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Maximizing Genetic Response in Breeding Schemes of Dairy Cattle with Constraints on Variance of Response

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ABSTRACT

Predicted genetic progress in dairy cattle breeding schemes was maximized with the variances of selection responses constrained, i.e., restricted effective population sizes. This restriction would also lead to schemes with acceptable rates of inbreeding (<.5%/yr).

If the required coefficient of variation of the annual selection response was reduced from .32 to .16, numbers of animals selected, openness of schemes, and generation intervals increased. When elite cows produced 8 offspring annually, this reduction of the coefficient of variation tended toward a conventional progeny-testing scheme. If the number of donor cows was optimized, responses increased $\leq 2\%$, and the breeding schemes became virtually closed. Variances of responses were reduced by selecting fewer, but proven, bulls, as is done in hybrid multiple ovulation and embryo transfer schemes, which select progeny-tested bulls and young elite cows.

In spite of the constrained coefficients of variation, maximized genetic gains were high and were only reduced from .300 to .293 genetic standard deviations per year, when coefficients of variation were reduced from .32 to .16. Adoption of breeding schemes with low coefficients of variation is recommended, because responses are high and coefficients of variation are sensitive to accidental changes in the breeding structure.

(**Key words**: breeding schemes, restricted maximization of selection response, variance of selection response, simulated annealing)

Abbreviation key: MOET = multiple ovulation and embryo transfer.

INTRODUCTION

Optimization of breeding schemes of dairy cattle has generally been for increased genetic gain with only an implicit restriction on the risk of the breeding scheme (2, 3, 11, 13, 16). Components of this risk are variance of the response and inbreeding, which both increase as the numbers of sires selected decrease. For this reason, the restriction most commonly and most easily applied has been to fix the number of sires selected annually prior to beginning the optimization. However, annual rates of inbreeding and variance of response are also affected by generation intervals, accuracy of selection, coselection of sibs, and the number of dams selected. The introduction of MOET (multiple ovulation and embryo transfer) (16) and BLUP (7) has led to the development of a variety of schemes that differ greatly in some or all of these aspects. Optimization of breeding schemes that have an explicit constraint on variance of response or inbreeding and that do not fix a priori the number of sires selected is therefore very much needed. Woolliams (20), Woolliams and Wilmut (23), and Quinton et al. (18) constrained rates of inbreeding when comparing mating designs, new technologies, and BLUP with phenotypic selection, respectively.

The debate on the selection of young versus older animals or, equivalently, MOET versus

progeny-testing schemes is still open if schemes are compared at equal rates of inbreeding or by variances of responses. Nicholas and Smith (16) found increases in genetic gain of ≤50% when they compared MOET schemes with conventional progeny-testing schemes. This increase in genetic gain was mainly due to the markedly reduced generation intervals. However, with selection of a constant number of animals per year, inbreeding is proportional to the reciprocal of the squared generation interval because, when generation interval is smaller, fewer animals per generation are selected, and more selection cycles are undertaken per unit of time. Other compounding effects occur from the selection of younger bulls because selection is often based on indices containing only family information, which increases the probability of coselection of siblings (24). To compare MOET schemes and conventional progeny-testing schemes at equal rates of inbreeding or variances of responses, more animals should be selected in the MOET schemes, which decreases their rates of genetic gain.

Nicholas (15) argued that obtaining acceptable variation of responses forms a more stringent restriction on effective population sizes than does obtaining acceptable rates of inbreeding. Depending on the degree of risk aversion, coefficients of variation of the re-

sponse of 10 yr of selection of .05 to .10 and annual rates of inbreeding of .005 were considered to be acceptable. For an adult MOET scheme, Nicholas (15) found that the former constraint led to effective population sizes of 100 to 400 and the latter to 27 animals per generation. Hence, schemes that satisfy constraints on variance of response implicitly lead to acceptable rates of inbreeding, but the converse may not be true.

The aim of this study was to maximize selection response in breeding schemes of dairy cattle with an explicit constraint on its coefficient of variation. Optimization is for the number of animals selected, the ages at which selection takes place, and the openness of the nucleus. Open and closed nucleus schemes, with and without progeny testing of young bulls, were considered. In this optimization, open nucleus schemes with progeny testing of young bulls and selection of (few) old animals represent the conventional progeny-testing schemes.

MATERIALS AND METHODS

Breeding Schemes

The parameters of the breeding schemes are given in Table 1. Selection is for lactation production, an aggregate trait that might in-

TABLE 1. Parameters of the breeding schemes.

Size of nucleus, no. neonates/yr	256 ♂ + 256 ♀
Size of base (commercial cow population)	1,000,000
Test daughters per progeny-tested bull, no.	100
Progeny per elite dam, no./yr	8 or optimized[1]
Age classes available for selection of sires and dams, yr	2–10
No. selected in path	
Sires to breed nucleus replacements, no.	optimized
Sires to breed base replacements	same sires as those to breed nucleus replacements
Dams to breed nucleus replacements, no.	64 or optimized
Dams to breed base replacements	random selection
Parameters of milk production	
Heritability	.25
Repeatability	.40
Genetic correlation between lactation records	1
Involuntary culling	
Bulls, %	0[2]
Cows, %/yr	30

[1]Optimized indicates that the number of offspring per elite cow is not restricted as may be the case with in-vitro maturation and fertilization techniques (5).

[2]Semen supplies take over the role of a deceased bull.

clude milk, fat, and protein yield. The categories of breeding schemes considered were category 1, closed nucleus without progeny testing and with 8 progeny per elite dam; category 2, as category 1 but with progeny testing; category 3, as category 2 but with an open nucleus; categories 4, 5, and 6 repeated categories 1, 2, and 3 with the restriction on the number of offspring per elite dam removed completely and allowing an unlimited number of offspring per elite dam. In this context, "unlimited" means that the nucleus replacements can be produced by very few females, which becomes feasible with in vitro maturation and in vitro fertilization or other techniques in the future (5). In these latter categories, the optimized number of elite dams selected might be smaller than the optimized number of sires, which leads to the mating of several bulls to the same cow and a maternal half-sib family structure. If the number of sires is larger than the number of cows, several cows are mated to the same bull, and a paternal half-sib family structure results.

The same sires were selected to breed nucleus and base replacements to reduce the size of the optimization problem. If the number of sires selected is very low, selection of a few more sires to breed the 1,000,000 base replacements will probably decrease rates of genetic gain only marginally. Involuntary culling of sires was neglected, because stored semen can take over the role of a deceased bull. In the path of males to breed base replacement, this assumption may be somewhat optimistic, but, in practice, involuntary culling rates of bulls are low. The selection response in the path of dams to breed base replacement was assumed negligible because of the high proportion of cows selected in this path and because selection is not only for breeding value estimates of lactation production in commercial herds.

The Optimization Algorithm: Simulated Annealing

The method of simulated annealing is particularly useful for large problems of combinatorial optimization, which consist of finding, from among a set of alternatives, one that maximizes the value of an objective function (17). The present problem is combinatorial because the optimal combination of numbers of animals selected from each age class has to be found. Selection of 0, 1, 2, . . ., or 512 bulls from each age class is possible. Nine age classes are eligible for selection (age classes 2, . . ., 10); hence, the total number of possible combinations of predefined numbers of animals selected per age class is $513^9 - 1$. If the number of dams to select from each age class is also to be optimized, the number of combinations is approximately squared in a closed scheme and more than cubed in an open scheme. Hence, the combinatorial problem is very large indeed. This problem is usually solved by applying the same truncation point across age classes for the selection of the predefined number of animals, such as in the work of Meuwissen (11). This procedure may lead to large coefficients of variation and requires a predefined total number of animals selected.

The simulated annealing algorithm has an analogy in physics that is described here because it aids understanding of the process and introduces some of the terminology that has become associated with the algorithm. Annealing refers to the slow cooling of metal in order to harden it (17). During this process, the atoms find their optimal positions to achieve a state of minimum energy. At the beginning, individual atoms move in all directions, which may either increase or decrease the energy, but, as temperature decreases, directions that increase energy become less probable. In this way, the order with minimum energy is found for billions of atoms.

This optimization process, which occurs in nature, is simulated by the present algorithm. An objective function, Ω, which is to be minimized, is defined, and an initial solution is generated. In the case of cooling of metal, the objective function is the energy level, and a solution refers to the position of each atom. In the present case, a solution represents the number selected from each age class. At each iteration, a small random modification to the current solution is suggested (a change in the position of a single atom). If the modification decreases the object function, it is accepted and replaces the current solution. Otherwise, the modification is accepted with a probability that depends not only upon how much poorer the solution is but also upon an imaginary temperature; the poorer the modification is,

and the cooler the temperature, the less likely the modification is to be accepted. The probability that a change is accepted is from the Boltzmann probability distribution of a system (e.g., metal) being at a certain level of energy (17) and is

$$P_{acc} = \exp(-\Delta\Omega/T)$$

for $\Delta\Omega > 0$, and

$$P_{acc} = 1$$

for $\Delta\Omega \leq 0$,

where P_{acc} = probability of accepting the modification, $\Delta\Omega$ = change of the object function value, and T = imaginary temperature, which was initially set to .03. This initial value of T is of the same order of magnitude as the changes in genetic gain because of modifications, which leads to acceptance of most initially suggested modifications. As in results of Press et al. (17), the imaginary temperature was multiplied by .9 each time 20 or 40 modifications (10% of the number of age classes) were accepted for closed and open schemes, respectively. The optimal solution is found when the solution is not changed during 200 or 400 suggested modifications, respectively. If the solution does not change further, the current solution is very unlikely to be improved upon, and the temperature has reached a sufficiently low value.

In the present case, we want to maximize expected genetic gain, E(ΔG), which is identical to the problem of minimizing –E(ΔG). To apply the algorithm, we take a solution to be the number selected from each age class. Modifications to solutions were chosen at random from the following three: 1) select one additional animal from a selection path and age class chosen at random, 2) decrease the number of animals selected by one in a selection path and age class chosen at random, and 3) perform modifications 1 and 2 simultaneously for two age classes and one selection path chosen at random. Modification 3 changes the distribution of the animals selected for a selection path and keeps the total number of animals selected the same. This modification is required because an improvement in the objective function might result even though the single component changes, one of type 1 and

the other of type 2, may both decrease the objective function.

The objective function is chosen such that, in the optimal scheme, genetic gain is maximized, and the coefficient of variation of the response does not exceed CV_c (the critical coefficient of variation):

$$\Omega = -E(\Delta G),$$

if $V(\Delta G) \leq CV_c^2 \, E^2(\Delta G)$, and

$$\Omega = -E(\Delta G) + k(V(\Delta G) - CV_c^2 \, E^2(\Delta G)),$$

if $V(\Delta G) > CV_c^2 \, E^2(\Delta G)$, where $E(\Delta G)$ and $V(\Delta G)$ = expectation and variance of genetic gain, respectively, and k = large positive constant. In the present study, k = 10,000 was sufficiently large to give only coefficients of variation of optimized schemes $\leq CV_c$.

The simulated annealing algorithm is not guaranteed to find the global optimum, but the algorithm does not converge rapidly to an unfavorable local optimum as many other optimization techniques do (17). Generally, the algorithm finds a solution that is close to optimum, and significantly better solutions are unlikely to be found.

The Model

The basic model used was that of Meuwissen (13). In that model, the optimization of generation intervals maximized genetic gain, and improvement at each stage depended on the genetic gain achieved, which made an iterative algorithm necessary for calculating genetic gains. The optimization of the generation interval part of the model was omitted here, because generation intervals are defined by the annealing algorithm, which made possible faster calculation of E(ΔG) and V(ΔG). Also, fast calculation of E(ΔG) and V(ΔG) was necessary because the annealing algorithm required many evaluations of E(ΔG) and V(ΔG).

Let I_{xi} denote the selection index for animal category x and age class i, where each age class contains 1 yr, and categories of animals are SN, DN(N), DN(B), SB, and DB, which denote, respectively, sires to breed nucleus replacements, dams to breed nucleus replacements selected from the nucleus, DN selected from the base, sires to breed base replace-

ments, and dams to breed base replacements. Age class i is defined such that a selected animal in age class i will have offspring when it is i yr old (selected animals in age class i have a generation interval of i yr). The selection indices combine records available on the individual, its progeny, half- and full siblings, its parents, their half- and full sib, and its grandparents. Separate indices were calculated for males and females within each age class, within nucleus and base. Within sex, age, and tier classes, the same amount of information was assumed to be available for each individual. The extent of the information that was included enables the indices to approximate BLUP closely.

Mean values of selection indices of the selected animals were from

$$I_x = \Sigma_i c_{xi} \bar{I}_{xi} \; \sigma_{Ixi}(\infty),$$

where summation is over all age classes i of animal category x; c_{xi} = contribution of age class i to the animal category x, which is from the annealing algorithm; $\bar{I}_{xi}$ = selection intensity, which is corrected for finite population size and correlations between breeding value estimates of half- and full sibs (12); $\sigma_{Ixi}^2(t)$ = variance of the selection index of animal category x and age class i in yr t. $\sigma_{Ixi}^2(\infty)$ = equilibrium variance, which is reduced because of selection (1). Equilibrium variances are obtained from $\sigma_{Ixi}^2(\infty) = \sigma_a^2(\infty) - PEV_{xi}$, where $\sigma_a^2(\infty)$ = equilibrium additive genetic variance and PEV_{xi} = prediction error variances of estimated breeding values. Values of $\sigma_a^2(\infty)$ are obtained by a few iterations on formulas of Bulmer (1) until successive values converge. Because prediction error variances (PEV) are not affected by selection (6), $PEV_{xi} = \sigma_a^2(0) - \sigma_{Ixi}^2(0)$, where 0 denotes the unselected founder population.

With generation intervals defined by the annealing algorithm, genetic gains of open nucleus schemes are predicted by (11):

$$E(\Delta G) = \Sigma \bar{I}/\Sigma \bar{L} =$$

$$\frac{\bar{I}_{SN} + f_{NN}\bar{I}_{DN(N)} + (1 - f_{NN})(\bar{I}_{DN(B)} + \bar{I}_{SB} + \bar{I}_{DB})}{\bar{L}_{SN} + f_{NN}\bar{L}_{DN(N)} + (1 - f_{NN})(\bar{L}_{DN(B)} + \bar{L}_{SB} + \bar{L}_{DB})}$$

[1]

where $E(\Delta G)$ = expected steady state selection response; $\bar{L}_x$ = mean generation interval of selected animals of animal category x, respectively; and f_{NN} is the fraction of DN selected from the nucleus. If $f_{NN} = 1$, this equation reduces to the well-known formula for closed nucleus schemes: $E(\Delta G) = [\bar{I}_{SN} + \bar{I}_{DN(N)}]/[\bar{L}_{SN} + \bar{L}_{DN(N)}]$. And, with $f_{NN} = 0$, the formula for a progeny-testing scheme is obtained: $E(\Delta G) = [\bar{I}_{SN} + \bar{I}_{DN(B)} + \bar{I}_{SB} + \bar{I}_{DB}]/[\bar{L}_{SN} + \bar{L}_{DN(B)} + \bar{L}_{SB} + \bar{L}_{DB}]$ (19).

The approach of Johnson (10) was followed to derive a formula for the variance of the selection response $V(\Delta G)$. Let z_t denote a vector of length 20 with mean genetic merits of the first 10 age classes (age classes >10 yr are neglected) in the nucleus and the base at year t, and let $z_t(1)$ and $z_t(11)$ denote the first nucleus and base age class, respectively. Further, let s_t denote a vector with genetic selection differentials, which can be obtained by weighting the I_x values over categories of selected animals. The exact form is not important here. The vector z_{t+1} can be expressed in parameters of year t:

$$z_{t+1} = Pz_t + s_t + e_t, \text{ for } t \geq 1, \quad [2]$$

where P = a matrix that describes the flow of genes from year t to t + 1 (8), and e_t = deviations from the expected genetic level because of sampling. For an open nucleus scheme, the gene flow matrix $P' = [p_N \; u_1 \; u_2 \; .. \; u_9 \; p_B \; u_{11} \; u_{12} \; .. \; u_{19}]$, where p_N = vector of contributions all nucleus and base age classes to nucleus ($p_N(i) = \frac{1}{2}(c_{SNi} + f_{NN}c_{DN(N)i})$, for $1 \leq i \leq 10$; $p_N(i) = \frac{1}{2}(1 - f_{NN})c_{DN(B)i}$, for $11 \leq i \leq 20$); p_B = vector of contributions all nucleus and base age classes to base ($p_B(i) = \frac{1}{2}c_{SBi}$, for $1 \leq i \leq 10$; $p_B(i) = \frac{1}{2}c_{DBi}$, for $11 \leq i \leq 20$); and u_i = vector with all zeros and a 1 at position i.

The variance-covariance matrix of e_t is denoted by V_e and has only nonzero elements at positions (1,1), (11,1), (1,11), and (11,11). Elements $V_e(i,i)$, with $2 \leq i \leq 10$ or $12 \leq i \leq 20$, are assumed to be zero because the mean merit of age class i - 1 in year t - 1 is approximately equal to that of class i in yr t, if culling is not correlated with lactation yield. Similarly, $V_e(i,j) = 0$, where $2 \leq i \leq 10$ or $12 \leq i \leq 20$ and $1 \leq j \leq 20$. From Meuwissen (13),

$$V_e(1,1) = \frac{Var(\Sigma_i TBV_{SNi})}{4n_{SN}^2} + \frac{Var(\Sigma_i TBV_{DNi})}{4n_{DN}^2}$$

$$+ \frac{Cov(\Sigma_i TBV_{SNi} \Sigma_i TBV_{DNi})}{2n_{SN}n_{DN}} .$$

where TBV_{xi} = true breeding value of animal i selected for category x; and n_x = number of animals selected for category x. The value of $V_e(11,11)$ is calculated similarly with SN and DN replaced by SB and DB. Further,

$$V_e(1,11) = \frac{Cov(\Sigma_i TBV_{SNi} \Sigma_i TBV_{SBi})}{4n_{SN}n_{SB}}$$

$$+ \frac{Cov(\Sigma_i TBV_{SNi} \Sigma_i TBV_{DBi})}{4n_{SN}n_{DB}}$$

$$+ \frac{Cov(\Sigma_i TBV_{DNi} \Sigma_i TBV_{SBi})}{4n_{DN}n_{SB}}$$

$$+ \frac{Cov(\Sigma_i TBV_{DNi} \Sigma_i TBV_{DBi})}{4n_{DN}n_{DB}} .$$

Evaluation of, for instance, $Var(\Sigma_i TBV_{SNi})$ requires calculation of

$$Cov(TBV_{SNi};TBV_{SNj}) =$$

$$Cov(I_{SNi};I_{SNj}) + PEC_{SN;i,j}, \qquad [3]$$

where $PEC_{SN;i,j}$ = prediction error covariance of i and j. The terms in Equation [3] depend on the family relationship of the selected sires i and j. Only full and half-sib relationships are considered. Selection of animals within an age class was based on expected order statistics of their selection index values (13). If this selection led to the coselection of full or half-sibs, the $Cov(I_{SNi};I_{SNj})$ and $PEC_{SN;i,j}$ of full or half-sibs, respectively, were used in Equation [3]. The other terms, $V_e(1,1)$, $V_e(1,11)$, and $V_e(11,11)$, were calculated similarly.

Because e_t in Equation [2] represents the variable part of selection response, $Var(z_{t+1}) = Var(\Sigma_{i=0}^t P^i e_i)$. Hence, $Var(z_{t+1} - z_t) = Var(P^t e_t) = P^t V_e P'^t$. Hill (8) shows that $\lim_{t\to\infty} P^t = qv'/(2\Sigma\bar{L})'$, where $\Sigma\bar{L}$ is as defined by Equation [1], v is the left eigenvector of P

associated with its largest eigenvalue, and q is a vector of ones. The variance of the steady-state selection response is $\lim_{t\to\infty} Var(z_{t+1} - z_t)$ $= \lim_{t\to\infty} P^t V_e P'^t = \frac{1}{4}(\Sigma\bar{L})^{-2} v'V_e v^* qq'$; hence, the variances of all elements of z_t increases at the same rate, which is the variance of the selection response. Prediction of the nonzero elements (1,1), (1,11), (11,1), and (11,11), of V_e has been described; hence, only the elements v(1) and v(11) are still required to calculate $v'V_e v$. Following a method of Hill (8), v(1) = 1, and v(11) = (1 - f_{NN}). Consequently, the steady-state variance of the selection response is

$$V(\Delta G) = \frac{1}{4}(\Sigma\bar{L})^{-2} (V_e(1, 1)$$
$$+ 2(1 - f_{NN})V_e(1,11)$$
$$+ (1 - f_{NN})^2 V_e(11,11)). \qquad [4]$$

Predicted variances of responses from this formula were virtually identical to the converged steady-state variances obtained from the model of Meuwissen (13). Computing times were much reduced if Equation [4] was used, which was desirable because many evaluations of $V(\Delta G)$ were required.

The correction of selection differentials for correlations between expected breeding values of full and half-sibs by the method of Meuwissen (12) requires a hierarchical breeding structure; i.e., each male is mated to several females, leading to a paternal half-sib family structure, or each female is mated to several males, leading to a maternal half-sib family structure. Input parameters for this method are the fraction selected, the number of half-sib families (n_{HS}), the number of full-sib families per half-sib family (n_{FS}), the number of males (or females) within a full-sib family (n_w), and intraclass correlations between full and half-sibs. With a paternal family structure, n_{HS} = the number of sires selected, n_{FS} = the number dams divided by the number of sires, and n_w = the total number of males (or females) divided by the number of dams. If n_{FS} and n_w were noninteger, n_{FS} and n_w were rounded to their nearest integer. Rounding only affected the family structure; fractions selected were not affected, hence, approximately accounting for the effect of family structure on intensities of selection.

RESULTS

We did not attempt to optimize the parameters of the annealing algorithm, e.g., start temperature, number of modifications within each temperature step. The number of evaluations of breeding schemes was large: 2000 to 4000 for closed nucleus and 7000 to 10,000 for open nucleus schemes. For a few schemes, the optimization was performed twice, and numbers of animals selected differed by ≤ 2 (results not shown). Solutions were not identical because suggested modifications were sampled at random. Genetic gains of the alternative schemes differed by <.1%.

The coefficient of variation of the annual selection response was restricted to .32 or .16; thus, the coefficient of variation of the response of 10 yr of selection was .1 or .05, respectively (CV(t) = CV(1)/$\sqrt{t}$, where CV(t) is coefficient of variation of responses of t year of selection). These figures were chosen because they had also been considered by Nicholas (15). The coefficient of variation of the optimized breeding schemes was, in all but one scheme, very close to its constraints.

Table 2 shows the results of the optimization for the schemes for which the number of elite cows to breed nucleus replacements was fixed at 64 with 8 progeny per elite cow. If the coefficient of variation was reduced from .32

to .16, expected genetic gains decreased by 11 and 5% for closed nucleus schemes without and with progeny tests, respectively. In the scheme without progeny testing, the reduction of the coefficient of variation was mainly achieved by increasing the number of sires selected; in the scheme with progeny testing, generation intervals were also increased. Paradoxically, this increase resulted in a smaller reduction in genetic gain in the progeny-testing schemes because the necessary changes in the number of bulls selected was less dramatic.

In the open nucleus schemes, the reduction of the coefficient of variation decreased response only 3% (Table 2). These schemes used the same means as the closed scheme with progeny testing but were more open, i.e., smaller f_{NN}. Variation of response decreased with decreasing f_{NN}, because ΣL in Equation [3] became substantially larger (see Equation [1]). By decreasing f_{NN}, the genetic gain in open nucleus schemes was reduced less than in closed schemes (Table 2). Table 3 shows the number of animals selected annually from each age class and path in the open nucleus scheme. The exact number of animals selected from each age class is of less interest than the qualitative changes in the age structure of selected animals when the coefficient of variation constraint is changed. The number of selected bulls that were progeny-tested (age

TABLE 2. The maximized expected response and corresponding structure of breeding schemes with 64 elite cows to breed nucleus replacements, for different required coefficients of variation (CV$_c$).

CV$_c$	E(ΔG)[1]	CV(ΔG)	N$_{SN}$[2]	L$_{SN}$[3]	L$_{DN}$[3]	f$_{NN}$[4]
	Closed nucleus without progeny testing of young bulls					
.32	.294	.316	12	2.7	2.3	1
.16	.262	.160	44	3.7	2.7	1
	Closed nucleus with progeny testing of young bulls					
.32	.297	.287	13	2.9	2.2	1
.16	.281	.160	20	4.3	2.4	1
	Open nucleus with progeny testing of young bulls					
.32	.300	.315	6	3.0	2.1	.67
.16	.293	.160	19	3.5	2.2	.47

[1]Expected genetic gain in σ_{a0}-units per year.

[2]Number of sires to breed nucleus replacements selected. In open nucleus schemes, N$_{SN}$ equals also the number males to breed base replacements.

[3]Generation intervals of sires to breed nucleus replacements (L$_{SN}$) and dams to breed nucleus replacements (L$_{DN}$) in year.

[4]The proportion of females to breed nucleus replacements that are selected from the nucleus.

TABLE 3. The number of animals selected per age class in an open nucleus scheme with progeny testing and 64 elite dams, when expected selection response is maximized for different required coefficients of variation (CV_c).[1]

	SN[3]		DN(N)[3]		DN(B)[3]	
Age class[2]	CV_c = .32	CV_c = .16	CV_c = .32	CV_c = .16	CV_c = .32	CV_c = .16
2	4	8	36	24	21	31
3	0	1	5	4	0	0
4	1	7	2	2	0	3
5	0	0	0	0	0	0
6	1	2	0	0	0	0
7	0	1	0	0	0	0

[1]The maximum number of animals selected per age class is 256 for bulls and follows from the number of neonates and involuntary culling rates for cows.

[2]Age is at birth of offspring of the selected animals.

[3]SN = Sires to breed nucleus replacements; DN(N) and DN(B) = dams to breed nucleus replacements selected from the nucleus and base, respectively.

classes 6 and 7) increased when the coefficient of variation was reduced; however, even with coefficient of variation constraint of .16, the majority of the bulls were young bulls (age class 2 and 3) and sib-tested bulls (classes 4 and 5). The elite cows selected were mainly young heifers. The reduction of the coefficient of variation hardly increased the generation interval for elite cows but increased substantially the number of elite cows selected from the commercial cow population.

When the total number of elite cows was allowed to vary and a paternal half-sib hierarchical structure was imposed, genetic gains increased only 2%. Table 4 shows the results for the three types of breeding schemes under consideration. The increased reproductive rate of elite cows led to nucleus schemes that were virtually completely closed.

When the coefficient of variation constraint was reduced, schemes with progeny testing selected fewer males per year but increased the

TABLE 4. The maximized expected response and corresponding structure of breeding schemes when the number of elite cows required is allowed to vary, for different required coefficients of variation (CV_c).

CV_c	E(ΔG)[1]	CV(ΔG)	N_{SN}[2]	N_{DN}[2]	L_{SN}[3]	L_{DN}[3]	f_{NN}[4]
	Closed nucleus without progeny testing of young bulls						
.32	.297	.320	17	34	3.1	2.4	1
.16	.266	.160	37	75	3.4	2.6	1
	Closed nucleus with progeny testing of young bulls						
.32	.304	.319	16	32	3.3	2.2	1
.16	.288	.160	4	30	6.3	2.3	1
	Open nucleus with progeny testing of young bulls						
.32	.304	.319	16	32	3.3	2.2	1
.16	.291	.159	4	30	6.3	2.1	.97

[1]Expected genetic gain in σ_{a0} units per year.

[2]N_{SN} and N_{DN} = Number of sires and dams to breed nucleus replacements, respectively. In open nucleus schemes, N_{SN} equals also the number sires to breed base replacements. To obtain a paternal half-sib family structure, the condition $N_{SN} \leq N_{DN}$ was enforced.

[3]Generation intervals of sires to breed nucleus replacements (L_{SN}) and dams to breed nucleus replacements (L_{DN}) in year.

[4]The proportion of females to breed nucleus replacements that are selected from the nucleus.

TABLE 5. The number of animals selected per age class in an open nucleus scheme with progeny testing and variable numbers of both bulls and cows, when expected selection response is maximized for different required coefficients of variation (CV_c).[1]

Age class[2]	SN[3]		DN(N)[3]		DN(B)[3]	
	CV_c = .32	CV_c = .16	CV_c = .32	CV_c = .16	CV_c = .32	CV_c = .16
2	8	0	28	27	0	1
3	0	0	3	1	0	0
4	6	0	1	1	0	0
5	0	0	0	0	0	0
6	2	3	0	0	0	0
7	0	1	0	0	0	0

[1]The maximum number of animals selected per age class is 256 for bulls and follows from the number of neonates and involuntary culling rates for cows (see Table 1).

[2]Age is at birth of offspring of the selected animals.

[3]SN = Sires to breed nucleus replacements; DN(N) and DN(B) = dams to breed nucleus replacements selected from the nucleus and base, respectively.

number of progeny-tested bulls (Tables 4 and 5). Without progeny testing, more sires and dams were selected when coefficient of variation constraint was reduced and the genetic gain decreased by 10% compared with the 5% decrease in progress for schemes with progeny testing. Thus, for an open nucleus scheme, a strong constraint on the coefficient of variation and a high reproductive rate of elite cows led to the use of progeny-tested bulls in a virtually closed nucleus scheme. This scheme resembles very closely the hybrid MOET schemes proposed by Colleau (2).

In schemes with unlimited reproductive rates of elite cows, the number of elite cows selected might be smaller than the number of males, which led to maternal half-sib family structures. Evaluations of these schemes were possible by the presented model as long as the mating design was hierarchical and the nucleus was closed. The latter restriction was due to the design of the computer program but was not a severe limitation in practice because schemes with selection of few dams were closed anyway (Table 4).

Table 6 shows the results for the schemes with maternal half-sib families. In the absence of progeny testing, genetic gains were up to 3% higher than that of the schemes with paternal half-sib families mainly because dams in age classes 4 and 5 have higher accuracy of selection than bulls of the same age, which is then combined with a higher intensity of selection of dams in the maternal schemes. Greater rates of gain for maternal than for paternal schemes were also found by De Boer and van Arendonk (3) for adult MOET schemes. The number of animals selected and generation intervals of the maternal schemes are very similar to those of their corresponding paternal schemes; the dams replaced the sires and vice versa. With progeny testing and coefficient of variation constraint of .16, the superior paternal scheme used only a few proven bulls. This scheme resulted in a 4% higher genetic gain of the paternal than the maternal scheme.

DISCUSSION

The number of animals selected and the generation intervals were optimized in breeding schemes that constrained variances of selection responses. This optimization should result in schemes with both acceptable variances of selection responses and acceptable rates of inbreeding. Maximized genetic gains were high, about .3 and .28 to .29 genetic standard deviation units per year, and coefficients of variation were .32 and .16, respectively. These rates of gain were as high as the highest ranking scheme of Meuwissen (13), which had a genetic gain of .299 σ_{a0} units/yr and a coefficient of variation of .66. Hence, the optimization resulted in remarkably high genetic gains when coefficients of variation

TABLE 6. The maximized expected response and corresponding structure of breeding schemes when the number of elite cows required is allowed to vary, for different required coefficients of variation (CV_c).

CV_c	$E(\Delta G)^1$	$CV(\Delta G)$	N_{SN}^1	N_{DN}^1	L_{SN}^3	L_{DN}^3
		Closed nucleus without progeny testing of young bulls				
.32	.305	.319	36	17	2.2	2.9
.16	.271	.160	76	28	2.6	3.5
		Closed nucleus with progeny testing of young bulls				
.32	.307	.320	36	13	2.3	3.1
.16	.276	.160	74	30	2.7	3.3

[1]Expected genetic gain in σ_{a0}-units per year.

[2]N_{SN} and N_{DN} = Number of sires and dams to breed nucleus replacements, respectively. In open nucleus schemes, N_{SN} equals also the number sires to breed base replacements. In order to obtain a maternal half-sib family structure, the condition $N_{DN} \leq N_{SN}$ was imposed.

[3]Generation intervals of sires to breed nucleus replacements (L_{SN}) and dams to breed nucleus replacements (L_{DN}) in year.

were constrained, mainly because the number of animals selected per path was not optimized by Meuwissen (13). Also, Meuwissen's (13) main interest was in MOET schemes with short generation intervals; hence, young nucleus bulls were not progeny tested.

Prediction of genetic gains and its variances ignored inbreeding. At a fixed coefficient of variation of the selection response, the rates of inbreeding would be similar because a close relationship exists between variance of response and inbreeding (9) and rates of gain are similar, and thus the schemes would be affected in the same way. Because rates of genetic gain for schemes with coefficients of variation of .16 and .32 were similar, we might assume that schemes with a coefficient of variation of .16 have reduced rates of inbreeding and that, over the long term, genetic gains would be more favorable than those of schemes with a coefficient of variation of .32.

Woolliams and Meuwissen (21) decreased the variance of the selection response by selecting for estimated breeding values minus a factor k times their prediction error variances, thus penalizing for prediction errors. Variance of response is not only due to prediction errors on breeding value estimates but is also due to Mendelian sampling of genes. The latter is reduced by reducing the number of samplings per unit of time (i.e., increasing generation intervals, or by selecting more animals, which reduces sampling effects). The method of Woolliams and Meuwissen (21)

does not aim at a predefined variance of the response, and it did not optimize the number of animals selected, although it could be easily implemented in practice. The present method could be implemented by using the approximate numbers of animals selected given in Tables 3 or 5, but this method is not optimal because of sampling effects. A sequential optimization rule for controlling risk, such as that of Woolliams and Meuwissen (21), could be more optimal.

The coefficients of variation considered were the same as those considered by Nicholas (15) and cover a substantial range of degrees of risk aversion. In particular, when national breeding schemes are considered, risk aversion seemed reasonable. But, in a competitive situation, a breeding firm may lag behind its competitors, and an increase of the lag may not harm the firm much (e.g., the firm has to buy improved breeding stock anyway). In this case, breeding schemes with high risk may be preferred, because there is at least a chance to outperform the competition, and a criterion regarding the probability of getting a response larger than a certain level is appropriate, as was studied by Dekkers (4). Woolliams and Meuwissen (21) considered risk preference by putting a reward on prediction error variance.

The assertion of Nicholas (15) that the variance of the response forms a more stringent restriction than the rate of inbreeding, may be criticized for two reasons. First, he used the coefficient of variation of the difference be-

tween a selection and a control line for this purpose. The variation of the genetic levels of both lines contributed equally to this variance, but, in practice, no control lines exist, and only the variation of the selected line remains. Thus, variances and effective sizes are halved. Second, Nicholas (15) made implicit use of the formula $V(\Delta G) = 2\Delta F\sigma_a^2$, which assumes random mating and overpredicts the variance of the response when selection is carried out. Meuwissen (13) showed that, in some cases, variance of response was only 42% of that predicted from this formula. Hence, effective sizes required for coefficients of variation of .32 and .16 may be as little as .21 (= .5 × .42) of those given by Nicholas (15), resulting in sizes of 21 and 84, respectively. This population size is of the same order of magnitude as the population size required for annual rates of inbreeding of .005, namely, effectively 27 animals per generation (generation interval is 3.67 yr in an adult MOET scheme). However, this effective size of 27 animals per generation is still rather small to prevent deterioration of fitness (14). In conclusion, if the coefficient of variation constraint is .32, the annual rate of inbreeding is probably about .005, but lower rates of inbreeding might be required. If the coefficient of variation constraint is .16, rates of inbreeding will be substantially lower and, probably, acceptable.

If more than 8 offspring could be obtained from an elite cow, genetic gain increased by 2% (Tables 2 and 4), which is substantially less than the increases predicted in other studies (11, 16, 21) because the variance of the response was restricted here. The variance of the response probably depended more on the actual number of animals selected than on the proportion of the animals selected and thus the selection differentials. Hence, larger nuclei could have both a sufficiently large number of elite cows selected and a small proportion selected, which yield high selection differentials. Therefore, the benefit of high reproductive rates of elite cows increases as nucleus size increases.

In general, the results showed that breeding schemes changed considerably when a more stringent coefficient of variation was required, but genetic gains were not much reduced. To test the robustness of the optimized schemes,

the open nucleus schemes with 8 offspring per elite cow (see Tables 2 and 3) were altered such that all the elite cows selected from the base (DN(B)) were rejected (e.g., did not pass quarantine requirements) and all nucleus progeny were obtained from the selected nucleus animals by increased MOET efforts. This modification hardly affected rates of genetic gain, but coefficients of variation of those animals were increased from .160 to .290 and from .315 to .397 for the schemes in which the coefficient of variation constraint = .16 and .32 schemes, respectively. Hence, the coefficients of variations are much more sensitive to deviations from the optimal schemes than the rates of gain. Because coefficients of variation are sensitive to variations in the breeding scheme and genetic gains are only slightly reduced by decreasing the required coefficients of variation, recommendations to adopt breeding schemes with low coefficients of variation, e.g., .16, seem reasonable.

Strong restrictions on variance of responses and implicitly on rates of inbreeding favored progeny testing of young bulls and open nuclei, which contrasted with the MOET nucleus schemes of Nicholas and Smith (16) that were obtained when higher variances of responses were allowed. High reproductive rates of elite cows favored closed nuclei, which led to hybrid MOET schemes (2). Generally, progeny testing of young bulls proved to be the most effective method to reduce variances of responses and maintaining high rates of genetic gain.

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