Original article

Strategies for controlling rates of inbreeding in MOET nucleus schemes for beef cattle

B Villanueva[1], JA Woolliams[2], G Simm[1]

[1] *Scottish Agricultural College, West Mains Road, Edinburgh, EH9 3JG;*
[2] *Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS, UK*

Summary – A closed MOET (multiple ovulation and embryo transfer) nucleus scheme, with overlapping generations, was modelled for beef cattle by stochastic simulation. Selection was carried out for 25 years on a trait measurable in both sexes and with a heritability of 0.35. Different strategies to control the rate of inbreeding were investigated: 1) decreasing female selection intensity whilst keeping the number of donors constant; 2) culling selected animals after having been used for a period of time; 3) using more donors; 4) using factorial mating designs; and 5) selecting on modified indexes. Comparisons among different schemes were made on the basis of equal number of transfers per year. Strategies 1, 2, and 3 reduced inbreeding but also reduced response. When the schemes were compared at the same level of inbreeding, culling of animals gave higher rates of genetic progress than decreasing selection intensity. Factorial designs decreased the rate of inbreeding by up to 19% in comparison with nested designs, with no effect on response. The most successful strategies were those that reduced the emphasis on family information in the selection criterion and especially selection on estimated breeding values obtained by BLUP (best linear unbiased prediction) using a deliberately increased heritability. With this method, it was possible to reduce inbreeding by up to 30% without affecting genetic progress. The reduction in inbreeding with different raised heritabilities averaged 42% and ranged from 26 to 61%. Under all the strategies studied to control inbreeding, proportional reductions in rates of inbreeding were always higher than those in genetic response.

beef cattle / breeding scheme / MOET / genetic gain / inbreeding

Résumé – **Stratégies pour contrôler la consanguinité dans des schémas de sélection fermés avec transfert d'embryons chez les bovins à viande.** *Un schéma de sélection fermé de bovins à viande, utilisant le système MOET (ovulation multiple et transfert d'embryon), et avec des générations imbriquées, a été soumis à un modèle de simulation stochastique. La sélection pendant 25 ans a porté sur un caractère mesurable dans les 2 sexes et d'héritabilité 0,35. Différentes stratégies pour contrôler le taux de consanguinité ont été examinées : i) réduction de l'intensité de sélection en sélectionnant un nombre plus*

grand de femelles, tout en maintenant un nombre constant de donneuses ; ii) élimination des animaux (donneuses ou pères) après une seule période d'évaluation (6 mois) ; iii) utilisation de plus de donneuses ; iv) utilisation de plans factoriels de croisement ; v) sélection selon des indices modifiés. Des comparaisons ont été faites entre les différents schémas, à nombre égal de transferts par an. Les stratégies iii), ii), i) conduisent à une réduction du taux de consanguinité, mais la réponse aussi est réduite. Quand on compare les différents schémas à niveau égal de consanguinité, l'élimination précoce des animaux donne un taux de progrès génétique plus élevé que la réduction de l'intensité de sélection. Les plans factoriels réduisent le taux de consanguinité d'une quantité pouvant aller jusqu'à 19% par rapport aux plans hiérarchiques, sans aucun effet sur les réponses. La stratégie qui donne les meilleurs résultats est la sélection sur les valeurs génétiques additives obtenues au moyen du BLUP en utilisant une héritabilité délibérément augmentée. Avec cette dernière méthode, la consanguinité est réduite jusqu'à 30% tandis que le progrès génétique reste constant. Une autre stratégie qui réduit le taux de consanguinité consiste à sélectionner sur un indice modifié pour diminuer la contribution de l'information familiale. Dans chacune des stratégies examinées pour contrôler la consanguinité, la réduction proportionnelle de la consanguinité a toujours été plus grande que celle de la réponse.

schéma de sélection / bovin à viande / ovulation multiple et transfert d'embryon / gain génétique / consanguinité

INTRODUCTION

Improved reproductive rates of females through multiple ovulation and embryo transfer (MOET) can lead to an increase in genetic response, due to increased selection intensities and reduced generation intervals. In the absence of the effects of inbreeding, Land and Hill (1975) indicated that the rates of genetic progress for growth rate in beef cattle could be doubled by using MOET in comparison with conventional schemes. Gearheart *et al* (1989) extended these results to different selection criteria and heritabilities and also found increases in genetic responses from MOET. These studies predicted response after a single generation of selection. Stochastic simulations, which have accounted for factors which influence medium or long-term responses, have shown that these theoretical predictions substantially overestimated the advantage of MOET schemes (Wray and Simm, 1990).

Comparisons among alternative breeding schemes have usually been made on the basis of expected rates of genetic progress. However, in practice, breeding schemes are operated with restrictions on rates of inbreeding, either implicitly or explicitly, to limit its negative effects (loss of genetic variation and inbreeding depression). One of the main drawbacks of MOET nucleus schemes is the increased rates of inbreeding resulting from their small population size. Faster inbreeding occurs with any selection scheme involving between-family selection (Robertson, 1961). The larger family sizes created by MOET amplifies this effect. Wray and Simm (1990) have shown that when comparing MOET with conventional beef breeding schemes at the same level of inbreeding, the advantage of MOET in genetic response was reduced to around 50%.

Several strategies have been proposed to control the rate of inbreeding in selection programmes (*eg*, Toro and Perez-Enciso, 1990). All of these strategies have either

direct or indirect effects on restricting the magnitude of the variance of family size and the expected relationship of long-term genetic contribution of ancestors with their breeding value (Wray and Thompson, 1990). For a given number of transfers, the variance of family size is least when all females contribute equally to descendants in subsequent generations. Increasing the opportunity of a female to be used as a donor decreases the variance of family size. This can be achieved by increasing the number of donors used in a period and by culling donors immediately following a designated number of flushes.

Best linear unbiased prediction (BLUP) is generally accepted as the optimum procedure for genetic evaluation. By using all information on relatives, the accuracy of estimating the breeding value is increased. However, selection methods in which the accuracy of prediction is gained by using ancestral information, can lead to higher rates of inbreeding due to the higher probability of selecting related animals (Robertson, 1961). Dempfle (1975) showed that, in the long term, selection within families could give higher selection response than individual selection, mostly due to the maintenance of genetic variability resulting from the increase in effective population size. He showed that, with selection on phenotypes, the advantage of within-family selection increases when the heritability is high and with large families. MOET schemes, with the use of BLUP, benefit progress, in the short term, by increasing family sizes and accuracies. By using a selection criterion in which the weight given to family information is reduced, inbreeding rates might be decreased without greatly affecting response.

Once the selection decisions have been made, the choice of the mating system can also affect the rates of genetic progress and inbreeding. Factorial mating designs, in which each dam is mated to more than one sire, were proposed by Woolliams (1989) for MOET breeding schemes to reduce rates of inbreeding with no loss in response.

In this paper, different strategies to control inbreeding are investigated through Monte-Carlo simulation of a closed MOET beef nucleus herd.

METHODS

Description of simulations

Basic scheme

A MOET nucleus scheme with overlapping generations was simulated for beef cattle. An additive infinitesimal genetic model was assumed. True breeding values of unrelated base animals (9 males and 18 females) were obtained from a normal distribution with mean zero and variance (σ_A^2) 0.35. Phenotypic values were obtained by adding a normally distributed environmental component with mean zero and variance 0.65. Thus, initial heritability was 0.35. Equal numbers of animals of 2, 3 and 4 years of age were simulated. To mimic selection for beef trait, it was assumed that the trait under selection was recorded in both sexes at around 400 d of age (between 385 and 415 d), at the end of a performance test. Selection was carried out for 25 years. The number of breeding males and females (donors) was constant over years and equal to the number of base males and females (9 males

and 18 females). Animals were genetically evaluated twice every year (evaluation period = 6 months). An estimate of breeding value (EBV) was obtained for each animal using an individual animal model-BLUP. The only fixed effect included in the model was the overall mean. All the information available at the time of evaluation was used to obtain the EBVs. Males and females with the highest EBVs were selected. There were no restrictions on the number of sires or dams selected from any one sibship. In the absence of the culling policies described below, animals were selected irrespective of whether they had been selected in previous periods. Animals not selected were culled from the herd.

Values for reproductive parameters (minimum age of donors, frequency of collection and proportion of calves per transfer) were taken from Luo *et al* (1994) and represent the current realistic situation in embryo technologies. Each donor was flushed 3 times in each evaluation period (embryo collections were carried out every 2 months). The number of transferable embryos collected was obtained from a negative binomial distribution (Woolliams *et al*, 1994). The mean number of transferable embryos per flush and per donor was 5.1, with a coefficient of variation of 1.25 and repeatability of 0.23. These values were obtained from analyses of extensive data on embryo recovery (Woolliams *et al*, 1994). Thus, the average number of embryo transfers per year was around 550. All calves were born from embryo transfer, *ie* there were no calves from natural matings. Embryos transferred survived until birth with probability 0.55 and the sex ratio was expected to be 1:1 (sex was assigned at random with probability 0.5). Males were assumed capable of breeding at 12 months of age and females at 15 months of age. At all ages after birth, individuals were subject to a mortality rate that varied with age. The maximum age of the animals was 15 years. Selected donors and sires were randomly mated according to a nested mating design (each donor was mated to the same sire in consecutive flushes, within an evaluation period). Each sire was used the same number of times.

After year zero, true breeding values of the offspring born every year, were generated as

$$TBV_i = (1/2)(TBV_s + TBV_d) + m_i$$

where TBV_i, TBV_s and TBV_d are the true breeding values of the individual i, its sire and its dam, respectively, and m_i is the Mendelian sampling term. The Mendelian term was obtained from a normal distribution with mean zero and variance $(1/2)[1 - (F_s + F_d)/2]\sigma_A^2$, where F_s and F_d are the inbreeding coefficients of the sire and dam, respectively. The inbreeding coefficients of the animals were obtained from the relationship matrix, using the algorithm proposed by Quaas (1976).

Alternative schemes

In order to control rates of inbreeding, several modifications of the basic scheme described in the previous section were considered. The different strategies studied are described below. Unless otherwise stated, the simulations were run as described for the basic scheme. Some combinations of different alternatives were also studied.

Selection intensity in females

The number of selected females in one period was increased from 18 (basic scheme) to 27, 36, 54, 72, 90, 108 and 144. In all cases, only 18 females, chosen at random from these selected females, were used as donors. In this way, the number of transfers was kept constant.

Limited use of selected parents

In a given period, each of the 18 donors was flushed 3 times and was then ineligible for further selection. Culling of males after use in one period was also examined.

Number of donors

At each evaluation period, 27 cows were selected and flushed twice. Thus, on average, the number of embryos was equal to that obtained with 18 donors flushed 3 times.

Mating design

A factorial mating design, in which donors were mated to different sires in consecutive flushes, was also considered. Each selected bull was used the same number of times and randomly assigned to donors.

Selection criteria

Three alternative selection criteria were studied. Firstly for each animal, a modified index ($IND1$) was computed as

$$IND1_i = EBV_i - \lambda_s EBV_s - \lambda_d EBV_d$$

where subscripts i, s and d refer to the individual, its sire and its dam and the EBV_s are those obtained from BLUP. Different values of λ_s and λ_d were used to explore the effects of a range of weights given to family information. Note that when $\lambda_s = \lambda_d = 1/2$, selection is based on the estimated Mendelian sampling component and so a form of within-family selection is practised. Animals with the highest index values were selected.

Secondly a selection criterion ($IND2$), which has been recently used by Grundy and Hill (1993), was evaluated. Individuals were selected according to their EBV obtained from BLUP using an artificially raised heritability (h_{AR}^2). Different values for h_{AR}^2 were examined (from 0.5 to 0.9).

Finally, for each animal, a modified index ($IND3$) was computed as

$$IND3_i = EBV_i - |EBV_i \gamma F_i|$$

where subscript i refers to the individual; the EBV is that obtained from BLUP and F is the inbreeding coefficient. Different values for the factor γ were investigated. Again, selected animals were those with the highest index values. This index can

be seen as a method to achieve retrospective minimum coancestry matings. By penalizing individuals with high inbreeding coefficients in the selection decisions, matings of highly related animals are penalized retrospectively.

Comparison among breeding schemes

The basic scheme was used as a point of reference for comparisons. Average true breeding values (G_i) and inbreeding coefficients (F_i) of individuals born at the ith year were obtained. Rates of response between years j and i were calculated as $\Delta G_{i-j} = G_j - G_i$, where $j > i$. Rates of inbreeding were obtained every year as $\Delta F = (F_i - F_{i-1})/(1 - F_{i-1})$. Other parameters calculated in the simulations were: 1) genetic variance of animals born every year; 2) accuracy of selection (correlation between the true breeding values and selection criteria of the candidates for selection); 3) genetic selection differentials (difference between the mean values of selection criteria of selected individuals and candidates for selection) and selection intensities for males and females; 4) generation intervals (average age of parents when offspring are born) for males and females; and 5) variance of family sizes for male and female parents. To calculate the variance of family size, the cohort of calves born at year 11 was chosen (each year should be similar to any other after genetic parameters approach equilibrium). Let M_{11} and F_{11} represent, respectively, males and females born at year 11, which are selected to produce offspring at any time. The variance of family size for males was calculated as $\mathrm{Var}(n_m) + \mathrm{Var}(n_f) + 2\,\mathrm{Cov}(n_m, n_f)$, where n_m and n_f are, respectively, the number of male and female offspring of M_{11} that are selected at any time. The variance of family size for females was calculated in a similar way by counting offspring of F_{11} that are selected in successive years. Appropriate variances and covariances of family sizes were calculated at the end of each replicate. The number of replicates ranged from 20 to 50. Values presented are the average over all replicates.

The number of transfers per year was expected to be the same for all the schemes studied. The criteria for comparing different schemes were the rates of response and inbreeding at different time periods. The cumulative response and inbreeding at year 15 were also compared.

RESULTS

Selection intensity

Genetic responses and inbreeding coefficients obtained per year, for different female selection intensities, are shown in figure 1. The number of selected females initially varied from 18 to 144, although in all cases, only 18 females were used as donors. Rates of response decreased substantially after year 5 due to the decrease in genetic variance by linkage disequilibrium (Bulmer, 1971). This decrease in variance is greatest during the first generation of selection (selection of animals born from base animals starts at the third year) and then slowly approaches an equilibrium. After that, the change in genetic variance is due to inbreeding. Rates of inbreeding become approximately constant after year 15 (around 5 generations of selection). The same pattern of response and inbreeding over years was observed for all the
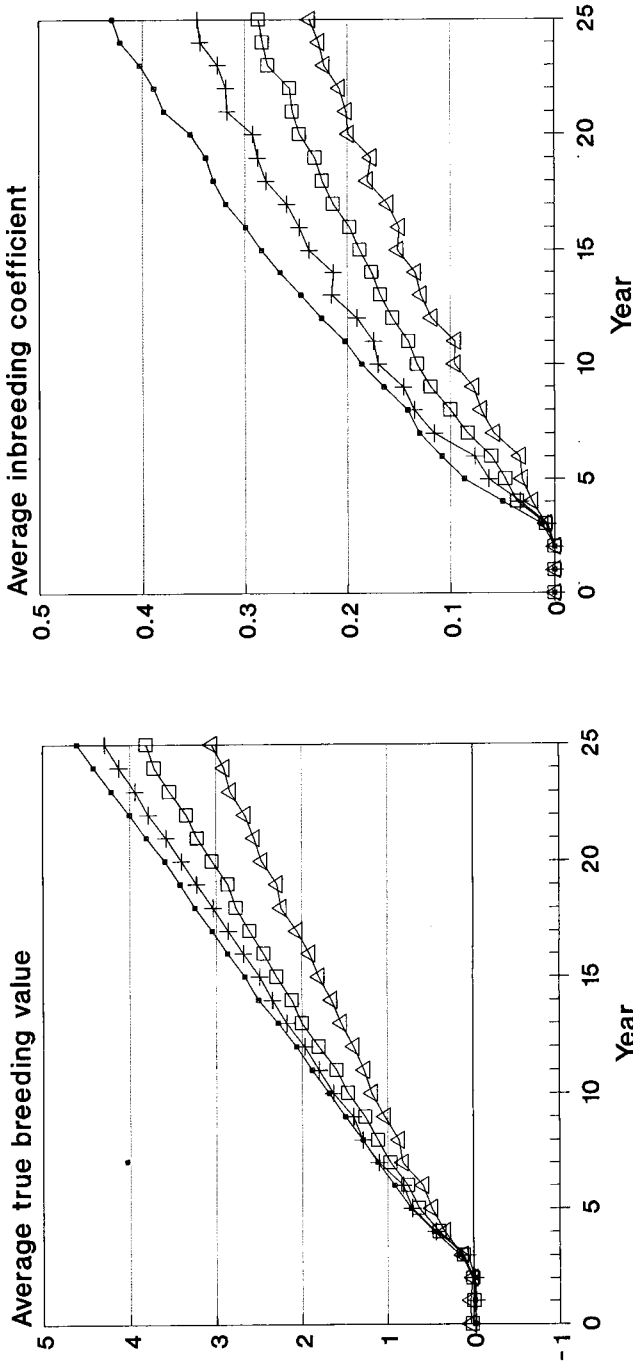
Fig 1. Change in genetic mean (phenotypic standard deviation units) and inbreeding coefficient (%) over years with different female selection intensities. The number of donors was 18 in all cases. ■: 18 selected; +: 27 selected; □: 54 selected; △: 144 selected.

schemes studied. For these reasons, 2 times periods were considered. Average rates of response from year 5 to 15 (ΔG_{5-15} and ΔF_{5-15}) and from year 15 to 25 (ΔG_{15-25} and ΔF_{15-25}) under different female selection intensities are shown in table I. Cumulative selection responses to year 25 (G_{25}) and average inbreeding coefficients at this year (F_{25}) are also presented. As expected, decreasing intensity of selection led to a decrease in rates of response and inbreeding. Decreasing selection intensity reduced rates of inbreeding (ΔF_{15-25}) by 34 to 58%, whereas rates of response (ΔG_{15-25}) were reduced by 7 to 36%, compared with the case where 18 females were selected. Rates of response and inbreeding were, in general, slightly higher in the early years ($5-15$) than in later years ($15-25$). Table II shows selection intensities and generation intervals obtained in the last time period for males (i and L) and females (i and L). Decreasing selection pressure in females led to a decrease in L (fewer donors are repeatedly used over successive periods). However, this was accompanied by a small increase in male generation interval, probably due to the slower genetic progress achieved. The average generation interval ranged from 2.94 to 3.09 years.

Limited use of selected parents, number of donors and mating design

Table III shows the effect of different culling policies, number of donors and mating designs on rates of response and inbreeding. Culling of females after each evaluation period reduced inbreeding but also reduced response. For the different number of donors and mating designs considered, the culling of females reduced the rate of inbreeding by 24–37%. Corresponding proportional reductions in response were lower (4–12%). When males were also culled from the herd after each period, there was, in general, a further reduction in inbreding rates. However, the rates of response were similar to those obtained when only females were culled. Although culling of males led to decreased generation intervals, there was no further reduction in the intensity of selection. Culling of animals resulted in a better strategy for decreasing inbreeding than reducing selection intensity (see also table I). That is, for the same level of inbreeding, there was a smaller reduction in genetic progress by culling animals than by reducing intensity of selection. Generation intervals for males and females obtained for the different schemes are shown in table IV. The values presented are averages from year 15 to 24. Culling of animals decreased generation intervals by around 16%.

Increasing the number of donors used from 18 (3 flushes per period) to 27 (2 flushes per period) led to reductions in inbreeding and in response. Differences in rates of inbreeding between schemes using 18 and 27 donors were smaller under the factorial mating design. For the different culling policies and mating designs considered, increasing the number of donors decreased rates of inbreeding by 2–38% and rates of response by 2–13%. Generation intervals were slightly increased by increasing the number of donors used (table IV).

The factorial mating design gave, in general, a slightly higher response (not statistically significant, $P < 0.05$) than the nested design and significantly lower rates of inbreeding (table III). When the number of donors was 18 and animals were allowed to be repeatedly selected (*ie* no culling), the factorial design reduced the rate of inbreeding by 19%. The average variance of family sizes after selection for female parents (over replicates) was 6.71 and 4.48 with nested and factorial designs,

Table I. Rates of genetic progress (phenotypic standard deviation units) and inbreeding (%) and their standard errors (se) for different female selection intensities under a nested mating design.

No of females selected	Genetic progress						Inbreeding					
	ΔG_{5-15}	(se)	ΔG_{15-25}	(se)	G_{25}	(se)	ΔF_{5-15}	(se)	ΔF_{15-25}	(se)	F_{25}	(se)
18**	0.194	(0.003)	0.194	(0.003)	4.60	(0.06)	2.33	(0.13)	2.15	(0.18)	42.93	(1.16)
27*	0.178	(0.005)	0.180	(0.005)	4.28	(0.07)	1.96	(0.25)	1.42	(0.17)	34.64	(1.80)
36*	0.179	(0.005)	0.170	(0.005)	4.15	(0.08)	1.68	(0.14)	1.28	(0.13)	31.69	(1.71)
54*	0.167	(0.004)	0.152	(0.004)	3.81	(0.07)	1.53	(0.10)	1.24	(0.12)	28.68	(1.18)
72*	0.146	(0.005)	0.148	(0.005)	3.43	(0.08)	1.32	(0.12)	1.32	(0.11)	25.93	(1.35)
90*	0.139	(0.004)	0.125	(0.004)	3.15	(0.08)	1.29	(0.10)	0.90	(0.11)	22.45	(1.30)
108*	0.139	(0.007)	0.132	(0.006)	3.16	(0.09)	1.37	(0.07)	1.04	(0.14)	23.96	(1.14)
144*	0.132	(0.004)	0.125	(0.003)	3.05	(0.08)	1.29	(0.09)	1.04	(0.13)	23.67	(1.20)

* 20 replicates; ** 50 replicates; the number of donors was 18 in all cases.

Table II. Selection intensities (i and i) and generation intervals (L and i , in years) for males and females and their standard errors (se) for different female selection intensities under a nested mating design.

No of females selected	i	(se)	i	(se)	L	(se)	L	(se)
18	1.36	(0.006)	1.63	(0.009)	3.18	(0.014)	3.00	(0.013)
27	1.15	(0.009)	1.65	(0.011)	2.93	(0.008)	3.04	(0.019)
36	0.98	(0.012)	1.65	(0.012)	2.82	(0.007)	3.07	(0.026)
54	0.63	(0.013)	1.67	(0.013)	2.72	(0.005)	3.17	(0.026)
72	0.34	(0.014)	1.67	(0.015)	2.68	(0.006)	3.20	(0.022)
90	0.10	(0.011)	1.66	(0.012)	2.67	(0.005)	3.24	(0.026)
108	0.01	(0.007)	1.65	(0.016)	2.66	(0.007)	3.32	(0.021)
144	−0.01	(0.005)	1.68	(0.015)	2.68	(0.006)	3.33	(0.036)

The number of donors was 18 in all cases.

respectively. Corresponding averages for the variance for male parents were 39.24 and 41.68, but there was enormous variation among replicates in these values. The variance of family size for males varied from 0 to 256 in the nested and from 0.5 to 174 in the factorial design. The efficiency of factorial designs for controlling inbreeding rates was smaller when 27 females were used as donors. There were no differences in generation intervals between mating designs (table IV).

Selection criteria

The rates of response and inbreeding, obtained by using different selection criteria, are presented in table V. Three different modified indexes ($IND1$, $IND2$ and $IND3$), as described above, were studied as alternatives to selection on BLUP breeding values. Males and females were culled after each selection period. For all schemes considered, the generation intervals ranged from 2.42 to 2.56 years for males and from 2.54 to 2.65 years for females. Selection on the index $IND1$ (table V) indicated that, by decreasing the contribution of family information, inbreeding levels were greatly reduced. The reduction in response was mostly due to a decrease in the accuracy of selection. Average accuracy from year 14 to 24 was 0.57 with BLUP and 0.46 with $IND1$ and $\lambda_s = \lambda_d = 1/2$. As would be expected, the decline in genetic variance was smaller with selection on the index. Average values from year 14 to 24 for the genetic variance ranged from 0.24 (BLUP) to 0.28 ($\lambda_s = \lambda_d = 1/2$). With culling, generation intervals were kept approximately constant (2.55 years for males and 2.65 years for females) by varying λ_s and λ_d. For values of $\lambda_s = \lambda_d = \lambda$, response decreased up to around 19% whereas inbreeding decreased up to 31% ($\lambda = 1/2$). For values of λ between 0.2 and 0.33, inbreeding decreased substantially whereas the change in response was very small. For higher values of λ, the decreases in inbreeding and response were notable. Figure 2 shows trends in rates of response and inbreeding obtained for different values of λ. It can be observed that rates of inbreeding are much more sensitive to the change in λ than rates of response.

Results obtained when λ_s and λ_d differ are also presented in table V. Genetic response (and inbreeding) was slightly higher when $\lambda_s > \lambda_d$ (when the weight given,

Table III. Rates of genetic progress (phenotypic standard deviation units) and inbreeding (%) and their standard errors (se) for different culling policies, number of donors and mating designs.

Mating design	No of donors	Culling		Genetic progress				Inbreeding			
				ΔG_{15-25}	(se)	G_{25}	(se)	ΔF_{15-25}	(se)	F_{25}	(se)
Nested	18	No	No**	0.194	(0.003)	4.60	(0.06)	2.15	(0.18)	42.93	(1.16)
		Yes	No**	0.184	(0.003)	4.49	(0.05)	1.58	(0.13)	39.00	(1.32)
		Yes	Yes**	0.185	(0.003)	4.37	(0.05)	1.22	(0.13)	35.13	(0.96)
	27	No	No*	0.186	(0.004)	4.42	(0.08)	2.06	(0.23)	38.10	(1.80)
		Yes	No*	0.164	(0.004)	3.99	(0.05)	1.27	(0.15)	30.01	(1.44)
		Yes	Yes*	0.174	(0.005)	3.85	(0.08)	0.75	(0.23)	30.02	(1.63)
Factorial	18	No	No**	0.188	(0.003)	4.66	(0.04)	1.73	(0.12)	36.31	(1.09)
		Yes	No*	0.181	(0.005)	4.29	(0.07)	1.31	(0.13)	31.12	(1.33)
		Yes	Yes*	0.186	(0.005)	4.41	(0.06)	1.15	(0.17)	30.11	(1.27)
	27	No	No*	0.184	(0.005)	4.43	(0.08)	1.69	(0.19)	33.35	(2.14)
		Yes	No*	0.173	(0.006)	4.05	(0.07)	1.13	(0.12)	27.20	(1.16)
		Yes	Yes*	0.161	(0.004)	3.78	(0.06)	0.79	(0.14)	25.66	(1.65)

* 20 replicates; ** 50 replicates.

Table IV. Generation intervals (years) for males and females and their standard errors (se) for different culling policies, number of donors and mating designs.

Mating design	No of donors	Culling		L	(se)	L	(se)
Nested	18	No	No	3.18	(0.014)	3.00	(0.013)
		Yes	No	2.64	(0.003)	3.04	(0.013)
		Yes	Yes	2.64	(0.003)	2.54	(0.004)
	27	No	No	3.30	(0.024)	3.12	(0.025)
		Yes	No	2.66	(0.004)	3.13	(0.028)
		Yes	Yes	2.66	(0.003)	2.61	(0.005)
Factorial	18	No	No	3.18	(0.011)	3.00	(0.011)
		Yes	No	2.64	(0.004)	3.01	(0.023)
		Yes	Yes	2.64	(0.004)	2.54	(0.006)
	27	No	No	3.32	(0.026)	3.14	(0.027)
		Yes	No	2.65	(0.004)	3.10	(0.025)
		Yes	Yes	2.67	(0.004)	2.62	(0.005)

in the selection criterion, to family information from the male side is smaller than that given to information from the female side) although difference between $\lambda_s > \lambda_d$ and $\lambda_s > \lambda_d$ were unclear. Also, there were no clear differences in components of response (selection intensity, accuracy, genetic variance and generation interval).

Results obtained when some artificially raised values for the heritability (h_{AR}^2) were used in the BLUP evaluations (*IND2*) are also presented in table V. The true heritability was 0.35. For values of h_{AR}^2 equal to or smaller than 0.7, response was kept practically constant whereas the rate of inbreeding decreased by 26–42%. For values of h_{AR}^2 greater than 0.7, response decreased by 4–6% whereas the rate of inbreeding decreased by 48–61%. Trends in rates of response and inbreeding can also be observed in figure 2, which shows that *IND2* is more efficient than *IND1* in controlling inbreeding. Of all schemes considered these were the most effective for decreasing inbreeding without affecting response.

When the modified index *IND3*, which penalizes individuals with high inbreeding coefficients in selection decisions, was used, there was no decrease in the rate of inbreeding. However, the response was affected.

DISCUSSION

The control of rates of inbreeding has become important in the design of breeding programmes since several procedures, introduced in the first instance to produce extra gains (MOET, BLUP), can in fact have a dramatic impact on inbreeding. These procedures can result in proportionally higher increases in rates of inbreeding than in rates of response compared to conventional schemes and mass selection. All the strategies evaluated for decreasing rates of inbreeding in a closed nucleus MOET herd were efficient in the sense that rates of inbreeding were reduced proportionally more than rates of response. The best strategy (to reduce inbreeding with little

Table V. Rates of genetic progress (phenotypic standard deviation units) and inbreeding (%) and their standard errors (se) for different criteria under a nested mating design with limited use of parents.

Selection criterion	Genetic progress				Inbreeding			
	ΔG_{15-25}	(se)	G_{25}	(se)	ΔF_{15-25}	(se)	F_{25}	(se)
BLUP**	0.185	(0.003)	4.37	(0.05)	1.22	(0.13)	35.13	(0.96)
IND1								
$\lambda_s = \lambda_d = 1/9^*$	0.183	(0.006)	4.36	(0.08)	1.16	(0.28)	35.17	(2.11)
$\lambda_s = \lambda_d = 1/8^{**}$	0.183	(0.003)	4.35	(0.04)	0.80	(0.18)	33.52	(1.28)
$\lambda_s = \lambda_d = 1/7^{**}$	0.184	(0.003)	4.33	(0.05)	1.30	(0.13)	34.62	(1.17)
$\lambda_s = \lambda_d = 1/6^{**}$	0.185	(0.003)	4.35	(0.04)	0.98	(0.14)	32.38	(1.09)
$\lambda_s = \lambda_d = 1/5^*$	0.179	(0.006)	4.27	(0.08)	0.83	(0.18)	28.88	(1.83)
$\lambda_s = \lambda_d = 1/4^*$	0.175	(0.005)	4.25	(0.06)	0.79	(0.17)	29.41	(1.38)
$\lambda_s = \lambda_d = 1/3^*$	0.175	(0.005)	4.13	(0.04)	0.69	(0.18)	27.65	(1.12)
$\lambda_s = \lambda_d = 1/2^*$	0.151	(0.006)	3.53	(0.04)	0.74	(0.17)	24.15	(0.79)
$\lambda_s = 1/2, \lambda_d = 0^*$	0.184	(0.005)	4.20	(0.08)	0.62	(0.33)	29.35	(1.41)
$\lambda_s = 0, \lambda_d = 1/2^*$	0.177	(0.005)	4.15	(0.08)	0.65	(0.14)	27.23	(1.07)
$\lambda_s = 1/2, \lambda_d = 1/8^*$	0.175	(0.004)	4.07	(0.06)	1.02	(0.20)	27.85	(1.27)
$\lambda_s = 1/8, \lambda_d = 1/2^*$	0.166	(0.006)	3.97	(0.05)	0.71	(0.24)	27.63	(1.52)
IND2								
$h^2_{AR} = 0.5^{**}$	0.182	(0.003)	4.39	(0.04)	0.90	(0.11)	27.67	(1.04)
$h^2_{AR} = 0.6^*$	0.185	(0.006)	4.23	(0.06)	0.84	(0.14)	24.38	(0.95)
$h^2_{AR} = 0.7^*$	0.187	(0.005)	4.33	(0.07)	0.71	(0.11)	22.75	(1.19)
$h^2_{AR} = 0.8^*$	0.175	(0.005)	4.19	(0.08)	0.63	(0.11)	19.27	(1.04)
$h^2_{AR} = 0.9^*$	0.170	(0.004)	4.11	(0.07)	0.48	(0.08)	17.23	(1.27)
IND3								
$\gamma = 1^*$	0.171	(0.005)	4.27	(0.07)	1.27	(0.20)	34.94	(1.56)
$\gamma = 2^*$	0.159	(0.007)	4.01	(0.09)	1.01	(0.27)	34.00	(1.63)

* 20 replicates; ** 50 replicates; the number of donors was 18.
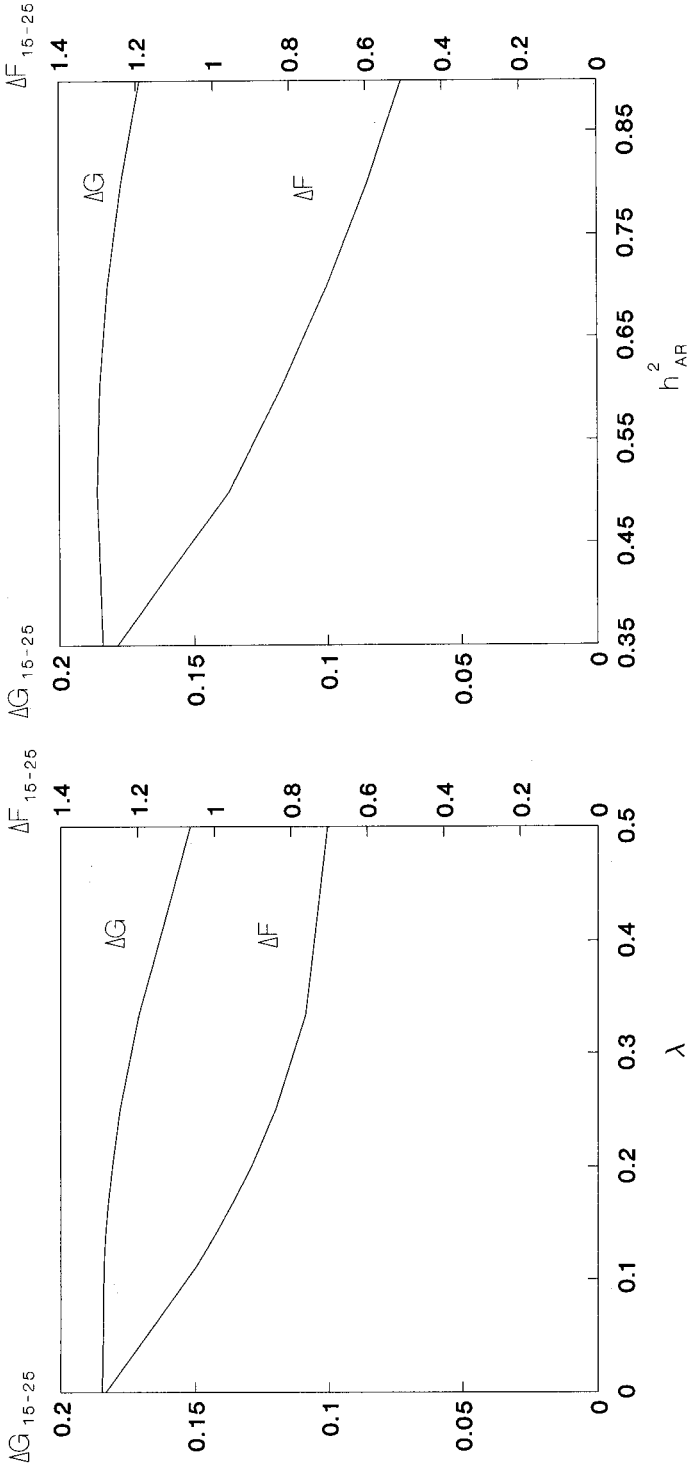
Fig 2. Rates of response (ΔG_{15-25}) and inbreeding (ΔF_{15-25}) obtained by using the modified indexes $IND1$ (with different values of $\lambda_s = \lambda_d = \lambda$) and $IND2$ (with different values of h^2_{AR}).

effect on response) was selection on modified indexes (especially *IND*2) in which the weight given to family information is reduced. Factorial designs were also capable of keeping gain constant and decreasing inbreeding although this decrease was smaller than with *IND*2. The other strategies led to clear reductions in response. Of these, the best was culling of animals after being used for a period of time since for a given level of inbreeding, the response was higher than that obtained using more donors or reducing selection intensity. Costs of implementing the different schemes for beef cattle would be similar if it were assumed that the most critical cost factor is the overall number of embryos transferred.

Rates of genetic progress and inbreeding greatly depend on parameters of embryo yield distributions. When previous studies on possible benefits from MOET in beef cattle (Land and Hill, 1975; Gearheart *et al*, 1989; Wray and Simm, 1990) were carried out, good estimates of the necessary reproductive parameters were not available. Now we have reliable estimates for these parameters. In the present simulations, parameters for embryo recovery and embryo transfer were obtained from an extensive literature review and a survey of experts (Luo *et al*, 1994) and analyses of data (Woolliams *et al*, 1994). The number of transferable embryos was obtained from a Poisson distribution whose parameter is distributed according to a gamma distribution. Thus, extra variation in embryo yield was introduced in comparison with a strict Poisson (with constant parameter). Without control this will influence the rates of inbreeding observed through additional variation in family size.

The rate of inbreeding increases, in general, with the variance of family size. An indirect method for decreasing this variance is to decrease the intensity of selection. Culling of animals from the herd after being flushed a given number of times and flushing more donors, can directly reduce the variance of family sizes. The results presented show that with these strategies, although inbreeding was reduced, response was also affected. If schemes are compared at the same level of inbreeding, limiting the use of selected parents (*ie* culling animals) could give better results than unrestricted selection. One of the advantages of BLUP is that selection can be made across generations. In the light of these results, this advantage could be arguable when a longer term response is considered.

Woolliams (1989) proposed the use of factorial mating designs in MOET schemes either to increase response while keeping rates of inbreeding unchanged, or to decrease rates of inbreeding while keeping response constant. Previous simulation studies (Ruane, 1991; Stranden *et al*, 1991; Toro *et al*, 1991) restricted the number of sons (or daughters) from a full-sibship eligible for selection. With more full-sibships produced with factorial designs, selection intensity (and consequently response) were increased with no additional inbreeding. In the situation considered here, where selection intensities are maintained, factorial designs are expected to give the same genetic progress as nested designs but with lower rates of inbreeding. These predictions were consistently found in all simulations where 18 donors were used and rates of inbreeding were decreased by up to 19%. Increasing the number of donors to 27 leads to a reduction in the variance of family size and the advantage of factorial designs is reduced. For the same reason, culling of animals under the factorial design led, in general, to smaller reductions in inbreeding than under the nested design (table III).

Selection on BLUP breeding values is expected to give the highest response in the short term. These higher responses are, however, accompanied by higher rates of inbreeding. In addition, the use of family information in genetic evaluation increases the correlation among estimated breeding values causing lower than expected selection differentials and response (Hill, 1976). Finally, the decline in genetic variance due to linkage disequilibrium (Bulmer, 1971) increases with the accuracy of selection. Therefore, responses obtained with methods that predict breeding values more accurately decrease proportionally more than responses from less accurate methods. Selection on modified indexes that decrease the family contribution seems to be a promising method to control inbreeding since genetic progress appears very robust to different weights given to family information. The use of *IND*1 can substantially decrease inbreeding with a small change in response. These results have also been found by Verrier *et al* (1993) using an index equivalent to *IND*1 when $\lambda_s = \lambda_d$. Grundy and Hill (1993) have utilized an alternative approach, initially proposed by Toro and Perez-Enciso (1990), to reduce the weights attached to family information. This involves artificially raised heritabilities in the BLUP evaluations in order to reduce the weight given to the family mean and therefore reduce co-selection of relatives. They showed that, in this way, inbreeding rates can be reduced with only a small loss in response. This also agrees with the results obtained by Toro and Silio (1993). The procedure has been evaluated in the present study (*IND*2) showing that methods exist which can reduce inbreeding by more than 40% with little effect on response.

Although both *IND*1 and *IND*2 are based on the same principles (reducing the weight given to family information), their efficiencies differ, with *IND*2 givin better results. *IND*2 not only reduces the weights given to pedigree information but also affects the evaluations of the sire and the dam. Genetic progress can be viewed as the covariance of long-term contributions and Mendelian sampling terms (Woolliams and Thompson, 1994). The breeding value of an individual is the sum of the Mendelian sampling term specific to that individual, plus the average breeding value of its parents. The breeding value of the parents can also be decomposed into Mendelian sampling components and the average of the breeding values of the respective parents. This decomposition can be carried out for each generation, back to the base generation. Thus, the estimated breeding value of an individual is a sum of estimated Mendelian sampling terms weighted by $1/2^t$ for an ancestor occurring t generations previously. To reduce inbreeding the expected short-term gain must be sacrificed to some degree (maybe small) and this may be seen as a decision on which information on genetic merit to ignore. The further back from the current generation, the greater the potential for inbreeding relative to the amount of information obtained. With *IND*2, by increasing the heritability, the weights attached to information from previous generations are progressively reduced each generation and therefore inbreeding is greatly reduced with little effect on response (the difference in weighting of information with respect to standard BLUP is greater for generations furthest from the current generation). With *IND*1, whilst extra weight is being given to the Mendelian sampling terms in the current generation, Mendelian sampling terms of all previous generations are weighted according to BLUP weights. Consequently, the reduction in inbreeding is less than that obtained

with *IND*2 and there is a higher reduction in response to obtain a given reduction in inbreeding.

The results obtained for *IND*2 assume a single value of the true heritability (0.35). Simulations were run for schemes with different levels of heritability and results showed, in all cases, the high efficiency of *IND*2. By using $h^2_{AR} = 0.5$ in a scheme with heritability 0.2, the rate of inbreeding was reduced by 41% whereas response was only reduced by 5%. Corresponding reductions in rate of inbreeding and response by using $h^2_{AR} = 0.8$ in a scheme with heritability 0.5 were 38 and 1%. The method was also efficient in a larger scheme with 36 donors (1 100 transfers/year) and 9 sires. By using $h^2_{AR} = 0.7$ (where the true heritability was 0.35) and limiting the use of parents, the rate of inbreeding was reduced by 55% whereas response was reduced by 4%.

Previous studies comparing different selection procedures have considered non-overlapping generations. Results presented in this paper for different selection criteria (table V) correspond to cases where animals are culled from the herd after being used during one period. This situation is therefore similar to that considered in previous studies in the sense that comparisons are only among contemporaries. It could be argued that the efficiency of *IND*2 for decreasing the rate of inbreeding at minimal cost in gain would be reduced when comparisons are made across animals born in different generations. Simulations were run with no culling of animals and the results show that the method is also very efficient when generations overlap. For example, when the heritability was artificially raised to 0.7, the rate of inbreeding decreased by 23% but the rate of response was not greatly affected (in comparison with the basic scheme in which the heritability used was 0.35). One disadvantage of this method is that breeding values, and therefore genetic trends, are wrongly estimated. However, unbiased trends and estimates of fixed effects could be obtained by running the evaluations with the unbiased estimate of heritability. Selection would be carried out on the data corrected for the fixed effects but reanalysed using the artificially raised heritability.

In this study, selection and mating procedures have been analysed separately. When the best selection and mating strategies (*IND*2 and factorial mating design) were combined in one single scheme, the rate of inbreeding was reduced by around 52% whereas response was not substantially affected. Thus, the change in rate of inbreeding from using both strategies simultaneously was similar to the sum of the changes from using both strategies separately.

With the exception of factorial mating designs and selection on *IND*2, in general, the strategies considered here will also decrease the response to selection, for the number of generations considered in this paper (around 8). If selection was to be carried out for long enough, within family selection could give higher responses than mass selection (Dempfle, 1975; Verrier *et al*, 1993). Moreover results for Quinton *et al* (1992) have indicated that, in the long term, phenotypic selection can result in higher genetic gains than BLUP selection. Verrier *et al* (1993) have shown that, after 30 generations of selection, selection on a modified index (*IND*1 with $\lambda = 0.25$), can give higher responses than BLUP selection if the size of the population is small. Some of the modified heritabilities would have an even more dramatic effect. However, in practice, selection for the same objective is rarely practised for this length of time in closed populations.

The results discussed here assume additive genetic models, which account for the loss of genetic variance due to inbreeding. Models including inbreeding depression need further investigation. Variation in response, which also depends on the effective population size, is also an important parameter to be considered in comparisons among breeding programmes (Nicholas, 1989). Theoretical work is needed to compare objectively the different procedures suggested to control rates of inbreeding and to find optimum schemes setting the genetic gains from selection against the losses due to inbreeding.

ACKNOWLEDGMENTS

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