PARAMETER-BASED STOCHASTIC SIMULATION OF SELECTION AND BREEDING FOR MULTIPLE TRAITS

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INTRODUCTION

To increase the adaptability and economic value of plantations, tree improvement professionals often manage multiple traits in their breeding programs. When these traits are unfavorably correlated, breeders must weigh the economic importance of each trait and select for a desirable aggregate phenotype. Stochastic simulation allows breeders to test the effects of different breeding and selection strategies without the costs associated with empirical tests. However, most available simulation programs have limited applicability because they only model the management of a single trait. To solve this problem, we are developing a parameter-based stochastic simulation program that can model a variety of multiple-trait tree improvement strategies.

METHODS

Five Excel™ and Simetar™-based* subprograms were written to simulate tree improvement for multiple traits in elite and mainline populations. Each subprogram incorporates a different mating design, but all have the same general organization. A variance/covariance structure is specified for a base population of undefined size, which serves as the initial source of genetic material for the tree improvement program. Then, either an elite breeding population is generated by selecting 30 trees at random from the base population, or a mainline population is generated by selecting 360 trees at random from the base population. All trees in the initial elite and mainline populations are assumed to be unrelated and non-inbred. Selections are crossed according to the designated mating designs to produce full- and half-sibling families for evaluation. Full-sibling families are ranked based on progeny mean index value, and the top individuals from the top families are selected for generation advancement. Where sublines are used, initial selections are first randomly assigned to different sublines; then all crosses and subsequent selections for generation advancement are made within sublines. In each generation, polymix tests are used to select individuals for the establishment of seed orchards. These tests are also used to rank selections for the positive assortative mating option based on breeding values. Selection, breeding, and testing are repeated for five generations, and summary statistics are output to a blank worksheet.

For the elite population simulations, four breeding strategies have been designed:

- 30 trees in one subline with trees randomly assigned to crosses and mated according to a circular mating design
- 30 trees in one subline with trees assigned to crosses using a positive assortative mating design where rankings are based on breeding value
- 30 trees in one subline with trees assigned to crosses using a positive assortative mating design where rankings are based on phenotypic value
- 30 trees divided into six sublines with trees randomly assigned to sublines and mated according to a five-tree modified half-diallel design

For the mainline simulations, only one breeding strategy has been designed thus far: 360 trees divided into 20 sublines (18 trees per subline) with trees randomly assigned to crosses within sublines and mated according to a circular mating design.

DISCUSSION

In each subprogram, the user specifies the method of selection and defines the initial base population in terms of the phenotypic mean and the variance and covariance components of up to three traits. Selection options include direct selection for one or more traits, indirect selection for one or more traits, restricted selection for one trait while another trait is held constant, and modified base index selection in which economic weights and heritabilities are used. Simulations are run for a user-specified number of iterations, and the means and variances of each model variable (across iterations) are output to a blank spreadsheet. Model variables in the overall, selection, and seed orchard populations include the phenotypic mean of each trait; the additive, dominance, environmental, and phenotypic variances of each trait; and the mean level of inbreeding in the population. In the overall population, the heritability of each trait and the genetic correlations between traits are also calculated, while in the seed orchard population, the percent gain and estimated progeny mean phenotypes are calculated.

At present, the user determines which mating design is employed by running the corresponding subprogram. We hope to combine the subprograms into one general program and allow users to specify their breeding and selection strategies at start up. Future versions will allow users to apply different selection indices for generation advancement and for seed orchard establishment and will include additional breeding schemes for the mainline population.

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