

COMPARING SUGARCANE BREEDING STRATEGIES BY MONTE CARLO SIMULATION

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The aim of most breeding programmes is to optimise the genetic gain, as measured by the performance of released varieties and the changes in the population mean for important traits, while at the same time maintaining genetic diversity within the population. The success of a breeding programme depends to a large degree on the breeding strategy that is used. Important factors in determining the outcome of a particular strategy are the number of parents used, the mating design employed, the number of progeny tested and the generation interval. The choice of these depends in turn on factors such as the number of traits that are selected for, and the genetic and phenotypic variances of these traits. The relative success of different strategies cannot be tested in field experiments, and so other methods are needed in order to make objective comparisons between different breeding options.

A Monte Carlo or stochastic simulation model is being developed as a tool for evaluating different breeding strategies. The simulation is based on the genetic model

$$P = A + D + I + E$$

where P represents the phenotypic value, A is the additive genetic value, D is the dominance value, I is the epistatic interactions and E is the environmental value. For simplicity, sugarcane is assumed to be an octoploid, and the dominance effect includes trigenic and tetragenic interactions, as well as digenic (dominance) interactions. A and D have both between- and within-family components, while I and E are assumed to be random, with no between-family component.

Population means and variances for each of these components are chosen by the user for six traits, viz sucrose content, cane yield and four disease reaction traits (scored on a 1 = resistant to 9 = susceptible scale). Sucrose yield is calculated as the product of sucrose content and cane yield. The variance components are summarised as narrow-sense heritability and the degree of genetic determination (DGD). The number of crosses or families to be used in the simulation, and the number of progeny per cross are also chosen. Selection

thresholds can be set for individual traits, so that no individual with a phenotypic value above or below the set threshold will be selected as a parent in the simulation. The field testing strategy is simulated very simply, by choosing the number of trials in which the 'varieties' are to be tested. Environmental deviations are then simulated for each trial, and the average deviation is used in the model.

The simulation consists of four basic steps as shown below, which then loop for the desired number of generations:

- Step 1.** Generate base population of family means for A and D for each cross.
- Step 2.** Generate individuals within each family, around individual cross means generated previously, with random effects I and E.
- Step 3.** Select individuals according to set criteria for use as parents of next generation.
- Step 4.** Cross parents according to set formulae to produce family means of next generation.
- Step 5.** Loop to Step 2, and continue for *x* generations.

The output is summarised in terms of the population means, variances and heritabilities for each trait in each generation, the best 'virtual variety' in each generation, and the mean of the best five varieties per generation. The best variety is defined as the one with the highest sucrose yield, and with disease ratings of 1–5 for all four disease traits.

To illustrate the model, a number of different breeding strategies have been simulated. The results will be presented, and the relative merit of each strategy evaluated. The simulation is based on statistical genetic models, and it is important that results are interpreted within the limits of the assumptions implicit in the models. These assumptions will be discussed, and the use of the simulation model in testing the assumptions will be examined.

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