Analysis of Genetic Variability from Generations of Plant-Progeny Lines in Soybeans

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FREQUENTLY in plant breeding programs with self-pollinated plants, lines have been evaluated from a series of selfed generations. The variability structure considered would be a sequence of generations which have been evaluated as single plant-progenies from a randomly selected plant within each line. Generations and years are confounded. Horner and Weber (8) generalized the genetic variances and covariances for such data. However, even though one assumes a negligible genotype by environment interaction, the analysis is difficult to interpret since the estimate of a genetic variance may vary considerably between years. A partition of genetic variability depends upon the magnitude of the variance estimates, and one must conclude that a partition could reflect the expansion and contraction of the measurement scales rather than the true genetic partition. However, reliable estimates of genetic variability may be available from such data. An objective of this paper was to generalize the variance structure for such data and to evaluate and interpret the data from the F2 through F6 generations from a soybean cross, Adams X Hawkeye. The generalized variance structure would have utility for analyzing data from other self-pollinated crops and for predicting genetic progress.

Partitioning of genetic variability into additive and non-additive genetic variances contributes basic information necessary for the proper evaluation of selection procedures. Fisher (2) and Fisher et al. (3) derived several genotypic variances and covariances for early generations of a self-fertilized population. These were described and extended by Mather (11). Horner et al. (7) derived an expression for the set of variances and covariances for a self-fertilized population. The genetic parameters in these studies were defined with reference to the F2 population. Hanson and Weber (4) considered the resolution of genetic variability with reference to the population of homoyzous lines generated by a segregating population which will serve as the basis for partitioning in this paper. However, the genetic parameters defined by this method are directly commutable by a factor of 1/2 for the additive component and 1/4 for the additive by additive component to those defined previously. The additive and epistatic genetic variances defined relative to homoyzous line variability will be designated as \( \sigma^2_{A\|} \), \( \sigma^2_{A\|A\|} \), etc., to avoid confusion with existing nomenclature.

MATERIALS AND METHODS

Experimental material—Two soybean varieties, Adams and Hawkeye, were selected as parents for the study. Both have desirable agronomic and chemical traits and, as far as is known, are unrelated. The F2 plants were grown in 1949 and the F6 through F10 generations, one generation per year, from 1950 through 1954 at the

Agronomy Farm, Ames, Iowa. General growing conditions and growth response were considered satisfactory except that the F2 (1950) and F6 (1953) generations were slightly below normal in growth response because of moisture deficits during the growth season.

Two random plants were selected from each of 94 F2 lines to provide 2 F3 lines from each F2 line. One of the 2 F3 lines per F2 line was randomly selected and 2 random plants were then taken to provide 2 F4 lines for each F2 progeny. The sampling procedure was continued through the subsequent generations of selfing. About 70 seeds were planted per 8-foot yield plot in 40-inch rows. The F6 through F9 generations were grown each year in a simple lattice design and adjusted means were used if the lattice design gave a gain in precision over the randomized block.

Data were recorded for 8 characters as described below for each plant in the F2 (except as noted) and for each plot in succeeding generations:

- **Flowering time**—recorded every other day after May 31 when 50% of the plants in a plot had started to flower. Recorded at the first flower on each F2 plant.
- **Period from flowering to maturity**—recorded in days from flowering to maturity.
- **Maturity date**—recorded every 3 days after August 31 when 95% of the pods had turned brown.
- **Height**—measured at maturity in inches from ground level to the highest part of the main stem.
- **Lodging**—scored on a mature row; scale ranged from 1, nearly all plants erect, to 5, most plants prostrate.
- **Seed yield**—threshed, air-dried seed recorded in grams and converted to bushels per acre for F2 plant yields (grams).
- **Seed weight**—recorded in grams per 100 random whole seeds after air-drying to uniform moisture.
- **Oil percentage**—expressed in percent on a moisture-free basis.

Genetic expectations for generation sequences—All entries are identified with 1 of 94 lines of descent. Consider only those progeny rows which gave rise to lines in the subsequent generation. Entries are random genotypes in a sequential line of descent. Let \( g_{ij} \) be the genotypic value for the \( i \)th generation sequence averaged for \( (r + 1) \) generations \( (r) \) in a line of descent. The phenotype \( y_{ij} \) for an entry is

\[ y_{ij} = [g_{ij} + s_{ij}] + e_{ij} \]

where \( g_{ij} \) results from genetic segregation, the second pair of terms represent deviations due to genotype by environment interaction and the last term is a random error. These expectations are available (Hornet et al., 7). The expected component for the average of lines over generations, \( \sigma^2_L = E[g^2_{ij}] \), can be determined. The proportion of the genetic variability of an observation associated with dominance with the assumption of complete dominance is summarized in Table 1. Formulation of these expectations for an additive model with dominance is not important. The presentation includes the partition between the line and the genotype by environment components. Dominance variability associated with years was included in the total genetic variability. Whether one includes or excludes the F2 generation in the analyses, dominance variability is negligible and can be ignored.