MATING STRATEGIES IN A SMALL NUCLEUS SCHEME

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INTRODUCTION
Present breeding programmes for dairy cattle provide high genetic response because accuracy of breeding values is high when best linear unbiased prediction (BLUP) method is used, and a large number of progeny from a few selected individuals can be produced. At the same time, the rate of inbreeding tends to mount, because the effective population sizes decrease, selection based on BLUP favours relatives, and generation intervals are short. Most often, financial benefit on the short run is essential, and genetic response cannot be compromised. Therefore, breeding schemes yielding high genetic response with low risks need to be developed.

Literature gives guidelines for the optimal schemes, but as concluded by Quinton and Smith (1995), there is no universally best system. Population size, heritability, planning horizon etc. affect the factors that form the optimal scheme. Setting restrictions on mating pairs may alter inbreeding in the population, and several mating systems has been proposed (e.g. Caballero *et al.*, 1996). Although non-random mating mostly only delays inbreeding, it seems reasonable to avoid mating of close relatives. First, animals with extreme inbreeding coefficients may suffer from inbreeding depression. Second, reduced genetic drift of family means reduces the probability of favouring certain families, which, in turn, may lower the rate of inbreeding.

This paper continues the project of devising schemes for the improvement of Nordic Red Dairy Cattle (Strandén *et al.*, 2001; Korpiaho *et al.*, 2002). Therefore, the studied schemes concern a small nucleus combined with a progeny testing programme. Hierarchical and factorial mating strategies are simulated using algorithms to generate random, avoidance of close relatives, compensatory, and minimum coancestry mating systems. Genetic response (ΔG), coefficient of variation in genetic response (CVR), rate of inbreeding (ΔF) and level of inbreeding are investigated in order to find a practicable procedure for the actual nucleus herd.

MATERIAL AND METHODS
The simulation program has been outlined in Strandén *et al.* (2001). An additive infinitesimal model for one trait with initial heritability of 0.30 was assumed. Estimated breeding values (EBV's) were obtained using BLUP method. The program followed the actual structure of Finnish Ayrshire population, referred as large population, and nucleus herd 'ASMO', except for ignoring genetic flow from the nucleus to the large population due to computational limits. Breeding programme using artificial insemination had been in operation before starting the nucleus. Therefore, equilibrium genetic variances were used for the founder animals of the nucleus, and real pedigrees were sampled from the large population. ΔG and ΔF in the nucleus were monitored between simulation years 5 to 20. Each scheme was replicated 200 times.
Bulls born in the nucleus and in the large population were progeny tested, and eligible at age of six years (PTN scheme). Alternatively, bulls with the best EBV's were selected across age

classes (PTNAJ-1 scheme), i.e. three-year-old adult bulls and one-year-old juvenile bulls could be selected with progeny tested bulls. To avoid co-selection of full sibs, only one non-proven bull per full sib family could be selected. In both bull selection strategies, a bull was eligible in maximum for three successive years. Number of selected bulls was 10 or 5 per year.

Size of the nucleus was 80 cows on first lactation per year. The cohort produced embryos as heifers, performed first lactation test, and the progeny of the best cows were selected to the next generation. Hence, generation interval was two years on female side. Female reproductive rate was assumed relatively low : an average of 30 cows contributed to the next generation annually (Korpiaho *et al.*, 2002). Family size was simulated by assuming 20 % of matings to fail, and for the successful matings, the number of progeny was derived from the Poisson distribution with an average outcome of eight progeny per cow; however, in maximum, four males and four females were accepted. Sex of the progeny was derived from binomial distribution with equal probability for males and females.

Mating strategies.
Hierarchical (H) and factorial mating (F4). In hierarchical mating, each heifer was mated to one bull, and in factorial mating to four bulls. Factorial mating affects the rate of inbreeding by reducing the probability of co-selection of full sibs (Woolliams, 1989). Strategies H and F4 were applied under the following four systems:
Random mating (R). Mates were generated at random, however, each animal had a fixed number of mates. Results from this system are given as a reference, since it was applied in previous studies (Strandén *et al.*, 2001; Korpiaho *et al.*, 2002). The alternative systems are expected to lower level of inbreeding, ΔF, CVR and/or increase ΔG (Caballero *et al.*, 1996).
Avoidance of close relatives (AR). Mates were generated as for random mating, but sib matings or sire-daughter matings were not allowed, whenever possible to pick another mate. This system is easy to implement, and widely used in actual breeding programmes. However, the following more complex systems may be more efficient.
Compensatory mating (C). Animals to be mated were ranked according to their average relationship to the whole mating cohort. Heifers with the highest rank were mated to the bulls with the lowest rank, in sequence. Compensatory mating reduced the rate of inbreeding up to 20% in a scheme with low rate of inbreeding (Caballero *et al.*, 1996). However, this might not be the optimal system in a small population with relatively high rate of inbreeding.
Minimum coancestry mating (MC). Mates were ordered so that the sum of relationship between mating pairs was in minimum. The optimal solution was computed by applying the simulated annealing algorithm (Press *et al.*, 1992). The algorithm tries solutions by switching two mating pairs, accepts improvements (in this case lower sum of relationships), and also poorer solutions with a probability that depends on the change in coancestry and 'temperature', which cools down during the process. Similar to Sonesson and Meuwissen (2000), the starting solution was mating pairs from the compensatory mating, and the initial 'temperature' 1.0 was decreased by 10 % after either 100*na tested mating sets or 10*na accepted mating sets, where na is number of animals in mating. When no replacement was made after the last reduction of 'temperature', the algorithm had found the best solution.

RESULTS AND DISCUSSION

Genetic response and CVR. Mean annual genetic response ranged from 0.112 to 0.130 σ_p, standard errors being in range from 0.002 to 0.003 σ_p. Selection of bulls across age classes increased ΔG from 2 to 11 %. Use of 5 bulls instead of 10 increased ΔG from 4 to 10 %. CVR values were from 0.057 to 0.093. CVR was up to 19 % higher in schemes with 5 selected bulls than in schemes with 10 selected bulls, and up to 60 % higher in the PTNAJ-1 schemes than in the PTN schemes. Mating strategies had no clear effect on CVR, and were expected to affect little on ΔG, because the same animals were used in breeding and had on average the same number of progeny in each mating scheme. However, factorial schemes gave up to 5 % higher ΔG, when selection of bulls was across age classes. This can be explained by the number of eligible young bulls. There was one bull per dam in the hierarchical schemes, but four in the factorial schemes. Indeed, young bulls were selected more in the factorial than in the hierarchical schemes: mean generation interval in males reduced from 5.9 to 5.3 years.

Inbreeding. Mean rate of inbreeding per generation ranged from 0.0078 to 0.0197 (table 1), standard errors being in range from 0.0001 to 0.0005. Values below 0.01 per generation, concluded as tolerable by Bijma (2000), were obtained only in the PTN schemes with 10 selected bulls per year. ΔF was from 7 to 98 % higher in the PTNAJ-1 schemes than in the PTN schemes, and from 18 to 78 % higher in the schemes with 5 than with 10 selected bulls (table 1). Compared to hierarchical random mating, alternative strategies gave lower ΔF per generation in the PTN schemes, but not in all PTNAJ-1 schemes. Minimum coancestry mating delayed inbreeding substantially (figure 1). Also strategies AR and C delayed inbreeding compared to random mating, but the effect was less than half of that attained with MC. Factorial mating reduced ΔF most in the PTN schemes, where it also delayed inbreeding. In the PTNAJ-1 schemes, however, level of inbreeding was higher in the factorial than in the hierarchical schemes (figure 1). Also, the ΔF was higher, especially if calculated per year. As noted above, factorial mating in PTNAJ-1 schemes yielded larger number of eligible young bulls than hierarchical mating. Obviously, the reduction in ΔF due to improved family structure was smaller than the increase due to short generation intervals and selection of young bulls closely related to their mates.

Table 1. Mean rate of inbreeding ($\Delta F \times 10^{-2}$) per generation in the simulated schemes

Sire selection[A]	PTN_{10}		PTN_5		PTNAJ-1$_{10}$		PTNAJ-1$_5$	
Mating system[B]	H	F4	H	F4	H	F4	H	F4
Random	1.042	0.806	1.659	1.425	1.491	1.596	1.855	1.883
Avoid relatives	1.045	0.874	1.652	1.420	1.279	1.298	1.852	1.910
Compensatory	0.976	0.899	1.571	1.404	1.290	1.522	1.873	1.966
Min coancestry	0.970	0.782	1.579	1.392	1.159	1.143	1.687	1.660

[A] PTN, progeny test; PTNAJ-1, progeny tested, adult and juvenile bulls; 5 or 10 selected bulls
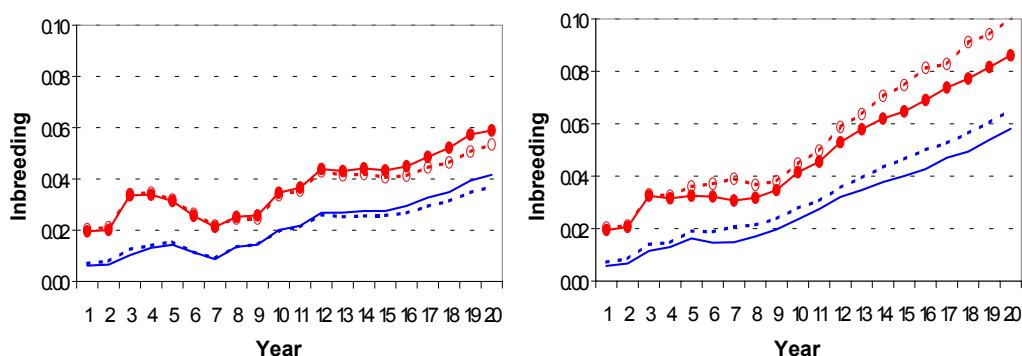[B] H, hierarchical; F4, factorial

Figure 1. Inbreeding in the PTN scheme (on the left), and in the PTNAJ-1 scheme (on the right), both with 10 selected bulls per year. Solid marked line = hierarchical random mating; dashed marked line = factorial random mating; solid bare line = hierarchical minimum coancestry mating; dashed bare line = factorial minimum coancestry mating

CONCLUSION

Schemes with 10 selected progeny tested bulls gave rates of inbreeding lower than 1 % per generation. For those schemes, combination of factorial and minimum coancestry mating proved to be the best strategy to decrease rate of inbreeding. Minimum coancestry mating also delayed inbreeding most. However, in the actual nucleus the sum of relationships between mates may get sub-optimal, because selection and mating decisions are made among small groups during the year.

When selecting bulls across age classes, the studied strategies failed to reduce the rate of inbreeding on generally acceptable levels. However, use of promising juvenile bulls is a tempting option to improve genetic response. In further research, breeding schemes with high genetic response and low risks are sought by taking into account relationships in the selection.

REFERENCES

Bijma, P. (2000) Doctoral Thesis, Wageningen Agricultural University, The Netherlands

Caballero, A., Santiago, E. and Toro, M. A. (1996) *Anim. Sci.* **62** : 431-442.

Korpiaho, P., Strandén, I. and Mäntysaari, E. A. (2002) *Acta Agric. Scand.* Submitted.

Press,W. H., Teutolsky, S. A., Vetterling, W. T. and Flannery, B. P. (1992) In "Numerical recipes in Fortran – the art of scientific computing", p. 436-448, Cambridge Univ. Press, UK.

Quinton, M., Smith, C. and Goddard, M. E. (1992) *J. Anim. Sci.* **70** : 1060-1067.

Sonesson, A. K. & Meuwissen, T. H. E. (2000) *Genet. Sel. Evol.* **32** : 213-248.

Strandén , I., Korpiaho, P. and Mäntysaari, E. A. (2001) *Acta Agric. Scand.* **51** : 235-245.

Woolliams, J. A. (1989) *Anim. Prod.* **49** : 1-14.