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AN INDEX OF ESTIMATED BREEDING VALUE, PARENTAL COANCESTRY AND PROGENY INBREEDING TO HELP MAXIMISE GENETIC GAINS.

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SUMMARY

Under mate selection, decisions on animal selection and mate allocation are made simultaneously. This makes a natural framework for accommodating many of the key issues in animals breeding - and this paper considers genetic gain (via EBV's) and inbreeding. By avoiding the selection of fewer and more related animals as parents, we can decrease mean parental coancestry. This in turn increases the size of the genetic pool and reduces long-term inbreeding, but at the expense of genetic gains, in the short term at least. Avoiding the mating of relatives reduces short-term inbreeding. However, under mate selection, short-term inbreeding is reduced even further, as emphasis to reduce progeny inbreeding affects which animals get selected as parents, and the extent of their use. The best results are achieved by using mate selection with an index that considers all three factors: EBV, progeny inbreeding and parental coancestry.

Keywords: Selection, inbreeding, coancestry, genetic algorithm

INTRODUCTION

This paper reports preliminary findings from a study aimed at managing inbreeding in populations under selection. The simple simulated populations used were bred using mate selection to generate all breeding decisions. This means that rather than selecting animals as a first step, and deciding on mate allocation as a second step, both these activities were accommodated in the one mate selection step.

Mate selection improves the flexibility and efficiency of the breeding program, because the best animals to select can depend on how you would allocate mates, and the best pattern of mate allocation depends on which animals you select. This is shown in the current paper by the result that, contrary to common doctrine, avoiding inbreeding in the next generation can result in useful and sustained reductions in inbreeding levels.

MATERIALS AND METHODS

Results in this short paper come from 1000 replicate simulations of a very small population. This has discrete generations with 8 dams per generation, a maximum of 4 sires per generation, and a maximum of 4 dams mated per sire (otherwise mating ratio is flexible), and with 2 progeny of each sex raised by each female mated. Heritability of the single trait measured was 0.25 and phenotypic standard deviation was 1. Estimated breeding values were calculated using BLUP.

Mate selection was carried out in order to maximise an index containing three elements:

- Predicted progeny mean genetic merit - reflecting genetic gains

- Mean inbreeding coefficient of progeny - reflecting short-term inbreeding
- Mean coancestry of parents - reflecting long-term inbreeding

These are weighted by weighting factors b_G, b_F and b_A respectively to give:

$$Index = b_G\, x'G \;+\; b_F\, \overline{F} \;+\; b_A\, x'Ax$$

$x'G$ is the weighted mean EBV of selected parents, which is also the expected mean progeny genetic merit. $\overline{F}$ is the predicted progeny mean inbreeding coefficient and $x'Ax$ is the weighted mean coancestry of selected parents. x is a vector of contributions from candidates. Following Meuwissen (1997), the elements of x sum to _ for each sex of candidates, as each sex contributes half of the genes in the next generation. G is a vector of BLUP EBV's and A is the numerator relationship matrix.

RESULTS

Table 1 shows the weightings put on each component of the index for the five treatments, T1 to T5. Mate allocations under T1 and T3 were made at random. These weightings are not optimised in any way, but serve to show the pattern of results from putting emphasis on avoidance of progeny inbreeding, avoidance of parental coancestry, or both. Resulting genetic merit and inbreeding level are shown by generation in Figure 1.

Table 1. Index weightings for mate selection

Treatment	Weight on EBV (b_G)	Weight on progeny inbreeding (b_F)	Weight on parental coancestry (b_A)
T1	1	0	0
T2	1	-1	0
T3	1	0	-1
T4	1	-0.1	-1
T5	1	-10	-10

Contrasting T1 and T2 in figure 1, it can be seen that avoiding inbreeding in progeny does in fact lead to a sustained reduction in level of inbreeding, together with an increased level of genetic merit in later generations. In results not shown, stronger emphasis against progeny inbreeding gave extra genetic gains in more distant generations.

Contrasting T1 and T3 in figure 1, it can be seen that avoiding coancestry has a much more beneficial effect than avoiding progeny inbreeding, both for inbreeding levels and genetic gains. Adding some emphasis on progeny inbreeding, in treatment T4, led to some further reductions in inbreeding levels at all generations, and extra response in all generations except generation 2. Increasing emphasis against both progeny inbreeding and parental coancestry, in treatment T5, led to big reductions in inbreeding levels, but with big reductions in genetic gain, especially in early generations

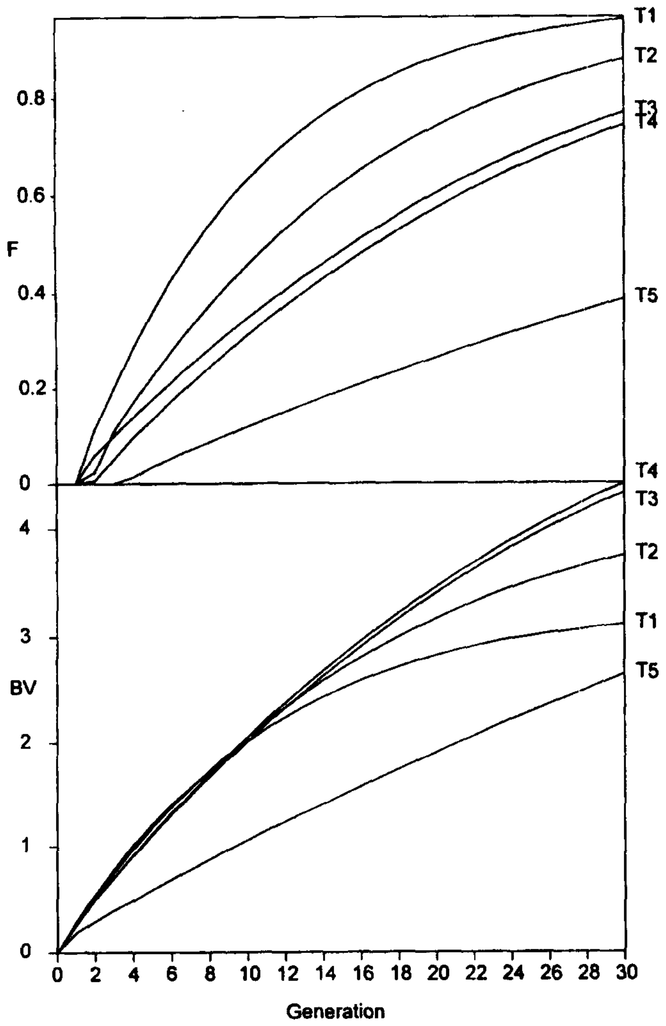

Figure 1. Average of 1000 replicate population means for inbreeding coefficient (F) and true breeding value (BV) to generation 30 for mate selection under treatments T1 to T5 (see Table 1, and the text).

The contrast between T3 and T4 was investigated further by varying weight on progeny inbreeding, and running simulations for 80 generations. Table 2 shows that a small weighting of -0.1 on progeny inbreeding, as in T4, gives a useful reduction in inbreeding levels compared to T3 and increases genetic merit as from generation 4. Increasing b_F to -1 delays the advantage in genetic merit over T3 until generation 26. From generation 37, the -1 weighting gives more genetic merit than does the -0.1 weighting. Increasing the weighting to -10, delays the advantage in genetic merit until well after generation 80, with little benefit in reduced inbreeding level at that late stage.

Table 2. Mean breeding value (top half) and inbreeding coefficient (bottom half) for different index weights b_G, b_F and b_A on EBV, progeny inbreeding, parental coancestry. Figures are means of 2002 replicates. Standard errors at generations 10 and 80 average 0.0093 and 0.0145 for breeding value, and 0.0007 and 0.0001 for inbreeding coefficient

	Generation number					
Weights (b_G b_F b_A)	2	4	10	30	50	80
(1 0 -1) (= T3)	**0.4947**	0.9104	2.0087	4.3254	5.2507	5.6101
(1 -0.1 -1) (= T4)	0.4933	**0.9132**	**2.0427**	**4.4004**	5.3720	5.8029
(1 -1 -1)	0.4872	0.8843	1.9668	4.3578	**5.4812**	**6.0722**
(1 -10 -1)	0.4848	0.7556	1.5869	3.4868	4.4937	5.1367
(1 0 -1) (= T3)	0.0581	0.1379	0.3474	0.7715	0.9329	0.9913
(1 -0.1 -1) (= T4)	0.0054	0.0943	0.3102	0.7446	0.9136	0.9844
(1 -1 -1)	0.0009	0.0793	0.2759	0.6949	0.8806	0.9729
(1 -10 -1)	0.0000	0.0610	0.2423	0.6360	0.8293	0.9464

DISCUSSION

The distinguishing feature of this work on balancing inbreeding and selection is that full mate selection has been used to drive the breeding program. With selection followed by a separate mate allocation step to avoid progeny inbreeding (results not shown in figure 1), inbreeding levels lagged only about one generation behind random allocation (as in T1). In this case, both inbreeding and genetic gain results were much less favourable than when using full mate selection under T2.

The biggest impact on reducing inbreeding and maintaining good genetic gains is made by placing some emphasis on avoiding parental coancestry, as in treatment T3. This increases the effective population size, while permitting more use of better parents, and Wray and Goddard (1994) and Meuwissen (1997) have shown this to be quite effective.

However, this paper shows that some further improvements can be made by also putting emphasis on avoiding progeny inbreeding. In the current simulations, there was no relationship between members of the foundation population. It is likely that the value of paying attention to progeny inbreeding will be higher when applied to populations that already have a high level of mean coancestry. It should be noted that the values used for weighting factors b_G, b_F and b_A have not been optimised, and more favourable results than those in this paper can no doubt be achieved. In conclusion, when practicing mate selection it is worth placing some emphasis on avoiding progeny inbreeding, in addition to avoiding parental coancestry.

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