UTILITY OF THE MULTIPLE-SEED PROCEDURE OF SINGLE-SEED DESCENT FOR BEAN IMPROVEMENT

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Single-seed descent permits plant breeders to maintain genetic variability while advancing generations. In Puerto Rico, as many as four generations of soybeans [Glycine max (L.) Merr.] can be grown within a period of 14 months, permitting the rapid development of advanced (Fg) lines. The multiple-seed procedure of single-seed descent (SSD) is used by soybean breeders to avoid high labor costs associated with the single-seed procedure. Pods containing 2 to 3 seed are harvested and bulked from soybean plants in segregating populations. Although this practice is known to reduce genetic variability, the magnitude of the reduction had not been quantified.

Macchiavelli and Beaver (2001) conducted a study to estimate the effect of number of seed bulked and population size on genetic variability when using the multiple-seed procedure of SSD. Simulations were conducted to estimate the number and proportion of Fj families which were represented in the Fg generation after bulking and randomly selecting seed. The effect of differences in number of seed per pod bulked and different population sizes on genetic variability was studied. Increasing the population size from 100 to 600 plants had little effect on the mean proportion of F2 plants represented in the Fg generation. Increased population size, however, did reduce the standard deviation and the range of the expected proportion of F2 plants that would be represented in the Fg generation. Number of seed bulked had a greater effect on the proportion of F2 plants represented in the Fg generation. At a population size of 600, the mean proportion of F2 plants declined from 0.39 to 0.35 when the number of seed per pod bulked increased from 3 to 6.

Using the multiple-seed procedure, bean breeders could expect, on the average, that at least every third line would be derived from a different F2 plant. Single-seed descent permits each F2 plant to be represented only once in the Fg generation. Unlike single-seed descent, the multiple-seed procedure would allow plant breeders to benefit from divergence in segregation patterns in lines derived from the same F2 plant. Therefore, the multiple-seed procedure of SSD would generate considerable genetic variability for the selection of quantitatively inherited traits.

Soybean breeders have been successful in using the multiple-seed procedure of SSD to improve traits with low heritability such as seed yield (Empig and Fehr, 1971). This approach would be most appropriate for dry edible bean populations derived from crosses between elite lines within a market class. Bean breeders may consider using a larger population size to compensate, in part, for the loss in genetic variability resulting from the use of the multiple-seed procedure of SSD.

The use of the multiple-seed procedure of SSD and winter nurseries would permit bean breeders to develop Fg lines within a two-year period. In recent years, plant breeders have placed greater emphasis on the development of bean germplasm and cultivars with specific combinations of genes. Greater use of marker-assisted selection would be expected to accelerate this trend. Recent releases of bean germplasm, such as, BelDakMi RMR 18, combine several specific genes (Ur-3, Ur-4, Ur-6, Ur-11, J, and bc3) for disease resistance (Pastor-Corrales et al. 2001). In order to maintain these very useful combinations of genes, bean breeders may be inclined to use conservative plant
breeding approaches such as backcrossing. This approach, however, may impede the improvement of quantitatively inherited traits such as seed yield and tolerance to abiotic stress. The multiple-seed procedure of SSD and winter nurseries can be used to rapidly produce inbred lines, which would increase likelihood that desired alleles would be fixed.

Single seed descent drastically reduces the minimum number of plants that need to be evaluated in order identify at least one plant with the desired genotype (Beaver and Macchiavelli. 1998). If a population were segregating for five specific genes, it would be necessary to evaluate 4,714 F2 plants to have a 99% probability of identifying at least one plant with the desired genotype. Using single-seed descent, it would be necessary to evaluate only 171 F6 plants to have a 99% probability to identify at least one plant with the desired genotype. Using the multiple-seed procedure, where every third plant would be derived from a different F2 plant, it may be necessary to evaluate as many as 500 plants to have the same level of confidence of identifying the desired genotype.

References