

Variation in Estimation of Genetic Parameters from Small Disconnected Diallel Mating

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Abstract

Diallel mating designs are widely used in plant improvement programs to estimate additive and dominance genetic variances, and to provide a base population for advanced selection. It is very common to limit the number of parents in a diallel small (4-8) in order to keep the number of crosses in a manageable size and complete the diallel breeding within a short time period. Many such diallels are created in a breeding program, and often are disconnected. Thus there are generally large sampling errors among diallels for genetic variance components. In this study, we examined variation in estimates of variance components and heritabilities of two loblolly pine breeding populations. Over 100 diallels (105) from the Coastal breeding population and 114 from Piedmont breeding populations were examined for the distribution of these parameters. Frequency distribution of GCA variance and narrow-sense heritability showed an approximate normal distribution, while SCA variance showed a considerable skewness and displayed a significant departure from normality. Genetic parameter estimates fluctuated considerably from one diallel to another as expected due to the effect of the small population size. Individual heritability ranged from 0.0 to 0.62 in the Coastal breeding population and from 0.0 to 0.52 in the Piedmont population. Some theoretical considerations regarding to the optimum sample size to estimate reliable genetic parameters from diallel tests were addressed.

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