Of course, it depends on genetic (co) variance structure in a given population and merits of the component traits of individual sires.

Genetic gains by GA in BMS, the main breeding objective in Japanese Black cattle, were higher in JS-Data than in BMS-Data (Table 3). The average PBV of BMS in 15 sires and 574 dams was 0.195. After the selection based on PBV, however, the averages were 0.192 in JS-Data and 0.301 in BMS-Data. Thus selection

differentials of -0.003 and 0.106 in JS- and BMS-Data were obtained, respectively. These differences would contribute to the gains at the next generation, and GA was used to add extra gains on them. Hence, total gains (*i.e.*, gain by selection and gain by GA) in BMS at constraint of mating frequency 0.30 were 0.184 and 0.236 in JS- and BMS-Data, respectively. In the practical selection of Japanese Black dams, the evaluation based on phenotypic JS has been conducted, and nowadays it is shifting to PBV of carcass traits, especially to BMS. Selection by BMS plus GA was expected to produce 28.3% more gain in BMS than selection by JS plus GA nevertheless selection intensity was very low.

Numbers of sires utilized were 14 in JS-Data and 15 in BMS-Data at constraint of mating frequency 0.10 as shown in Table 4. As expected, diversity index and effective number of sires decreased as the constraint value was weakened. The sire with the highest AGM

(Sire 1) had low average relationships with dams. Therefore as Sire 1 was utilized more intensively, the expected inbreeding level decreased (Table 3).

Under all constraint values the GA found the solutions and could designate the mating design. The GA should be applicable to practical breeding situation where AI or a nucleus breeding scheme have been employed. Using linear or quadratic programming techniques of Toro and Pérez-Enciso¹⁶⁾ and Klieve *et al.*⁹⁾ gave similar information. Those techniques are computationally demanding and require the constraint function to be linear. However, the GAs require no condition, and if necessary any constraint can be added once the fitness is expressed. Constraint values can be easily determined by breeders themselves according to given population structures. However the choices of appropriate operator values are important to operate GAs properly. Since no theoretical method to choose the values is developed, they should be determined empirically. Although this is one of the weak points of GAs, the advantage of GAs is that these operators make GAs applicable to various kinds of data structures. Of course other searching algorithms can be used to optimize mating design. The uniqueness of hill climbing or simulated annealing for GAs is discussed by Michalewicz¹¹⁾, and the algorithms must be effective to find global maximums.

The present research can be one solution to the problems the cattle breeders are confronted today. However it dealt with mating design for optimizing the genetic gains and inbreeding levels in the next generation. Evaluation and selection methods also have large influences on accumulation of inbreeding, and negative impact of the accumulation is more serious in long-term. Many studies have been conducted on these issues^{2,15,17)}, and GA can be combined with those methods to deal with long-term selection and mating.

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遺伝的アルゴリズムによる集団の近交度ならびに種雄牛の 供用頻度に制限を加えた交配計画の最適化

大山憲二・向井文雄*

神戸大学大学院自然科学研究科, 神戸市灘区 657-8501

* 神戸大学農学部, 神戸市灘区 657-8501

育種価予測値による選抜が普及するにつれ、近交度を抑制し改良量を最大にする交配計画の重要性はますます大きくなることが予想される。しかしながら、次世代の近交度のみを考慮すれば、血縁関係の薄い特定の種雄牛に供用が集中し、中・長期の育種改良に弊害が生じる危険性がある。したがって本報では、現実の集団の育種価予測値 (PBV) を用い、集団の近交度、種雄牛の供用頻度および個々の後代の近交係数に制限を加えた交配計画の最適化を遺伝的アルゴリズム (GA) により試みた。最適化の対象とした牛群は、種雄牛 15 頭および繁殖雌牛 574 頭からなっており、この牛群の繁殖雌牛に対して審査得点の PBV (JS-Data) あるいは脂肪交雑評点の PBV (BMS-Data) により 400 頭の選抜を行った。交配計画により改良対象とした形質は枝肉 5 形質、審査得点ならびに繁殖能力 2 形質を総合した遺伝的水準 (AGM) とした。ただし、枝肉形質以外には重み付けを行わず、枝肉形質を主体とした交配の影響を考察するとどめた。両データで制限をまったく加えない交配計画を探索したところ、1 頭の種雄牛に供用が集中したが、種雄牛の供用頻度を 0.30 に制限した場合でも、制限を加えない場合と比較して AGM の改良量は JS-Data および BMS-Data でそれぞれ 31.3% および 35.6% 小さくなる程度にとどまった。交配計画に起因する脂肪交雑評点の改良量は JS-Data の方が大きかったものの、選抜に起因する改良量では BMS-Data の方が大きく、脂肪交雑評点の合計の改良量では BMS-Data が 28.3% 大きな改良量を示した。また、GA は設定したすべての制限値の下で交配計画の決定に成功し、3 つの制限に対応できることが認められた。

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