

SIMULATION OF ASPECTS OF SUGARCANE SELECTION

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Abstract

A model to simulate aspects of sugarcane selection has been developed to assess various selection techniques. The consequences of testing for response to disease at the beginning of the selection programme, and the benefit, where the soil exhibits an appreciable trend in fertility, of selecting within small groups of adjacently planted clones, rather than merely within whole families, were studied.

Introduction

Sugarcane breeding is expensive. This is because it is a large, perennial plant which requires large areas of land and other resources, and also because the frequency of 'good' clones in the progeny of a cross between two existing varieties is invariably low. Selection must therefore be carried out on as large and efficient a scale as possible to help ensure that at least some agriculturally acceptable clones are produced in the breeding programme. Simulation of selection methods with the aid of a computer provides some insight into the efficiency of various selection procedures (Choo and Kannenberg,^{1,2} Cress³).

A simple model for simulating successive stages of sugarcane selection has been developed and used to study the effect of screening for resistance to a disease at the first stage of selection on the yield potential and response to disease of clones reaching the final stage of selection. It has also been used to ascertain the effect on genetic advance of selecting either the phenotypically best 10% of all the clones in a family or the phenotypically best single clone from each group of ten contiguously planted clones, assuming either a small or a large trend in soil fertility.

Theory and Methods

Assumptions

The genotypes for yield and for response to a disease of the clones originating from a cross between two sugarcane varieties are distributed normally, and both distributions have a characteristic mean and standard deviation (SD). There is no genetic correlation between yield and disease response. When a group of clones derived from a cross (a family) is grown in the field, the measured (phenotypic) yield of a clone will differ from its genetic yield as a result of a random environmental deviation and (if needed for the simulation) by its position in the field relative to a trend in soil fertility. Random deviations have a normal distribution and the degree of variability is determined by the size of the SD of this normal distribution. The soil fertility level for a clone is calculated by an equation which produces a curve of the shape shown in Figure 1. The magnitude of the trend in fertility is varied by changing the values of the constants in the equation. (The shape of the fertility trend was chosen simply for convenience; it is given by a simple mathematical expression.)

In summary, the observed (phenotypic) yield of a clone in the field is family mean \pm genetic deviation \pm random environmental deviation [\pm deviation due to trend in soil fertility]; the last term is included only where the effect of a soil fertility trend is being considered.

Screening of clones for response to disease is done by means of a test in which the observed disease rating is correlated with its true response to disease (Figure 2). The computer allows the observed rating of a clone with a particular true response to

vary randomly between the limits shown; thus high resistance and high susceptibility are assessed comparatively accurately, but intermediate levels of resistance are assessed much less accurately.

A selection programme with sugarcane consists of successive stages. The genotypes for yield (and disease response, where appropriate) of mn clones (m = number of families; n = number of clones per family) are derived, with the aid of a random number generator, from normal distributions with the appropriate mean and SD. If no test for disease response is carried out, all the clones of every family are planted in the field. A proportion, O , of the clones of each family is selected according to yield phenotype. These are carried forward to the next stage(s) of selection, where a proportion is again selected according to yield phenotype.

A test for disease response may be carried out between two successive stages of selection. If it is carried out before the first stage and a fraction, p , of the clones from each family eliminated, then $n-pn$ clones per family will be planted in the field at the first stage (in practice the value of p will vary slightly because of sampling variation). The proportion of clones selected will then increase to $O/(1-p)$ to maintain the number of clones in the following stage of selection.

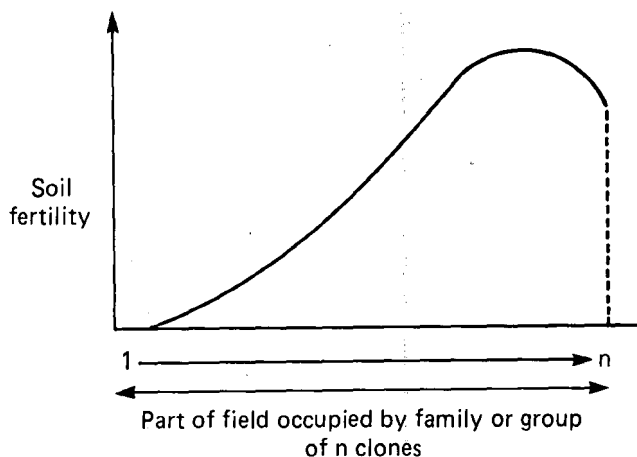


FIGURE 1 'Shape' of trend in soil fertility.

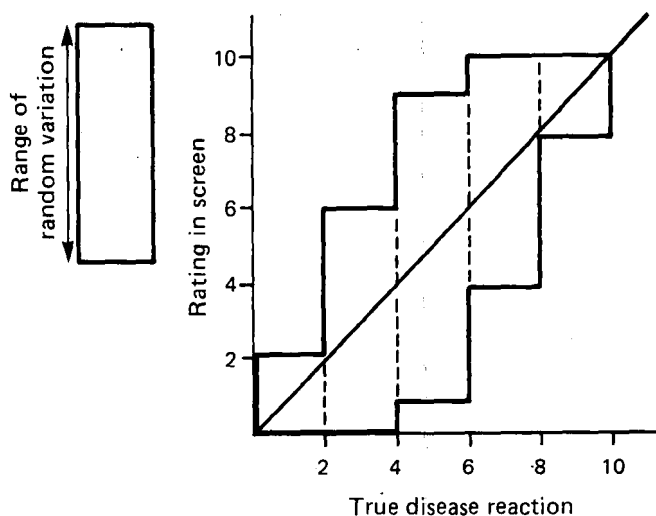


FIGURE 2 Method of relating observed and true response to disease.

Details of the selection programmes which were simulated are shown in Tables 1 and 2. Three stages of selection were simulated in the one case and two stages in the other case. The sizes of genetic and environmental standard deviations for yield were chosen so as to give phenotypic standard deviations and clonal repeatability values which seemed reasonable in the light of observations in local selection programmes (RS Bond, personal communication). The mean and SD for disease response were chosen so that virtually all the responses fell between the limits of the standard scale of disease response (ie from 1 to 9), where conventionally, the smaller the value, the greater the degree of resistance. The simulated relationship between observed and true response to disease (Figure 2) gave a correlation coefficient of 0,69 which is approximately the degree of correlation that should be expected with a satisfactory screening technique (RA Bailey, personal communication). Clones were screened for disease before the selection programme was started, and only those with a rating less than or equal to 5 were included in the first stage of selection.

TABLE 1

Details of selection for yield with or without screening for response to disease

Details	Programme	
	1 Without screening	2 With screening
Initial number of clones	60 000 (300 families, 200 clones per family)	
Genotypes	yield [mean SD]	100 17
	disease response [mean SD]	5 1,9
Correlation coefficient, observed vs 'true' disease response	—	0,69
No of clones planted in the field:		
1st stage of selection	60 000	c 30 000
2nd stage of selection	6 000	6 000
3rd stage of selection	600	600
SD of environmental deviations:		
1st stage of selection	26	26
2nd stage of selection	17	17
3rd stage of selection	11	11

Results and discussion

Screening for disease

Testing for response to disease at the beginning of a selection programme is expensive, because of the large number of clones to be screened. On the other hand, carrying many clones which are too susceptible to be of commercial use through the successive stages of selection is wasteful of resources.

The inclusion in the selection programme of a test for disease response caused only a slight decrease in the average yield, but a somewhat greater average level of resistance to disease in the clones which were selected for the second stage of selection (Table 3).

Similarly, the yield of clones selected for the third stage was slightly greater when the test for disease response had not been conducted. The average level of resistance did not change after the first stage because it was assumed that the only selection for disease response was that carried out at the beginning of the programme.

TABLE 2
Details of selection strategies with either a large or a small trend in soil fertility

Details	Programme			
	3	4	5	6
Initial number of clones	50 000 (250 families, 200 clones per family)			
Fertility trend	large	small	large	small
Yield genotypes [mean SD]	100 17			
Selection strategy, select on phenotype	the highest yielding 20 clones in each family at Stage 1 (= 5 000 clones) and highest yielding 50 clones from each group of 500 at Stage 2 (= 500 clones)		the highest yielding clone from 10 contiguously planted clones at both Stages 1 & 2 (= 5 000 clones at Stage 1 & 500 clones at Stage 2)	
No of clones planted at Stage 2	5 000			
No of clones remaining after two stages of selection	500			
SD of environmental deviations*:				
Stage 1 [total [random component]	26 14,9	26 24,6	26 14,9	26 24,6
Stage 2 [total [random component]	17,2 9,9	17,2 16,4	17,2 9,9	17,2 16,4

* the magnitude of the fertility trend was varied to give the same total environmental variation with both smaller and larger random components

TABLE 3

Results of simulation of selection, with or without screening for response to disease

Details	Programme	
	1 Without screening	2 With screening
Stage 1		
Number of clones planted	60 000	c 30 000
Mean values of [yield (SD) selected clones [disease response]	116 (14,4) 5,0	113 (14,8) 3,9
Stage 2		
Number of clones planted	6 000	6 000
Mean yield, selected clones (SD)	130 (11,9)	128 (12,8)
Stage 3		
Number of clones planted	600	600
Mean yield of 10 best clones with disease response: disregarded	159	156
≤5	153	154
≤3	145	153
Number of clones with:		
yield ≥150 disease ≤5	15	18
≥150 ≤3	5	8
≥150 ≤4	8	16
≥150 ≤5	48	60
≥140 ≤3	14	28
Incidence of clones with disease response ≤5 (≤3) in 120 clones (20% of number in Stage 3) selected on yield phenotype for inclusion in variety trials	61 (18)	85 (42)

The object of selection in sugarcane is, however, to produce a small number of outstanding varieties; average values of yield or response to disease in a population of clones are of little importance in themselves. The outcome of the selection programmes can be compared in a number of ways (Table 3). There was little difference between them at Stage 3 in respect of the yields of the ten highest yielding clones with at least an average degree of resistance to disease (153 vs 154). A requirement for a relatively high degree of resistance (≤ 3) resulted in a fairly small difference in yield of the best clones (145 vs 153). Thus it would appear that unless exceptionally high resistance to a disease is of overriding importance it is not worth expending resources to screen the many clones in the initial stage of a selection programme. At the same time, if the initial number of clones in the programme is decreased by 50%, the effect on the yield of the best clones is small (159 vs 156). The question of numbers of clones at the different stages of selection could therefore warrant examination by means of a simulation exercise.

At Stage 3, there was relatively little difference between programmes in the number of clones with an exceptionally high yield (not less than 150, which was 50% greater than the mean yield of the unselected progeny of a cross) and at least average resistance to disease (≤ 5). However, the number of clones with a comparatively high degree of resistance (≤ 3) as well as a high yield (≥ 150) was substantially greater when screening for disease response had taken place (5 vs 8). (Sampling error can be sizeable when numbers are so small, but the large difference in the number of clones with a resistance ≤ 4 (8 vs 16) between the two programmes, tends to confirm the difference in the number of clones with a resistance (≤ 3). Similarly, if the yield level is set lower at 140, the proportion of resistant clones amongst those with acceptable yield was much greater when the test for disease response had been conducted (14 vs 28).

Genotypic yield has so far been regarded as an invariable property of a clone, but considerable genotype-environment interaction can be expected in breeding work. Accordingly, the clones selected at Stage 3 (on yield phenotype) for testing in yield trials should perhaps be considered as a group, because their commercial value in respect of yield would only be evident once variety trials had been conducted. In such circumstances, the more clones with acceptable resistance to disease that are included in variety trials, the less the danger of an outstanding variety (in respect of yield) being rejected because of its susceptibility to disease. When the test for disease response was included in the selection programme there was a marked increase in the number of highly resistant and an appreciable increase in the number of at least moderately resistant clones amongst those selected for testing in variety trials (Table 3). So these results suggest that considerable resources should be devoted to screening for response to an important disease at the beginning of the selection programme.

Soil fertility trend (Table 4)

Whether there was a large or a small trend in soil fertility the selection strategy had little effect on the mean yield of clones selected at either Stages 1 or 2. Similarly, the mean yield of the highest yielding 50 clones selected at Stage 2 (50 clones would be an appropriate number for inclusion in variety trials) was hardly affected by the method of selection.

It appears that greater precision resulting from selecting within small groups of contiguously planted clones was offset by a small loss of yield caused by the enforced selection of one clone from every small group. Thus, the mean genotypic yields of two samples of 100 clones chosen from 1 000 thrown up by the random number generator, were determined. The first sample was chosen as the highest yielding ten clones from each of

ten samples of 100 clones; the second sample was chosen as the highest yielding clone from each of 100 samples of ten clones. Mean yields of the first and second samples were 129,2 and 126,0 respectively.

On the other hand, it appears that even where trends in soil fertility are small, there is little disadvantage in selecting clones on the basis of comparisons (perhaps only visual comparisons at the earliest stage of selection) with their ten or so immediate neighbours in the field.

The greater mean yield at Stage 2 of selected clones when the trend in soil fertility was large than when it was small, was statistically significant (means 135 and 131, SE = 0,5). The reason for the difference is not clear. It is possible that selection can be more precise when the environmental variation is due largely to a gradual change in conditions than when it results mainly from deviations which vary randomly.

TABLE 4
Results of simulation to compare selection strategies on soils with large or small trends in fertility

Details	Programme			
	3	4	5	6
Selection strategy	Without 'grouping'		With 'grouping'	
Soil trend	large	small	large	small
Stage 1				
Selected clones	5 000	5 000	5 000	5 000
[number]	119	116	120	115
[mean yield]	13,0	14,5	13,2	14,8
[SD]				
Stage 2				
Selected clones	500	500	500	500
[number]	135	132	136	130
[mean yield]	9,6	10,6	9,9	11,8
[SD]				
Mean yield of 50 highest yielding selected clones:				
observed	152	150	153	150
calculated from mean and SD of Stage 2 selections	147	146	149	145

Conclusion

In sugarcane, all the genotypes which survive the successive stages of a selection programme are there from the beginning; with vegetative propagation no new genotypes arise during the course of selection. It follows that the greater the genetic progress made during the early stages of selection, the less the progress that remains to be made during subsequent stages. This inference is supported by the generally inverse relationship between the mean and the SD (ie the variability) of yield within selected groups of clones in both the simulated selection programmes (Tables 3 and 4.) Paradoxically, therefore, it seems that different selection strategies could produce genetic advances of similar magnitude, even if they differ somewhat in efficiency.

REFERENCES

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