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Abstract. -- Parameter based simulation modelling was used to look at mating designs and population structure for breeding population advancement. The use of balanced vs unbalanced parental contribution to gain and effective population size was investigated. Non-random unbalanced mating adds to gain but at marked reduction in effective population size. The trade-off between gain, and maintaining genetic diversity as described by effective population size, was best made using balanced mating and truncation selection than the use of unbalanced or assortative mating designs. The effect of subline size indicated smaller sublines provide lower gain but higher overall population diversity.

Keywords: Advanced generation planning, simulation models, genetic gain, effective population size, sublines.

THE SIMULATION MODELS

A Monte Carlo simulation model was designed to investigate features of breeding population advancement (King and Johnson 1993). The details of the model are based on the New Zealand radiata pine improvement program but have in common many of the features of tree improvement programs using recurrent selection for general combining ability (Burdon and Shelbourne 1971, Shelbourne et al. 1989). This includes: a complimentary mating design one for GCA testing and another to create a population for recurrent selection; different testing features including single-tree-plots for the GCA test and family blocks for within-family selection in the recurrent-selection population; assortative or non-random mating in the recurrent-selection crosses; the structuring of the breeding population into replicates or sublines – inbreeding is contained within sublines and outcrossing is assured in the production population by crossing between sublines. The modelling uses a Monte Carlo simulation of the advancement of the breeding population for five generations of recurrent selection for a single trait. The model is parameter based and estimates of genetic and environmental variances were used to produce independent normal distributions of true genotypic values and environmental deviations. Phenotypic values constructed from the sum of these two independent distributions provided the basis for the selection of a simulated breeding population. Mating and the generation of an offspring population were constructed under the assumption that

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genotypic values for the trait derive from a polygenic and purely additive gene effects model. King and Johnson (1993) provides the details of the model and the assumptions that were used. The simulation model was designed to address the last two features noted above particularly the effect on both genetic gain and effective population size of using non-random mating features and different population sub-structuring.

Model for Breeding Population Advancement

Lindgren (1986) proposed promoting some of the features of assortative mating by the use of imbalanced family contribution for breeding populations. This comprises having both more representatives of good families and more cross combinations with better genotypes. Increasing mating frequency provides another level of selection over initial truncation selection. Comparisons between mating designs for recurrent selection populations should include not just genetic gain (after all increasing family selection will produce higher gain) but also retaining genetic diversity within the framework of a fixed population resource. Effective family number involving the reciprocal of the sum of squares of each parent's proportional contribution to the breeding population offers a simple and effective way of measuring genetic diversity (Robertson 1961, Kang and Namkoong 1988).

The comparisons provided in these simulations are all made with a breeding population size of 60 parents and an offspring population of 6000. The details are provided in King and Johnson (1993) and include: double pair cross design random mated; imbalanced mating design with top third out of the 60 index ranked parents crossed three times, mid third crossed twice and the bottom third crossed once; double pair cross design with an additional group of crosses involving the top 6 parents in a half diallel; and the 60 parents crossed 8 times each randomly.

In brief, the results showed that imbalanced mating produced significantly more gain (about 10%) than random balanced mating, however having more cross combinations produced higher levels of gain (about 20%) (King and Johnson 1993). Heritabilities are not high enough that assortative mating can accurately match the best genotypes. Increasing mating frequency offers a better opportunity that the best genotypes will be matched. Effective population size was more quickly reduced with imbalanced mating than with random mating for a given level of gain at lower selection intensities. At high selection intensities this difference was less noticeable. Gain and diversity are best managed in the breeding population through the selection process. A combination of high mating frequency and assortative mating is best when selection objectives also incorporate the production population where genetic diversity is less of an issue.

MODELLING POPULATION SUBSTRUCTURE

Background

Wright (1922) concluded that improvement with artificial selection would be more rapid if a population were subdivided into small lines. Wright stressed that this conclusion was dependent on selection being for epistatic combinations. Reviews of many studies in artificial selection and animal improvement shows no advantage to population subdivisions when traits are under additive gene action (Barker 1989, Lopez-Fanjul 1989). Population substructuring is not expected to be as efficient as managing larger populations except: 1-selection across sublines may provide some rapid gain as small sublines are more quickly fixed for favorable alleles - this is temporary as larger sublines will soon overtake the smaller sublines (Madalena and Hill 1972); and 2-small sublines are expected to be more efficient for the elimination of deleterious recessives (Madalena and Hill 1972). Another potential advantage, however, to having population sub structure is to help in maintaining genetic diversity. Small sublines provides a method of maintaining many unrelated sub structures thus providing for a wider base. This is expected to occur at a loss to overall gain with the ability to use higher selection intensities in larger sublines.

The model here used a breeding population of 100 parents. The treatments comprised: the population maintained as one undivided breeding population; 5 sublines of 20 parents each; and 10 sublines of 10 parents each. The mating design comprised a random double pair cross and in addition the top selections were crossed in a half-diallel to produce elite crosses (e.g. EN; King and Johnson 1993). Each population treatment provided 100 crosses as random double pair crosses and 30 crosses in elite crosses. 100 individuals were created for each full-sib family for an offspring population of 13,000. Selections using combined index selection (King and Johnson 1993) were made in the offspring to choose 100 parents for the next generation of breeding. A restriction of a maximum of 4 individuals per full-sib family was made. Over 100 independent runs for two cycles of recurrent selection were made for these three treatments.

Results of Simulation Runs

The results of the simulation runs are summarized in Table 1. Gains are shown as percentage gain over the previous generation mean averaged over two cycles of recurrent selection. Effective population size calculated as per King and Johnson (1993) refers to the weighted parental contribution in the second cycle of recurrent selection from the 100 parents of the breeding population. There are higher levels of genetic gain in the undivided breeding population, nearly 30% more per generational gain than the smallest subline size but the effective population size is less than half of that present in the smallest subline size.

Table 1. Per Generation Gain and Effective Population Size for
         Differing Subline Sizes.

Treatment	Gain	Ne
1 x 100 parents	13.5%	17
5 x 20 parents	11.5%	30
10 x 10 parents	10.5%	38

Using small subline sizes thus presents a cautious way that genetic diversity can be maintained in the breeding population. These results should be treated as preliminary, many questions beg answering. For instance, can restrictions be used in the selection process to maintain higher effective population size in the larger subline and how will gain be affected this way? Is this cautious approach the best way of managing for genetic diversity? Small sublines would be expected to diverge with fixation of different alleles due to drift. Directional selection that allow divergence because of selection for different traits and objectives is another way that genetic variability can not only be maintained but enhanced. Selection in this way for multiple populations is different than the division of the breeding population into replicate populations or sublines. Sublines are not expected to have different selection objectives and in tree improvement are meant primarily to control inbreeding in the production population by containing it within sublines (Lowe and van Buijtenen 1981). Sublines should also be distinguished from breeding groups such as disconnected diallels that are established for manageability but can be selected across groups. The subline unit as a replicate of the breeding population is meant to contain useful genetic variation within lines (Lowe and van Buijtenen 1981). Multiple populations or varietal lines can be contained within sublines, although this would be difficult if unfavorable correlations exist. The use of multiple populations in this way may be a more active way of maintaining and enhancing the genetic resources of our tree species than the conservative approach of using small sublines (Namkoong 1984). Large sublines can provide more flexibility to provide selections for multiple breeding objectives.

CONCLUSIONS

Monte Carlo simulations offers a valuable tool in planning and quantifying strategies for advanced generation breeding programs. In a selective breeding program continued improvement and the management of diversity is best made in the selection process. Mating designs and population structure should be used to enhance the selection opportunities to meet these goals.

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