

LOSS OF GENETIC VARIATION IN CLOSED POPULATIONS

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INTRODUCTION

Selection based on BLUP estimated breeding values is optimal in terms of short-term genetic response. However, the use of family information in BLUP evaluation results in the selection of more closely related individuals and a greater reduction in the genetic variation compared with mass selection (Verrier *et al.*, 1993). As a result evaluation methods that make less use of family information may be preferable to BLUP in order to maintain long-term selection response (Verrier *et al.*, 1993). These methods include mass selection (Quinton *et al.*, 1992), indexes of family information and mendelian sampling (Verrier *et al.*, 1993) and the use of biased genetic parameter estimates and compensatory mating (Grundy *et al.*, 1994). Dynamic selection procedures have been proposed to maintain long-term genetic progress that optimise a function containing some combination of genetic merit and relationships among candidate animals (Meuwissen, 1997). This general mate selection or allocation function is defined as $\mathbf{x}'\hat{\mathbf{u}} + w\mathbf{x}'\mathbf{A}\mathbf{x}$, where \mathbf{x} is a vector of contributions of candidates to the next generation, $\hat{\mathbf{u}}$ is a vector of estimated breeding values, \mathbf{A} is the numerator relationship matrix among candidates and w is an applied weight. Additional functions, e.g. to include the average inbreeding of the progeny (Kinghorn *et al.*, 1999), can be appended to this general function. These methods focus on relationships among animals, rather than on the components defining these relationships. A selection procedure accounting for the expected loss of alleles or the contribution of alleles by founder or bottleneck animals, would improve upon existing technologies. Selection is not the only cause of a reduction in the genetic variance. Alleles will be lost by chance in any population. The expected number of genes from a parent that will not be inherited by any of its n progeny is $(\frac{1}{2})^n$. The purpose of this paper is to illustrate the loss of alleles and contributions from founders under random, mass and BLUP selection in a small, closed population representing a selection line of a small seedstock pig breeder.

MATERIAL AND METHODS

A single trait controlled by either 100 or 1000 unlinked, biallelic loci was simulated. The genotype effects were 1, 0 and -1 for the favourable homozygote, the heterozygote and the unfavourable homozygote at every locus. Founder allele frequencies were $\frac{1}{2}$ for all alleles and loci. Males and females were sampled from the base population and randomly mated to give the first recorded progeny. There were 100 female and 5, 10 or 20 male (constant within a simulation) parents used in each cycle. The population was maintained for 20 discrete cycles of random selection or either mass or BLUP selection with assortative mating. Litter size was fixed at 10, giving 1000 littermates recorded for the trait of interest in each of cycles 1 to 20. Parents of the current cohort were available to be selected as parents in the next cycle. The heritability among founders was set at 0.25 and random common litter of birth effects had a variance equal to 5% of the phenotypic variance. No dominance effects were simulated and no

effect of inbreeding on the phenotype of the trait of interest or on fitness and reproductive ability (litter size). In cycle t , the average genetic value was calculated as the sum of allelic effects across loci and animals born, divided by the number of animals born in that cycle. The genetic variance in each cycle (σ_{At}^2) was calculated as the sum over all loci of $2p_t(1-p_t)a^2$, where p_t is the observed frequency of a favourable allele in animals born in cycle t and a , the genotypic effect of the homozygous favourable allele, which was one across all loci. For every animal, the identity of the founder animal in which each allele originated was stored and used to generate the number of base males and females contributing alleles to each cycle. The frequency of favourable alleles (p) was calculated in the progeny of each cycle, and the percentage of loci at which the favourable allele had been lost ($p=0$) or fixed ($p=1$) recorded.

RESULTS AND DISCUSSION

The mean of 100 replicates from simulations using 100 and 1000 loci are presented in Table 1 and Table 2, respectively.

The genetic variance declined under random selection as a result of drift, and this was associated with both loss and fixation of favourable alleles, and reductions in the contributions of the parents selected from the base population.

For both mass and BLUP, selection at lower intensity produced the highest genetic gain over 20 selection cycles, but not in the early selection cycles (results not shown). For example, for BLUP selection with 100 loci, selection using 20 male parents per cycle led to higher average genetic merit than using 5 or 10 male parents from cycles 6 and 12 onwards, respectively. For mass selection with 100 loci these changeovers occurred at cycles 13 and 16. This is consistent with the reduction in genetic variance and the fixation of alleles associated with both mass and BLUP selection.

Loss of favourable alleles, i.e. when the allele frequency was zero in the progeny generated in cycle 20, was lower under mass selection than random selection, since those alleles were being actively selected for. However, under BLUP selection loss of favourable alleles was considerably higher than for either mass or random selection. This is the result of family selection taking place, with the loss of alleles resulting from unselected families. This can also be seen in the lower numbers of both male and female base parents contributing alleles to progeny born in cycle 20 under BLUP selection compared to either mass or random selection, and also when comparing more intense with less intense selection.

Generally, the results in Table 2 show the same trends across selection methods and selection intensities as for 100 loci. By cycle 20, when the trait was controlled by 1000 loci there was more genetic progress, less reduction of genetic variance, a higher percentage of favourable alleles lost and a lower percentage of favourable alleles fixed. Also more base parents contributing alleles were found compared to the equivalent selection strategies when 100 loci controlled the trait.

Table 1. Results of simulating a population of 100 female parents with a litter size of 10 and either 5, 10, or 20 male parents after 20 cycles; random, mass or BLUP selection was used and 100 loci affected the trait of interest. Values are averages of 100 replicates

Selection method	Random			Mass ^A			BLUP ^A		
	5	10	20	5	10	20	5	10	20
Male parents	5	10	20	5	10	20	5	10	20
Genetic merit (σ_{A0})	0.0	0.1	-0.1	8.4	8.8	8.9	10.3	11.0	11.4
Genetic variance (σ_{A0}^2 %)	63.6	77.5	86.1	41.5	46.0	50.2	10.2	13.2	15.8
Favourable alleles lost (%)	3.1	0.4	0.0	0.3	0.0	0.0	7.8	4.2	2.5
Favourable alleles fixed (%)	3.3	0.4	0.0	11.9	6.8	3.0	68.6	65.8	60.6
Base males contributing	5.0	9.7	18.3	4.5	8.3	14.5	2.5	3.6	5.0
Base females contributing	24.2	36.3	48.2	18.1	23.0	28.7	6.2	7.8	8.1

^A with assortative mating**Table 2. Results of simulating a population of 100 female parents with a litter size of 10 and either 5, 10, or 20 male parents after 20 cycles; random, mass or BLUP selection was used and 1000 loci affected the trait of interest. Values are averages of 100 replicates**

Selection method	Random			Mass ^A			BLUP ^A		
	5	10	20	5	10	20	5	10	20
Male parents	5	10	20	5	10	20	5	10	20
Genetic merit (σ_{A0})	0.0	0.0	-0.1	9.5	10.5	10.5	11.8	12.8	13.1
Genetic variance (σ_{A0}^2 %)	63.2	77.3	85.9	54.0	64.4	74.2	18.3	25.8	31.7
Favourable alleles lost (%)	3.3	0.4	0.0	1.9	0.5	0.1	22.4	16.7	13.5
Favourable alleles fixed (%)	3.3	0.4	0.0	6.0	2.7	0.7	43.7	38.0	33.7
Base males contributing	5.0	9.9	18.3	4.7	8.5	14.8	2.7	4.0	5.3
Base females contributing	28.8	39.5	48.2	18.8	24.4	30.9	7.9	8.5	8.9

^A with assortative mating

When the results from the simulation with 100 loci (Table 1) are compared with those with 1000 loci (Table 2) the most noticeable differences relate to the percentage of alleles being fixed. Under BLUP selection with five male parents per cycle the percentage of alleles fixed were 76.4% and 66.1% when 100 or 1000 loci were simulated, respectively. In the 100 loci case this value was made up of 68.6% and 7.8% of loci in which favourable alleles were fixed or lost, respectively. With a 1000 loci, 43.7% or 22.4% of loci had fixation or loss of favourable alleles. These results were also reflected in the inbreeding (results not shown). For BLUP selection with 5 males per cycle, the average inbreeding coefficients of animals born in cycle 20 were 0.78 and 0.80 for 100 and 1000 loci, respectively. The percentage of alleles that were identical by descent (IBD) in cycle 20 of these two simulations were consistent with these inbreeding levels (83% and 82% IBD, respectively). The IBD percentages can be partitioned into IBD for favourable and unfavourable alleles. The percentages of loci that were IBD for favourable alleles were 74% and 53%, respectively, consistent with the observed fixation of favourable alleles. With 1000 loci, the distribution of genotypes was more continuous than

with 100 loci. This allows to cycle 20, more selection across-families, resulting in contributions of more founder animals.

No effect of inbreeding on either the trait of interest or reproductive ability was included in the simulation. Inclusion of unfavourable inbreeding effects would be expected to have had a considerable effect on the outcome of this study. Inbreeding affecting the trait of interest would be expected to reduce the chance of selecting highly inbred animals (including from BLUP if no allowance was made for this in the analysis model). Inbreeding affecting fitness or reproductive ability (e.g. litter size) may force selection to be across more full-sib families in later cycles.

The large difference in the percentage of favourable alleles that are lost during BLUP selection with genetic control by either 1000 loci or 100 loci requires further investigation. The model of genetic control is simplistic, with all genes having equal effect. If there were genes of larger effect in the population, as well as many genes of small effect, the emphasis of selection will be on the genes of larger effect until they reach fixation. As a result the random loss of favourable alleles for the genes of small effect may be even greater than observed here.

CONCLUSION

Dynamic selection procedures using $\mathbf{x}'\hat{\mathbf{u}} + w\mathbf{x}'\mathbf{A}\mathbf{x}$ may be useful for controlling the loss of alleles, as a by-product of controlling the rate of inbreeding. Further simulations will be carried out in this area in order to ascertain values of w that minimise the loss of favourable alleles under different situations. There may also be alternative methodologies that are better able to maintain the long-term variability. For example, functions of founder animal contributions or predicted variance of progeny EBVs could be incorporated into mate selection procedures.

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