Computer simulation of family selection schemes suitable for kale (Brassica oleracea L.), involving half-sib, full-sib and selfed families

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Summary. Three recurrent selection schemes suitable for kale (Brassica oleracea L.), involving half-sib (HS), full-sib (FS) and selfed (S) families, were compared by computer simulation. All combinations of 6, 12 and 24 families selected, out of 120 and 240 assessed, were investigated for a range of genetical models. Selection was simulated for 20 generations from an initial allele frequency of 0.05 and for 16 generations from an initial frequency of 0.20. With an initial frequency of 0.05 there was a serious loss of desired alleles ranging from 0.31 out of 20 for the HS scheme with 24 out of 240 families selected to 9.19 for the S scheme with 6 out of 120 families selected. It was concluded that if as many as 20 cultivars were included in the initial population the selection scheme should be chosen to minimise the loss. With an initial frequency of 0.20 there were no losses with 12 and 24 families selected in the HS and FS schemes respectively, and the highest loss was 2.88 for the S scheme with 6 out of 120 families selected. It was concluded that if as few as five cultivars were included in the initial population a compromise between the initial response to selection and the loss of desired alleles should be sought. Selecting 6, 12 and 24 families for the HS, FS and S schemes respectively, resulted in average relative responses per generation of 2.28, 2.74 and 2.76, respectively for the first five generations, and losses of 0.22, 0.13 and 0.35, respectively after 16 generations. Practical considerations favour the FS scheme over the S scheme.

Key words: Kale breeding – Population improvement – Family selection – Computer simulation – Genetic drift

Introduction

With an outbreeding crop species such as kale (Brassica oleracea L.), population improvement by recurrent selection is an important component of any breeding programme. As kale is grown for feeding to cattle and sheep, an important selection criterion is the yield of digestible organic matter in the dry matter (DOMD yield). Single plant selection is impractical because assessment of DOMD yield involves a destructive harvest of the plants. Hence family selection is required so that in addition to a yield trial, selection plots of all the families can be grown to provide plants for seed production.

Plants must pass through a juvenile growth stage and be vernalised before they will flower. Self pollination is largely prevented by a sporophytic incompatibility system, although the breeder can produce selfed seed by bud pollination or special techniques, such as an atmosphere enriched with carbon dioxide (Taylor 1982). The easiest type of family selection scheme for the kale breeder to operate is therefore half-sib family selection on a biennial cycle, in which the half-sib families are produced either by the natural insect pollinators at an isolation site, or by blowflies in special cages or tunnels. Such a scheme has been operated at the Scottish Crop Research Institute (SCRI) since 1971 and has been described by Bradshaw and Mackay (1981). Half-sib matings are also commonly used in forage grass breeding and have been reviewed by Nguyen and Sleper (1983).

The production of full-sib and selfed families of kale involves more work than for half-sib families, but would be worthwhile if the rate of population improvement that could be achieved in practice was faster. As limited resources with a minor crop such as kale usually prevent more than one breeding programme being carried out at a time, decisions on whether or not to change the breeding method must be made on the basis of theoretical models and computer simulation studies. Extensive work has been carried out on recurrent selection methods in maize (Zea mays L.) which, unlike kale, is a monoecious, annual, wind-pollinated crop mainly grown for its grain (Hallauer and Miranda 1981). Thus,
the three breeding methods, mass, modified ear-to-row, and $S_r$ selection, chosen by Choo and Kannenberg (1979a, b) for comparison by computer simulation, as likely from theoretical studies to be the best for maize population improvement, are not the most relevant ones for kale improvement.

This paper therefore reports the results of a computer simulation study of three recurrent selection schemes which are feasible for kale and which involve half-sib, full-sib and selfed families. The effect of type of family, number of families assessed and number of families selected on the loss of desired alleles, as well as on the response to selection, is reported for a range of genetical models.

Materials and methods

Simulation program

The simulation program was written in IMP and run on the Edinburgh Regional Computing Centre’s ICL 2988 computer. The methods used were based on those described by Fraser and Burnell (1970). The algorithm of Wichmann and Hill (1982) was used to generate pseudo-random numbers.

Genetical models

In all models there were 20 unlinked loci with two alleles at each. In the additive genetical models the desired homozygote at each locus was assigned a genotypic score of 2, the heterozygote a score of 1 and the undesired homozygote a score of 0. In the dominance models the heterozygote was also assigned a score of 2 (complete dominance).

Four initial populations were considered. Two were in genetical equilibrium with initial average frequencies of the desired allele of 0.05 and 0.20, respectively, although the frequency at any given locus was allowed to deviate by up to one standard deviation from the average. (This constraint prevented extreme frequencies, in particular, zero frequencies.) The other two were disequilibrium models. In one 20 "inbred lines", each with a different locus homozygous for the desired allele and the other 19 loci homozygous for the undesired allele, were random mated for two generations. In the other, 5 "inbred lines", each with a different set of 4 loci homozygous for the desired allele and 16 homozygous for the undesired allele, were also random mated for two generations. Two generations were chosen as the minimum number required to generate genetical variation between families. The random mating was carried out by mating each member of the population to a different member chosen at random. The population size equalled the number of families subsequently produced.

In one set of models the phenotypic score of a family mean equalled the genotypic score whereas in another set it was determined by adding on to the genotypic score an environmental score which was normally distributed with a mean of zero and variance (E) of 2.5 (2.5 is the genetical variance between half-sib families when the frequency of the desired allele is 0.5 at all 20 loci).

Thus, all combinations of additive and dominance models, equilibrium and disequilibrium initial populations, and presence and absence of environmental contributions to the family means made 8 genetical models.

Selection schemes

In all of the schemes, from each plant in the initial population, families of 20 progeny were produced for assessment. The genotypic score of each individual was determined and the family mean calculated. The phenotypic score of the family was then determined. The families were then ranked according to their scores and the best ones chosen. Further progeny were then produced for each of the chosen families in order to form a new population of plants from which to produce the next generation of families to be assessed.

In the half-sib (HS) schemes each plant in the population was mated by 20 plants chosen at random (not necessarily different, but excluding the plant itself) in order to produce 20 half-sib progeny.

In the full-sib (FS) schemes each plant in the population was mated by another plant chosen at random and 20 progeny produced.

In the selfed (S) schemes each plant in the population was selfed to produce 20 progeny in one generation and then in the next generation full-sib families with 20 progeny were produced.

Thus all combinations of type of family, 120 and 240 families assessed and 6, 12 and 24 families selected made 18 selection schemes.

Selection was simulated twice for 20 generations from an initial desired allele frequency of 0.05 and twice for 16 generations from an initial frequency of 0.20, for all combinations of selection schemes and genetical models, making a total of 576 runs. (After these numbers of generations alleles had usually either been lost or had reached a relatively high frequency. There were some cases of just one locus with an allele frequency below the starting frequency, but loss of these in further generations would not alter the conclusions.)

Analyses

The number of desired alleles lost, out of 20, by generation 20 from a starting frequency of 0.05, and by generation 16 from a starting frequency of 0.20, was counted for each simulation.

The initial relative responses to selection per generation were assessed as the difference, divided by 5, between the population mean after five generations and the initial population mean.

The numbers of alleles lost and the responses to selection were analysed by analyses of variance with both the selection schemes and the genetical models as fixed effects.

Results

The analyses of variance are shown in Table 1. The differences between genetical models, between selection schemes, and their interaction were all statistically significant when tested against the pooled mean square for duplicate runs, for all four sets of data. As examination of the tables of means showed that the interactions did not involve major changes in ranking, the means for selection schemes and genetical models given in Tables 2-5 are adequate for discussing the main conclusions.

The analyses of variance were taken further by partitioning the 17 degrees of freedom for selection schemes into the three factors shown in Tables 2a to 5a and the 7 degrees of freedom for genetical models into the